(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
4 November 2004 (04.11.2004)

PCT

(10) International Publication Number
WO 2004/094467 A2

(51) International Patent Classification[7]: C07K 14/195, A61K 38/00, 39/106

(21) International Application Number: PCT/EP2004/004255

(22) International Filing Date: 22 April 2004 (22.04.2004)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
03450097.5 22 April 2003 (22.04.2003) EP

(71) Applicant *(for all designated States except US)*: **INTERCELL AG** [AT/AT]; Campus Vienna Biocenter 6, A-1030 Vienna (AT).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: **MEINKE, Andreas** [DE/AT]; Piettegasse 26/1, A-3013 Pressbaum (AT). **MIN BUI, Duc** [VN/AT]; Rudolf Zeller Gasse 70/6/9, A-1230 Vienna (AT). **NAGY, Eszter** [HU/AT]; Taborstrasse 9, A-1020 Vienna (AT). **HENICS, Tamas** [HU/AT]; Taborstrasse 9/4/15, A-1020 Vienna (AT).

(74) Agent: **SONN & PARTNER PATENTANWÄLTE**; Riemergasse 14, A-1010 Vienna (AT).

(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Declarations under Rule 4.17:
— *as to the applicant's entitlement to claim the priority of the earlier application (Rule 4.17(iii)) for all designations*
— *of inventorship (Rule 4.17(iv)) for US only*

Published:
— *without international search report and to be republished upon receipt of that report*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: H. PYLORI ANTIGENS

(57) Abstract: The present invention discloses isolated nucleic acid molecules encoding a hyperimmune serum reactive antigen or a fragment thereof as well as hyperimmune serum reactive antigens or fragments thereof from *H. pylori*, methods for isolating such antigens and specific uses thereof.

WO 2004/094467 A2

H. PYLORI ANTIGENS

The present invention relates to isolated nucleic acid molecules, which encode antigens for *Helicobacter pylori*, which are suitable for use in preparation of pharmaceutical medicaments for the prevention and treatment of bacterial infections caused by *Helicobacter pylori*.

Helicobacter pylori is a Gram-negative, microaerobic, spiral and flagellated bacterium representing the most prevalent human pathogen with nearly half the globe's population infected. Infection most likely occurs in early childhood (< age 10) in most cases and the pathogen specifically colonizes the stomach where it becomes a resident. Colonization lasts for years or even decades but it can persist for life, yet about 70-80 % of colonized individuals remain asymptomatic and never develop disease. It is now clear that the prolonged interaction of *H. pylori* with gastric epithelia is a complex and dynamic process, which leads to chronic acute inflammation of the gastric mucosa and to the development of peptic ulcer disease in 10-20 % of the cases. Nearly all duodenal ulcers are caused by *H. pylori* and, in the stomach ulcers can develop into gastric adenocarcinoma with a frequency of 0,1-4 %. The significance of this number is that gastric cancer is the second most common fatal malignancy after lung cancer and within twenty years, it is predicted to be the 8th leading cause of death of any origin worldwide. *H. pylori* infection is also associated with about 90 % of mucosa-associated lymphoid tissue lymphomas (MALT). Patients with *H. pylori* infection develop high titers of primarily IgG and IgA antibodies but their role in the immune response against the bacterium is not known. Presence of the bacteria within the mucosal epithelium is associated with massive neutrophil infiltration. Considerable evidence exists demonstrating that the *H. pylori* -induced Th1-biased $CD4^+$ T cell response with prominent IFN-γ production might be a strong contributing factor in the outcome of the local immune reaction linked to tissue damage.

H. pylori is inherently equipped with an array of extremely potent factors and mechanisms that enable the pathogen to uniquely adapt to the gastric mucosal environment leading to survival and long-term colonization in humans. However, the known virulence factors are only associated with increased risk of disease and are not absolute. Perhaps the most obvious system what *H. pylori* developed is its powerful urease enzyme, which by converting urea into ammonia and carbon dioxide allows survival under acidic conditions. Expression of the cytoplasmic apoenzyme is constitutive and its abundance can be as high as 15 % of total *H. pylori* protein. The activity of the enzyme is increased in low pH and the conductance of the inner membrane is also increased for urea under low pH conditions. The produced NH_3 diffuses to the periplasm protecting thereby the bacterium against the extremely acidic environment (Prinz, C. et al., 2003). The vacuolating cytotoxin product of the *vacA* gene of *H. pylori* induces vacuole formation and, thus, perturbation of structure and function in epithelial cells. The *vacA* gene is present in all strains but its expression varies. It is now known that VacA acts through a Z-type protein tyrosine phosphatase receptor by increasing its tyrosine phosphorylation activity on the G-protein coupled receptor kinase-interactor 1, leading to marked detachment of gastric epithelial cells from their base membrane, a possible mechanism behind *H. pylori* -induced epithelial cell demise and consequent peptic ulcer formation (Fujikawa, A. et al., 2003). A major virulence-associated genetic element in *H. pylori* is the 40 Kbp pathogenicity island, Cag (cytotoxin associated gene) PAI, contained in the majority of strains. The PAI harbors about 30 genes and one gene product, CagA was originally identified in serological studies as an important determinant of disease outcome in *H. pylori* infected individuals. The Cag PAI contains genes that have close sequence similarities to a type IV secretion system, known to provide a mechanism for direct transfer of bacterial effector proteins into eukaryotic host cells. Not surprising therefore that the CagA protein has been demonstrated as the effector protein that translocates from adherent *H. pylori* into epithelial cells *in vitro*. The subsequently phosphorylated CagA rearranges the host cytoskeleton, which then leads to pedestal formation adjacent to the bacteria (Bjorkholm, B. et al., 2003). Although, it is present in strains expressing VacA, the *cagA* gene is not linked chromosomally to *vacA*. Strains with the *cagA* PAI and the *vacA* genotype (type I strains) are associated with higher frequency with patients suffering from duodenal ulcer, atrophic gastritis and gastric carcinoma compared with those lacking CagA and VacA (type II strains) (Censini, S. et al., 1996). Human populations in distinct geographical regions can be differentiated based on genotypic variations located to the right end of the *cag* PAI (Kersulyte, D. et al., 2000).

Attachment of *H. pylori* to gastric epithelium is promoted by a number of factors. The Hpa hemagglutinin binds to sialic acid components of erythrocytes while the *babA2*-encoded BabA adhesion binds to the histo-blood group antigen Lewis^b, present on gastric epithelial cells. *babA2*-positive strains are more frequently isolated from patients with peptic ulcer disease and gastric carcinoma than type 1 strains and, when compared to type 1 strains lacking *babA2*, type 1 isolates that also harbor the *babA2* gene are more prevalent in patients with atrophic gastritis and intestinal metaplasia. The SabA adhesion protein is shown to associate with a glycoconjugate on the onco-fetal surface antigen sialyl-Le^x that is expressed on immature cells of the developing fetal gastric epithelium as well as on rapidly proliferating undifferentiated cells of cancerous and precancerous lesions {Dubreuil, J. et al., 2002}.

Another potent virulence-associated mechanism evolved in *H. pylori* is its natural competence for transformation together with the pathogen's highest rate of recombination of any known bacterial species. This mechanism makes *H. pylori* capable of acquiring new genetic material via horizontal gene transfer, a common phenomenon during colonization of an individual and this can result in the generation of novel pathogen subtypes (quasispecies) that exhibit profound changes in virulence markers, such as the *cag* PAI {Loughlin, M. et al., 2003}. Such extreme genetic variability, with any given isolate easily distinguishable from most others by DNA fingerprinting, has also been proposed to account for the expression diversity of many cell surface associated or secreted proteins {Ferrero, R. et al., 2001}. Although, it is not yet clear why only a relatively small portion of the infected population develop clinically manifest disease, the above mentioned pathogen-related factors together with emerging host-specific characteristics, such as IL-1β promoter allele polymorphism, are likely contribute to the complex mechanisms that lie behind *H. pylori* pathogenicity {Blaser, M., 2000}.

Today, patients diagnosed with *H. pylori* infection are treated with a combination of one or two antibiotics and a proton pump inhibitor or bismuth. There are a number of standard combinations but re-infection (most likely from parts of the stomach where eradication did not happen) can occur. Current combinational treatment regimes reach 80-90 % eradication rates in most cases but since *H. pylori* strains are emerging with resistance to one or more of the antibiotics that currently comprise any of the treatment combinations, development of new strategies is urgently needed for an effective treatment to prevent or ameliorate *H.pylori* infections. A vaccine could not only prevent infections by Helicobacter, but more specifically prevent or ameliorate colonization of host tissues, thereby reducing the incidence of gastric atrophy, peptic ulcer disease and gastric cancer. Elimination of severe chronic conditions would be a direct consequence of reducing the incidence of acute infection and carriage of the organism.

A vaccine can contain a whole variety of different antigens. Examples of antigens are whole-killed or attenuated organisms, subfractions of these organisms/tissues, proteins, or, in their most simple form, peptides. Antigens can also be recognized by the immune system in form of glycosylated proteins or peptides and may also be or contain polysaccharides or lipids. Short peptides can be used since for example cytotoxic T-cells (CTL) recognize antigens in form of short usually 8-11 amino acids long peptides in conjunction with major histocompatibility complex (MHC). B-cells can recognize linear epitopes as short as 4-5 amino acids, as well as three-dimensional structures (conformational epitopes). In order to obtain sustained, antigen-specific immune responses, adjuvants need to trigger immune cascades that involve all cells of the immune system necessary. Primarily, adjuvants are acting, but are not restricted in their mode of action, on so-called antigen presenting cells (APCs). These cells usually first encounter the antigen(s) followed by presentation of processed or unmodified antigen to immune effector cells. Intermediate cell types may also be involved. Only effector cells with the appropriate specificity are activated in a productive immune response. The adjuvant may also locally retain antigens and co-injected other factors. In addition the adjuvant may act as a chemoattractant for other immune cells or may act locally and/or systemically as a stimulating agent for the immune system.

Attempts to develop a Helicobacter vaccine have focused mainly on whole-cell and attenuated or subunit

vaccine approaches. The initial "proof of principle" studies to generate an *H. pylori* vaccine were performed using inactivated whole-cell preparations and cholera toxin as a mucosal adjuvant. Although, such vaccines were highly effective in inducing protective immunity against gastric infection in mice, their safety and licensing as well as difficulties in producing *H. pylori* preparations *in vitro* in large scale eliminated them from human trials {Ferrero, R. et al., 2001}; {Sutton, P., 2001}. For second generation subunit vaccines, candidate antigens were identified by empirical approaches. The selection criteria for these antigens were linked to known or suspected roles of the proteins in bacterial virulence. Such candidates include the urease holenzyme and its subunits, UreA and UreB, heat shock protein homologues of the chaperonins GroEL and GroES, the VacA cytotoxin and catalase (KatA) ({Prinz, C. et al., 2003}; {Svennerholm, A., 2003} and references therein). Another set of candidate proteins were identified in subsequent studies on the basis of their immunoreactivity in *in vitro* assays. *H. pylori* genomic expression libraries were screened with antibodies from mice that had been immunized with *H. pylori* whole cell sonicates or outer membrane vesicles in the presence of cholera toxin. Antigenic proteins were purified from selected *E. coli* clones and their identity determined by N-terminal sequencing. Among known antigens, such as UreA, UreB, the GroEL homologue and Lpp20 lipoprotein, four previously uncharacterized proteins were also identified. One had homology to L7/L12 ribosomal proteins and the rest were of unknown function. A similar screening strategy combined with a chimeric fusion technique confirmed the Lpp20 protein as a vaccine candidate antigen {Oliaro, J. et al., 2000}. There are other proteins under consideration for vaccine development that are based on recent identifications employing multiparameter selection criteria. These include an Hpa homologue (HP0410) and a novel protein of unknown function (HP0231), both with high protective efficacy {Sabarth, N. et al., 2002}. Despite the benefits of both prophylactic and therapeutic vaccination in animals as demonstrated in several studies, bacterial eradication (sterilizing immunity) has not been described in humans.

Since the above mentioned identification methods are either empirical or limited to a specific selection criterion, there is a demand to identify additional relevant antigens of *H. pylori* using an efficient and comprehensive identification and validation technology.

The present inventors have developed a method for identification, isolation and production of hyperimmune serum reactive antigens from a specific pathogen, especially from *Staphylococcus aureus* and *Staphylococcus epidermidis* (WO 02/059148). However, given the differences in biological property, pathogenic potency and genetic background, *Helicobacter pylori* is distinctive from Staphylococcus strains. Importantly, the selection of sera for the identification of antigens from *H. pylori* is different from that applied to the *S. aureus* screens.

Three major types of human sera were collected for this purpose. First, healthy adults below <45 years of age were tested for *H. pylori*-specific IgG and IgA serum antibody levels by ELISA using total bacterial lysate and culture supernatant proteins. High titer individuals were interviewed and seleted based on the absence of medical history, symptoms or complains related to *H. pylori* diseases. Based on correlative data, protective (colonization neutralizing) antibodies are likely to be present in exposed individuals who are not carriers of *H. pylori* or not susceptible to disease casued by *H. pylori*. High titer sera from symptom-free healthy adults were included in the genomic based antigen identification. This approach for selection of human sera is basically very different from that used for *S. aureus*, where carriage or noncarriage state cannot be associated with antibody levels.
Second, serum samples from patients with gastric cancer were characterized for anti-*H.* pylori antibody titers using ELISA and high titer sera were selected for the screens. The third group of serum samples was obtained from individuals with duodenal ulcer and high titer sera determined by ELISA were selected for the screens.

The genomes of the two bacterial species *H. pylori* and *S. aureus* by itself show a number of important differences. The genome of *H. pylori* contains approximately 1.65 Mb sequence information, while *S. aureus* harbours about 2.85 Mb. They have an average GC content of 39 and 33%, respectively. In

addition, the two bacterial species require different growth conditions and media for propagation. While *H. pylori* is a strictly human pathogen, *S. aureus* can also be found infecting a range of warm-blooded animals. A list of the most important diseases, which can be inflicted by the two pathogens, is presented below. *S. aureus* causes mainly nosocomial, opportunistic infections: impetigo, folliculitis, abscesses, boils, infected lacerations, endocarditis, meningitis, septic arthritis, pneumonia, osteomyelitis, scalded skin syndrome (SSS), toxic shock syndrome. *H. pylori* causes likely community aquired gastro-intestinal infections: self limiting traveler's diarrhea, corpus predominant or pangastritis, peptic ulcer disease (stomach and duodenum), gastric cancer (adenocarcinoma), chronic atrophic gastritis (CAG) and MALT (mucosa-associated lymphoid tissue, non-Hodgkin's type B cell lymphoma).

The problem underlying the present invention was to provide means for the development of medicaments such as vaccines against *H. pylori* infection. Particularly, the problem was to provide an efficient, relevant and comprehensive set of nucleic acid molecules or antigens from *H. pylori* that can be used for the manufacture of said medicaments.

Therefore, the present invention provides an isolated nucleic acid molecule encoding a hyperimmune serum reactive antigen or a fragment thereof comprising a nucleic acid sequence, which is selected from the group consisting of:

a) a nucleic acid molecule having at least 70% sequence identity to a nucleic acid molecule selected from **Seq ID No** 3-4, 16, 19-21, 28-29, 33-38, 41-42, 44, 48-52, 55, 57-58, 61, 63, 65, 67-68, 72, 74-75, 81, 84, 91, 94, 96-97, 101, 105-108, 112, 115-117, 119, 123-178.
b) a nucleic acid molecule which is complementary to the nucleic acid molecule of a),
c) a nucleic acid molecule comprising at least 15 sequential bases of the nucleic acid molecule of a) or b)
d) a nucleic acid molecule which anneals under stringent hybridisation conditions to the nucleic acid molecule of a), b), or c)
e) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid molecule defined in a), b), c) or d).

According to a preferred embodiment of the present invention the sequence identity is at least 80%, preferably at least 95%, especially 100%.

Furthermore, the present invention provides an isolated nucleic acid molecule encoding a hyperimmune serum reactive antigen or a fragment thereof comprising a nucleic acid sequence selected from the group consisting of

a) a nucleic acid molecule having at least 96% sequence identity to a nucleic acid molecule selected from **Seq ID No** 8-10, 13-15, 17-18, 24, 27, 32, 39-40, 45-47, 56, 59, 62, 69-70, 73, 77, 79, 82, 85-86, 88, 90, 103, 109-110, 114, 121,
b) a nucleic acid molecule which is complementary to the nucleic acid molecule of a),
c) a nucleic acid molecule comprising at least 15 sequential bases of the nucleic acid molecule of a) or b)
d) a nucleic acid molecule which anneals under stringent hybridisation conditions to the nucleic acid molecule of a), b) or c),
e) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid defined in a), b), c) or d).

According to another aspect, the present invention provides an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of

a) a nucleic acid molecule selected from **Seq ID No** 5, 7, 30-31, 53, 60, 66, 76, 83, 87, 92, 99, 120,
b) a nucleic acid molecule which is complementary to the nucleic acid of a),
c) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid defined in a), b), c) or d).

Preferably, the nucleic acid molecule is DNA or RNA.

According to a preferred embodiment of the present invention, the nucleic acid molecule is isolated from a genomic DNA, especially from a *H. pylori* genomic DNA.

According to the present invention a vector comprising a nucleic acid molecule according to any of the aspects of the present invention is provided.

In a preferred embodiment the vector is adapted for recombinant expression of the hyperimmune serum reactive antigens or fragments thereof encoded by the nucleic acid molecule according to the present invention.

The present invention also provides a host cell comprising the vector according to the present invention.

According to another aspect the present invention further provides a hyperimmune serum-reactive antigen comprising an amino acid sequence being encoded by a nucleic acid molecule according to the present invention.

In a preferred embodiment the amino acid sequence (polypeptide) is selected from the group consisting of **Seq ID No** 181-182, 194, 197-199, 206-207, 211-216, 219-220, 222, 226-230, 233, 235-236, 239, 241, 243, 245-246, 250, 252-253, 259, 262, 269, 272, 274-275, 279, 283-286, 290, 293-295, 297, 301-356.

In another preferred embodiment the amino acid sequence (polypeptide) is selected from the group consisting of **Seq ID No** 186-188, 191-193, 195-196, 202, 205, 210, 217-218, 223-225, 234, 237, 240, 247-248, 251, 255, 257, 260, 263-264, 266, 268, 281, 287-288, 292, 299.

In a further preferred embodiment the amino acid sequence (polypeptide) is selected from the group consisting of **Seq ID No** 183, 185, 208-209, 231, 238, 244, 254, 261, 265, 270, 277, 298.

According to a further aspect the present invention provides fragments of hyperimmune serum-reactive antigens selected from the group consisting of peptides comprising amino acid sequences of column "predicted immunogenic aa" and "location of identified immunogenic region" of Table 1, the serum reactive epitope of Table 3 especially peptides comprising amino acids 63-91, 95-101, 110-116, 134-148, 150-156, 158-164, 188-193, 197-209, 226-241, 247-254, 291-297, 312-319, 338-346, 351-358, 366-378, 404-410, 420-438, 448-454, 465-473, 482-488, 490-498, 503-510, 512-519, 531-543, 547-554, 568-575, 589-604, 610-631 and 239-308 of **Seq ID No** 179; 16-29, 35-47, 50-68, 70-79, 91-101, 143-149, 158-163, 185-191, 196-206, 215-224, 230-237, 244-251, 258-278, 290-311, 319-325, 338-351, 365-385, 396-429, 445-454, 458-466, 491-499, 501-521, 17-79 and 218-233 of **Seq ID No** 180; 4-10, 16-41, 46-66, 77-84, 91-97, 102-118, 125-144, 187-200, 202-214, 245-253, 255-261, 286-295, 300-330, 335-342, 350-361, 363-381, 385-392, 396-416, 435-450 and 460-470 of **Seq ID No** 181; 11-19, 27-48, 52-59, 77-82, 84-107, 118-125, 127-154, 178-183, 192-209, 215-221, 286-295, 302-313, 350-357, 402-415, 417-431, 453-463, 465-493 and 313-331 of **Seq ID No** 182; 19-26, 30-43, 47-55, 63-68, 72-80, 97-104, 107-119, 129-146, 160-175, 194-216, 231-251, 254-260 and 26-43 of **Seq ID No** 183; 7-13, 29-37, 65-81, 110-120, 123-131, 135-152, 230-249, 254-260, 284-290, 292-299, 317-326, 329-336, 403-444, 452-458, 466-477, 490-498, 510-519, 541-550, 557-566 and 533-567 of **Seq ID No** 184; 5-47, 71-77, 79-86, 89-95, 120-126, 137-144, 176-181, 184-196, 202-208, 211-232, 236-282, 301-313, 317-325, 341-347, 353-384, 394-400, 412-433, 436-443 and 59-75 of **Seq ID No** 185; 4-18, 22-38, 59-69, 106-112, 116-130, 138-149, 156-170, 175-197, 200-214, 216-223, 233-244, 255-261, 266-276, 279-286, 325-333, 342-348, 366-399, 402-420, 429-441, 1-104 and 130-147 of **Seq ID No** 186; 50-58, 69-95, 97-113, 131-136, 157-163, 170-175, 188-212, 220-226, 254-259, 265-277, 283-289, 297-308, 311-318, 347-358, 360-369, 378-401, 416-421, 440-450, 454-462, 470-476, 493-502, 506-514, 536-567, 585-590, 598-607, 613-618, 653-659 and 35-46 of **Seq ID No** 187; 16-29, 32-60, 65-87, 89-123, 128-134, 137-158, 162-173, 178-196, 210-216, 218-228 and 206-225 of **Seq ID No** 188; 10-20, 26-35, 51-64, 86-

91, 94-100, 113-122, 154-160, 185-191, 193-201, 211-217, 225-230, 237-246, 251-257, 298-304, 306-312, 316-328, 340-348, 357-389, 391-397, 415-421, 449-456, 458-471, 488-495, 502-511, 24-55 and 236-341 of Seq ID No 189; 5-22, 41-51, 87-93, 114-122, 127-136, 150-156, 158-166, 223-233, 245-263, 291-296, 9-126 and 127-285 of Seq ID No 190; 30-43, 46-56, 61-70, 72-83, 85-93, 103-113, 119-125, 151-166, 179-191, 212-218, 225-231, 236-243, 262-267, 291-307, 331-344, 349-355, 366-372, 380-386, 414-422, 428-447, 459-464, 469-478, 507-519, 525-544, 563-569, 576-590, 620-626, 633-643, 654-659, 665-671, 684-707, 717-723, 725-733, 747-779, 782-801 and 347-361 of Seq ID No 191; 4-12, 14-26, 37-80, 107-115, 133-139, 144-150, 154-165, 173-180, 191-199, 205-211, 221-231, 237-244, 254-284, 307-340, 342-353, 360-368, 370-380, 479-493, 495-503, 509-522, 525-536, 539-547, 554-560, 565-573, 578-583, 7-23 and 465-479 of Seq ID No 192; 4-17, 47-55, 76-83, 85-100, 104-112, 117-123, 126-135, 142-148, 156-167, 174-182, 267-273 and 258-283 of Seq ID No 193; 8-32, 36-42, 65-88, 102-108, 112-140, 147-163, 170-179, 183-193 and 117-124 of Seq ID No 194; 12-18, 45-50, 62-77, 82-95, 99-113, 115-123, 125-147, 155-177, 187-209, 211-223, 244-253, 259-270, 278-297, 302-307, 311-318, 329-334, 350-356, 359-365, 390-400, 402-413 and 333-350 of Seq ID No 195; 4-13, 15-27, 30-46, 53-58, 68-74, 82-95, 115-126, 134-139, 148-153, 159-176, 182-199, 201-217, 220-225, 227-235, 237-248, 253-266, 300-315, 322-336, 390-396, 412-426, 438-445, 448-459, 477-484, 502-508, 515-527, 529-537, 553-568, 643-651, 658-667, 690-703 and 376-400 of Seq ID No 196; 4-10, 24-32, 38-55, 59-67, 70-77, 80-87, 89-97, 123-129, 134-151, 166-172, 178-189, 191-216, 218-235, 245-259, 271-315, 326-339, 341-360 and 73-94 of Seq ID No 197; 13-25, 31-38, 43-57, 79-85, 92-99, 106-112, 117-128, 130-139, 146-158, 160-175, 194-204, 211-222, 225-232, 234-242, 263-270, 278-292, 299-320, 322-333 and 240-256 of Seq ID No 198; 4-17, 55-63, 66-101, 109-131, 135-143, 145-151, 155-161, 164-170, 177-185, 192-198, 213-218, 223-238, 246-256, 258-268, 273-283, 309-314, 322-328 and 195-221 of Seq ID No 199; 13-24, 31-39, 41-50, 63-69, 90-96, 104-109, 116-141, 148-153, 161-167, 173-178, 190-209, 253-258, 265-272, 279-289, 295-312, 317-343, 355-366, 376-389, 400-407, 430-451, 453-464, 466-472, 487-493, 499-505, 523-538, 554-559, 568-579, 584-601 and 344-363 of Seq ID No 200; 5-22, 30-36, 53-59, 61-70, 82-92, 99-106, 120-131, 135-148, 154-167, 169-183, 187-199, 204-212, 231-247 and 111-249 of Seq ID No 201; 17-36, 40-66, 71-144, 148-171, 173-191, 199-214, 220-252, 265-272, 278-288, 298-333, 342-385 and 287-307 of Seq ID No 202; 4-16, 22-28, 30-36, 42-48, 95-116, 154-162, 164-174, 239-252, 258-263, 273-285, 306-313, 323-333, 341-357, 363-369, 372-379, 395-401, 430-436, 438-453, 464-480, 33-44, 233-258 and 349-369 of Seq ID No 203; 4-21, 30-37, 46-53, 59-68, 80-92, 98-104, 118-143, 150-160, 165-185, 187-200, 204-211, 224-236, 241-246, 252-258, 271-280, 288-294, 311-320, 335-341 and 191-350 of Seq ID No 204; 4-16, 37-59, 64-70, 79-87, 93-102, 107-127, 143-165, 172-188, 197-204, 207-218, 221-227, 242-248, 258-277, 289-296, 298-316, 332-338, 344-365, 367-373, 375-382, 400-408, 415-425, 438-446 and 235-250 of Seq ID No 205; 4-37, 39-66, 84-98, 101-127, 140-149, 157-163, 166-172, 175-182, 184-193, 203-208, 215-232, 234-247, 250-299, 303-345 and 183-204 of Seq ID No 206; 10-20, 41-61, 73-87, 112-141, 176-192, 194-201, 205-222, 230-237, 257-264, 276-282, 284-310, 312-318, 330-337, 349-357 and 304-328 of Seq ID No 207; 4-31, 42-103, 105-113, 121-153, 160-181, 188-196, 210-226, 231-264, 272-287, 297-304, 328-336 and 304-318 of Seq ID No 208; 21-43, 46-52, 54-70, 72-79, 94-107, 133-141, 160-166, 217-253, 311-317, 359-365, 374-381, 390-395, 434-440, 488-494, 497-502, 511-522, 554-563, 565-574, 577-585, 591-598, 601-606, 617-625, 633-643, 658-664, 676-682, 694-702, 710-719, 754-760, 782-788, 802-808, 916-921, 942-948, 955-964, 973-979, 992-998, 1006-1011, 1016-1023, 1030-1038, 1046-1053, 1059-1066, 1088-1098, 1119-1126, 1129-1135, 1156-1171, 1173-1181, 1202-1210, 1255-1261, 1268-1280, 1295-1310, 1312-1320, 1375-1381, 1406-1417, 1450-1471, 1478-1492, 1498-1506, 1569-1578, 1603-1608, 1611-1624, 1648-1655, 1663-1670, 1680-1698, 1702-1707, 1713-1719, 1737-1742, 1747-1753, 1762-1769, 1771-1785, 1790-1804, 1811-1818, 1830-1836, 1838-1852, 1874-1886, 1893-1899, 1902-1909, 1942-1948, 1952-1962, 1980-1986, 2001-2017, 2020-2028, 2042-2050, 2052-2068, 2074-2079, 2083-2095, 2107-2113, 2147-2155, 2177-2194, 2203-2211, 2236-2241, 2251-2258, 2267-2274, 2285-2292, 2314-2328, 2330-2340, 2358-2365, 2390-2401, 2408-2418, 2432-2453, 2463-2476, 2486-2507, 2528-2537, 2540-2548, 2552-2558, 2568-2576, 2596-2601, 2610-2622, 2629-2638, 2653-2669, 2718-2727, 2749-2767, 2777-2784, 2789-2795, 2806-2815, 2817-2824, 2835-2843, 2847-2854, 2860-2881, 511-523, 612-630 and 1790-1803 of Seq ID No 209; 4-54, 61-68, 72-82, 86-93, 100-108, 115-130, 147-154, 187-194, 196-207, 224-229, 236-251, 275-287 and 96-109 of Seq ID No 210; 31-39, 62-69, 91-101, 158-172, 175-180, 186-193, 201-208, 210-223, 243-250, 273-286, 293-299, 319-325, 343-354, 356-365, 368-384, 414-435, 471-491, 512-518, 550-556, 567-581, 584-589, 633-639, 680-692, 697-708, 716-721, 747-754, 779-786, 810-816 and 366-503 of Seq ID No 211; 5-20, 22-48, 57-65, 96-101, 111-122, 130-145, 154-164, 170-181, 193-199, 201-216, 224-241, 244-262, 281-323, 342-351, 359-367, 369-396, 406-416, 424-433, 450-456, 485-491, 493-499, 501-515, 517-535 and 289-305 of

Seq ID No 212; 4-17, 22-44, 53-60, 66-83, 87-94, 101-106, 110-116, 131-137, 148-183, 189-207, 209-215, 233-242, 251-262, 264-272, 290-296, 308-327, 359-373, 375-380, 397-405, 415-420, 426-433, 444-475, 478-484, 529-536, 548-558 and 106-126 of Seq ID No 213; 4-38, 42-50, 58-64, 72-81, 92-118, 140-146, 157-165, 172-192, 198-204, 208-216, 227-234, 238-258, 271-278, 288-293, 311-322, 327-346, 357-370, 375-383, 395-409, 411-417, 425-432, 436-445, 109-129 and 370-380 of Seq ID No 214; 23-30, 36-49, 52-64, 86-94, 97-104, 121-129, 257-272, 279-286, 288-294, 307-327, 334-340, 369-375, 377-386, 406-412, 418-423, 430-438, 441-447, 459-465, 469-476, 482-488, 510-546, 550-580, 584-622, 638-645, 653-659, 675-683, 692-705, 723-731, 752-761, 788-795 and 54-72 of Seq ID No 215; 11-33, 36-46, 88-104, 116-126, 134-170, 189-195, 199-217, 225-250, 255-261, 266-273, 280-291, 296-313, 334-341, 343-349, 354-360, 362-369, 373-380, 387-401, 406-420 and 259-273 of Seq ID No 216; 9-14, 28-44, 57-64, 72-79, 86-93, 104-111, 116-126, 142-150, 159-164 and 61-86 of Seq ID No 217; 10-17, 26-33, 43-61, 69-95, 101-107, 109-125, 129-135, 137-144, 147-153, 158-169, 177-187, 209-219, 221-232, 235-247, 261-268, 271-282, 296-302, 306-347, 355-362, 364-379, 386-399, 409-418, 424-442, 451-460, 467-479, 490-498 and 60-74 of Seq ID No 218; 8-14, 20-31, 65-84, 94-99, 154-179, 193-207, 238-253 and 96-118 of Seq ID No 219; 4-24, 30-44, 47-62, 84-93, 108-116, 124-133, 136-141, 201-209, 217-223, 228-235, 238-245, 247-270, 275-285, 290-314, 328-338, 342-349, 353-365, 375-383, 386-392, 394-402, 417-427, 443-459, 465-481, 492-514, 516-524, 550-566, 602-617, 630-639, 666-676, 687-693, 719-730, 747-753, 783-790, 799-816, 824-831, 837-842 and 167-189 of Seq ID No 220; 6-15, 18-28, 58-66, 84-101, 106-129, 136-151, 154-165, 182-203, 205-211, 214-220, 222-228, 233-240, 251-260, 270-277, 284-291, 306-315, 322-328, 363-369, 378-388, 392-405, 443-452, 495-501, 512-523, 574-583 and 362-375 of Seq ID No 221; 5-25, 27-34, 47-59, 64-70, 76-86, 145-158, 166-183, 189-202, 217-231, 235-242, 260-270, 278-309 and 1-102 of Seq ID No 222; 4-19, 24-76, 78-83, 90-99, 102-109, 114-122, 137-147, 154-174, 177-188, 203-212, 217-223, 227-239 and 226-325 of Seq ID No 223; 7-37, 71-90, 94-109, 117-128, 141-153, 179-192, 199-206, 225-231, 237-243, 258-264 and 40-51 of Seq ID No224; 13-19, 25-30, 46-59, 75-91, 101-107, 114-124, 129-135, 137-145, 160-167, 171-179, 187-194, 209-215, 217-222, 229-239, 243-249, 257-265, 269-275, 299-308, 310-327 and 282-300 of Seq ID No 225; 86-100, 216-230, 342-369, 382-388, 424-430, 438-445, 452-458, 488-494, 501-518, 554-560, 568-574, 584-592, 603-609, 611-629, 639-645, 652-661, 669-699, 708-714, 726-738, 747-753, 763-775, 785-791, 794-807, 815-824, 826-845, 854-860, 863-868, 870-883, 892-898, 901-906, 909-921, 930-937, 946-959, 968-974, 977-990, 998-1007, 1009-1027, 1037-1043, 1046-1051, 1053-1066, 1075-1081, 1084-1089, 1092-1103, 1113-1119, 1122-1135, 1143-1152, 1154-1172, 1182-1188, 1191-1196, 1200-1210, 1220-1226, 1229-1235, 1237-1249, 1259-1265, 1268-1281, 1289-1298, 1305-1318, 1328-1334, 1337-1343, 1345-1357, 1367-1373, 1390-1396, 1405-1411, 1418-1423, 1426-1435, 1445-1455, 1474-1483, 1493-1500, 1505-1512, 1517-1524, 1538-1544, 1568-1578, 1595-1601, 1674-1682, 1687-1720, 1728-1736, 1738-1744, 1754-1761, 1764-1774, 1798-1824, 1836-1842, 1886-1893, 1895-1903, 366-781, 782-1518 and 1731-1747 of Seq ID No 226; 4-17, 20-39, 46-55, 60-66, 102-110, 114-122, 125-131, 161-167, 172-178, 185-190, 195-202, 218-232, 236-252, 264-291, 293-302, 309-315, 324-339 and 169-381 of Seq ID No 227; 5-10, 13-40, 42-53, 69-75, 83-89, 120-135, 150-161, 174-190, 203-225, 229-247, 257-287, 318-348 and 30-200 of Seq ID No 228; 7-19, 43-53, 64-72, 124-139, 52-84 and 120-131 of Seq ID No 229; 12-19, 39-48, 58-100, 117-123, 154-162, 164-187, 189-195, 202-216, 218-235, 241-246, 262-278, 315-328, 333-347, 354-366, 372-379, 391-405, 422-429, 431-442, 444-450, 458-466, 478-485, 494-501, 504-510, 520-535, 573-580, 589-598, 615-625, 666-676, 686-698, 722-729, 737-746, 756-767, 787-796, 805-816, 824-829, 833-848, 856-864, 866-876, 879-886, 898-904, 918-924, 927-934, 941-960, 967-978 and 561-575 of Seq ID No 230; 11-29, 49-55, 70-77, 84-100, 102-112, 148-155, 160-177, 181-204 and 1-104 of Seq ID No 231; 27-44, 64-71, 122-133, 151-156, 164-178, 214-220, 226-232, 235-244, 253-262, 282-288, 294-310, 317-325, 350-356, 362-368, 376-383, 438-443, 449-454, 459-464, 492-498, 500-511, 529-535, 538-546, 567-573, 597-603, 660-665, 674-679, 724-734, 763-769, 773-784, 791-801, 807-815, 821-826, 840-848, 863-868, 897-902, 908-928, 932-953, 956-975, 980-987, 990-996, 1012-1018, 1042-1063, 1095-1116, 1149-1157, 1160-1167, 110-357, 358-501 and 502-1161 of Seq ID No 232; 4-21, 64-71, 73-84, 128-138, 144-162, 203-217, 240-263, 288-298, 300-308, 310-317, 325-351, 369-380, 391-411 and 330-345 of Seq ID No 233; 5-11, 25-31, 39-48, 51-79, 89-98, 100-122, 135-148, 166-201, 203-227, 230-250, 254-260, 266-272, 274-282, 299-305, 328-337 and 31-45 of Seq ID No 234; 12-23, 29-48, 51-60, 66-72, 75-81, 83-93, 103-115, 133-148, 168-174, 195-204, 222-229, 231-240, 242-251, 270-280, 286-305, 322-344, 349-360, 364-370, 378-400, 421-441, 448-484, 486-493, 495-501, 504-534, 547-561, 567-590, 597-607, 621-635, 643-649, 658-685, 688-694, 702-711, 717-731, 737-742, 759-765, 767-772, 776-786, 803-809, 815-825, 854-908, 910-919, 923-930, 942-948, 961-975, 994-1014 and 915-940 of Seq ID No 235; 4-9, 32-47, 51-61, 75-96, 139-191 and 1-124 of Seq ID No 236; 4-13, 17-38, 43-49, 55-76, 88-

95, 110-121, 128-146, 151-157, 162-214, 222-240, 243-249, 251-273, 275-281, 292-298, 300-309, 312-320, 322-331, 355-369, 376-408, 446-460, 471-482, 485-509 and 191-203 of Seq ID No 237; 4-21, 72-82, 89-103, 106-115, 118-124, 140-146, 174-184, 191-200, 204-213, 218-224, 261-266, 282-293, 299-309, 311-340, 342-358, 362-372, 381-389, 391-402, 413-421, 438-447, 457-464, 470-478, 501-507, 545-560, 578-624, 631-641, 658-670, 680-689, 717-738, 753-759, 795-805, 816-822, 830-838, 842-848, 869-881, 892-898, 33-51 and 818-835 of Seq ID No 238; 4-21, 79-85, 156-177, 183-188, 206-214, 243-249, 261-269, 287-292, 315-322, 334-345, 360-366, 374-390, 402-411, 37-97 and 260-399 of Seq ID No 239; 4-9, 19-54, 58-78, 97-104, 111-120, 126-134, 137-145, 163-173, 178-188, 193-203, 211-224, 246-286, 288-324, 337-346, 355-362, 374-390, 392-398, 409-417 and 240-249 of Seq ID No 240; 5-12, 14-31, 35-41, 43-61, 82-92, 97-105, 134-145, 155-166, 184-203, 215-223, 225-251, 272-279, 281-306, 310-345, 358-418, 435-473, 482-490, 525-532, 538-547, 549-563, 578-604, 613-639 and 144-154 of Seq ID No 241; 53-59, 64-72, 74-100, 133-152, 154-172, 176-181, 207-214, 225-238, 275-297, 304-310, 331-340, 362-367, 384-395, 403-410, 437-443, 448-456, 482-490, 579-597, 602-610, 625-630, 633-651, 699-707, 709-715, 734-743, 750-762 and 544-685 of Seq ID No 242; 12-18, 22-40, 45-83, 89-97, 103-109, 147-153, 159-173, 195-204, 210-219, 243-253, 259-265, 273-282, 303-309, 315-325, 332-340, 346-358, 362-367, 377-390, 393-402, 418-426, 447-455, 467-480, 505-512, 514-525, 548-561, 566-576, 584-596, 619-626, 638-645, 649-659, 661-680, 699-708, 714-720, 753-759, 766-772, 775-781, 801-808, 202-218, 282-299, 339-350 and 617-628 of Seq ID No 243; 5-33, 52-62, 87-101, 111-135, 137-143, 145-152, 190-202, 209-221, 233-245, 253-270 and 151-215 of Seq ID No 244; 19-29, 32-39, 42-48, 75-94, 124-135, 137-145, 152-160, 176-182, 193-203, 215-236, 266-273, 275-291, 297-306, 311-319, 322-342, 348-360, 369-378, 394-401 and 48-64 of Seq ID No 245; 4-11, 13-33, 36-43, 53-63, 65-80, 112-129, 134-141, 143-155, 157-168, 178-188, 191-199, 201-207, 215-229, 242-255, 263-270, 283-315, 320-329, 333-338, 340-349, 412-426, 465-478, 485-490, 498-512, 540-554 and 390-516 of Seq ID No 246; 4-18, 23-32, 41-47, 54-70, 88-99, 104-111, 118-138, 143-148, 150-162, 168-175, 181-188, 203-211, 214-220, 227-245, 251-268, 275-281, 287-296, 323-333 and 1-90 of Seq ID No 247; 8-34, 38-49, 72-83, 85-91, 94-104, 112-125, 134-142, 148-168, 181-189, 191-198, 202-214, 222-233, 242-254, 256-262, 273-278, 287-294, 314-325 and 141-159 of Seq ID No 248; 4-24, 30-36, 47-75, 82-105, 124-134, 151-157, 192-202, 208-214, 219-226, 234-247, 285-290, 318-324, 332-340, 343-349, 380-386, 453-462, 472-478, 484-501, 531-540, 550-557, 604-612, 620-625, 642-648, 652-671, 64-84, 93-180 and 181-446 of Seq ID No 249; 12-18, 24-32, 68-75, 77-83, 96-101, 109-116, 129-136, 152-164, 175-184, 190-199, 206-215, 224-233, 241-250, 258-264, 273-292, 302-312, 319-331, 334-346, 348-368, 387-395, 408-416, 420-429, 437-452 and 364-374 of Seq ID No 250; 11-28, 36-52, 60-67, 74-79, 108-116 and 61-76 of Seq ID No 251; 20-27, 38-49, 69-74, 84-107, 138-145, 161-168, 179-195, 210-226, 228-252, 267-281, 283-296, 305-311, 333-340, 342-356, 361-372, 380-399, 401-414, 458-466, 475-481, 492-507, 515-520 and 146-160 of Seq ID No 252; 43-61, 68-74, 76-90, 120-128, 130-149, 156-161, 164-182, 206-234, 242-252, 269-274, 291-304, 332-345, 349-355, 360-371, 374-388, 434-440, 447-453, 459-465, 469-496, 504-522 and 261-285 of Seq ID No 253; 4-17, 24-30, 37-49, 87-98, 118-124, 126-136, 144-171, 176-188, 206-214, 216-228, 233-240, 246-252, 262-271, 277-297, 307-330, 333-342, 346-352, 355-361, 368-386, 391-400, 413-420, 474-480 and 401-427 of Seq ID No 254; 15-26, 31-46, 51-72, 80-93, 96-109, 131-137, 150-158, 179-185, 189-209, 211-219, 221-234, 241-247, 255-262, 265-271, 283-288 and 173-190 of Seq ID No 255; 28-37, 39-45, 51-58, 77-84, 89-97, 132-148, 171-180, 199-205, 212-218, 220-226, 257-265, 273-300, 307-327, 334-340, 344-365, 385-390, 402-408, 426-436, 450-468, 476-485 and 425-497 of Seq ID No 256; 4-25, 70-76, 80-88, 90-100, 120-128, 162-169, 183-203, 261-277, 279-289, 291-297, 302-308, 321-327, 339-353, 358-377, 392-401, 404-410, 414-422, 443-450, 456-461, 470-488, 490-497, 510-535, 570-611, 618-630, 639-647, 649-660, 668-690, 702-716, 718-724, 737-747, 750-764 and 497-509 of Seq ID No 257; 12-48, 50-64, 99-108, 216-223, 235-241, 244-254, 262-274, 287-293, 310-316, 320-326, 361-366, 377-383, 390-395, 408-414, 418-425, 438-444, 462-469, 494-505, 524-530, 536-547, 551-566, 592-598, 601-613, 678-685, 687-695, 709-717, 727-737, 751-757, 760-765, 772-778, 782-788, 801-807, 822-830, 859-868, 870-878, 884-890, 898-903, 909-919, 953-969, 973-980, 990-1000, 1002-1019, 1041-1047, 1059-1065, 1090-1095, 1116-1127, 1130-1139, 1143-1149, 1151-1168, 1178-1183, 1188-1195, 1197-1209, 1213-1220, 1226-1234, 1236-1247, 1255-1274, 1276-1282, 76-100, 270-284, 309-438, 493-505, 786-942 and 947-967 of Seq ID No 258; 4-9, 24-34, 46-95, 97-109, 119-130 and 138-156 of Seq ID No 259; 9-26, 28-35, 43-53, 55-68, 83-92, 99-105, 110-135, 139-149, 157-162, 164-170, 173-183, 193-208, 210-230, 239-245, 253-259, 263-271, 293-305, 310-320, 322-331, 336-343, 351-364, 367-376, 92-107 and 154-173 of Seq ID No 260; 19-39, 52-62, 108-117, 145-152, 160-168, 194-203, 229-240, 252-268, 280-287, 308-316, 333-339, 383-390, 403-412, 414-424, 438-445, 464-472, 479-484, 489-505, 510-526 and 247-260 of Seq ID No 261; 5-17, 25-52, 60-77, 105-113, 118-125, 162-167, 228-234, 272-279,

328-334, 341-357, 381-395, 400-406, 512-518, 557-569, 586-592, 645-651, 690-695, 701-709, 720-726, 733-743, 751-758, 781-786, 879-886, 929-934, 939-944, 952-960, 965-975, 994-1001, 1039-1045, 1102-1109, 1164-1181, 1198-1206, 1223-1229, 1253-1259, 1283-1292, 1312-1317, 1339-1349, 1360-1370, 1389-1398, 1400-1412, 1452-1465, 1470-1484, 1490-1497, 1519-1525, 1554-1564, 1578-1591, 1623-1636, 1638-1646, 1669-1679, 1685-1697, 1704-1711, 1713-1720, 1730-1736, 1738-1749, 1756-1764, 1778-1786, 1796-1803, 1817-1826, 1849-1866, 1975-1993, 2017-2032, 2044-2053, 2070-2086, 2091-2109, 2116-2127, 2156-2167, 2182-2188, 2197-2202, 2244-2252, 2281-2287, 2290-2307, 2350-2361, 2383-2404, 2425-2433, 2445-2455, 2495-2505 and 394-549 of Seq ID No 262; 9-24, 31-53, 57-67, 69-79, 84-114, 133-141, 144-172, 178-186 and 13-46 of Seq ID No 263; 4-25, 27-35, 43-52, 59-70, 79-91, 115-130, 136-152, 154-163, 170-179 and 1-58 of Seq ID No 264; 4-30, 49-55, 71-80, 96-105, 111-126, 139-146, 149-162, 239-245, 279-285, 290-296, 300-307, 331-337, 343-350 and 250-351 of Seq ID No 265; 9-27, 34-41, 43-51, 92-111, 114-120, 123-131, 139-150, 156-171, 176-186, 188-204, 229-241, 252-258, 266-279, 288-297, 319-334, 338-348, 373-379, 389-398, 431-439, 479-484 and 214-398 of Seq ID No 266; 4-15, 18-27, 47-52, 68-83, 91-97, 104-110, 115-121, 139-147, 157-164, 198-206, 227-236, 241-254, 264-273, 278-289, 311-320, 353-361, 372-383, 405-420, 426-434 and 232-386 of Seq ID No 267; 4-10, 24-34, 91-97, 129-141, 156-163, 184-190, 205-219, 229-235, 256-273, 278-285 and 93-116 of Seq ID No 268; 7-29, 35-54, 71-83, 85-91, 104-111, 122-134, 138-144, 146-154, 158-174, 177-183, 186-201, 207-215, 223-235, 240-247, 262-273, 275-283, 287-292 and 48-66 of Seq ID No 269; 7-27, 31-47, 49-70, 75-102, 110-149, 157-171, 217-223, 235-251, 294-302, 358-364, 367-375, 387-393, 395-412, 423-430, 441-451, 456-470, 472-486, 488-495, 499-509, 515-529, 536-549, 556-570, 574-603, 607-615, 625-633, 642-658, 670-676, 683-702, 708-716, 720-726, 747-756, 763-784, 803-812, 815-826 and 475-490 of Seq ID No 270; 7-22, 30-38, 53-59, 64-75, 83-95, 97-112, 120-131, 133-142, 145-151, 154-166, 172-180, 189-203, 227-238, 277-287, 9-156 and 174-287 of Seq ID No 271; 13-23, 25-32, 111-117, 150-164, 185-193, 207-212, 216-224, 230-236, 263-272, 304-311, 342-348, 374-385, 391-407, 444-458, 480-487, 489-499, 523-542, 544-558, 572-579, 620-640, 686-696, 703-710, 742-755, 765-772, 817-822, 830-837, 865-872, 931-937 and 66-86 of Seq ID No 272; 4-27, 49-56, 62-70, 86-92, 121-127, 151-163, 170-182, 195-202, 212-226, 237-243 and 234-254 of Seq ID No 273; 4-10, 13-24, 39-51, 62-78, 92-104, 107-117, 134-141, 156-161, 166-181, 210-216, 222-229, 256-266, 273-280, 297-304, 313-330, 336-349, 371-376, 433-439, 443-448, 488-493, 506-515, 527-534, 560-572, 575-583, 587-593 and 252-483 of Seq ID No 274; 4-15, 21-38, 45-56, 81-95, 102-108, 118-130, 133-147, 152-162, 166-171, 199-204, 211-218, 230-240, 253-261, 274-283, 288-294, 312-317, 325-336, 344-357, 391-414 and 24-146 of Seq ID No 275; 26-31, 38-56, 65-82, 90-101, 112-119, 123-153, 175-188, 197-216, 234-242, 249-265, 273-286, 290-305, 327-335, 338-346, 361-372, 394-404 and 290-306 of Seq ID No 276; 17-26, 43-48, 50-73, 81-93, 95-107, 139-146, 158-168, 171-176, 190-196, 202-212, 216-223, 243-266, 274-282, 308-313, 324-330, 344-378, 380-387, 403-422, 427-443, 448-455, 457-465, 491-515, 517-528, 553-567, 589-599, 610-617, 642-648, 670-697, 709-717, 726-743, 745-759, 769-803, 807-823, 840-849 and 820-851 of Seq ID No 277; 4-18, 39-48, 53-63, 66-90, 102-117, 125-134, 137-145, 156-162, 169-197, 26-40 and 56-80 of Seq ID No 278; 21-33, 36-42, 49-60, 68-76, 91-105, 123-130, 141-161, 169-178, 185-190, 192-199, 205-214, 223-233, 239-247, 260-269, 284-293, 300-314, 324-352, 357-364, 373-382, 389-403, 420-432, 438-446, 466-471, 477-484, 503-509, 549-556, 558-576, 600-623, 625-635, 654-661, 663-669, 671-687, 702-716, 735-741, 744-750, 757-766, 776-786, 807-815, 824-832, 854-860, 863-897, 909-915, 920-946, 952-959, 982-997, 1024-1038, 1049-1055, 1071-1085, 1104-1113, 1121-1132, 1138-1150, 1187-1196, 1212-1221, 1227-1236, 1257-1262, 1264-1278, 1282-1294, 1307-1318, 1353-1370, 1382-1388, 1396-1409, 1434-1440, 1446-1454, 1465-1478, 1485-1513, 1516-1529, 1540-1545, 1563-1568, 1575-1593, 1607-1616, 1628-1645, 1648-1661, 1676-1682, 1689-1697, 1713-1719, 1739-1749, 1753-1758, 1763-1774, 1797-1803, 1807-1846, 1855-1874, 1877-1891, 1893-1907, 1912-1925, 1931-1943, 1955-1965, 1976-1990, 2032-2043, 2045-2051, 2099-2105, 2131-2138, 2161-2179, 2188-2199, 2205-2216, 2219-2227, 2235-2245, 2247-2267, 2277-2288, 2294-2304, 2314-2326, 2346-2358, 2365-2377, 2383-2402, 2407-2423, 2437-2450, 2454-2473, 2489-2497, 2525-2531, 2557-2570, 2580-2587, 2589-2599, 2621-2641, 2647-2653, 2661-2677, 2685-2690, 2697-2717, 2722-2733, 2739-2777, 2786-2793, 2801-2808, 2811-2822, 2825-2835, 2838-2845, 2859-2871, 2877-2883, 213-344, 954-1080 and 2524-2733 of Seq ID No 279; 10-16, 18-23, 28-41, 63-69, 77-91, 101-109, 118-136, 146-153, 155-162, 168-179, 192-207, 217-226, 229-235, 239-254, 279-286, 294-307, 313-319, 334-341, 344-353, 363-377, 390-396 and 178-328 of Seq ID No 280; 18-42, 68-84, 89-95, 100-105, 107-115, 125-135, 154-177, 189-195, 205-228, 236-243, 252-259, 279-300, 309-316, 323-331, 340-351, 353-364, 377-402 and 85-97 of Seq ID No 281; 4-18, 26-32, 66-76, 100-126, 151-159, 178-186, 188-194, 200-210, 241-248, 253-259, 262-279, 284-291, 307-313, 315-322, 327-337, 376-386, 399-407, 432-441, 467-473, 487-497, 499-505, 543-549, 560-568, 585-593, 598-604,

608-614, 630-642, 647-653, 690-703, 717-730, 21-200 and 468-480 of Seq ID No 282; 17-49, 52-58, 62-73, 78-97, 100-117, 122-172, 185-190, 193-217, 225-236 and 33-42 of Seq ID No 283; 7-39, 50-58, 73-89, 96-107, 109-120, 126-142, 152-170, 178-202, 205-211, 224-244, 249-259, 261-270, 300-310, 312-325 and 158-169 of Seq ID No 284; 4-31, 40-64, 71-82, 85-92, 102-124, 126-139, 147-152, 159-173, 176-188, 195-207, 210-216, 234-241, 249-256, 258-276, 279-293, 296-302, 310-315, 349-356, 363-378, 380-403, 411-426, 435-441, 448-459, 463-476, 488-494 and 201-221 of Seq ID No 285; 5-13, 15-74, 87-104, 107-120, 123-129, 136-145, 150-191, 193-206, 227-248, 250-264, 278-302, 304-323, 332-378, 384-407, 409-419, 425-457, 462-471, 474-497, 511-545, 555-564, 571-578, 585-598, 640-647, 669-675, 682-691, 693-705, 729-743, 752-761, 772-780, 786-804, 808-818, 822-846, 858-880, 884-900, 910-939, 941-947, 962-971, 973-988, 998-1003, 1007-1027 and 236-259 of Seq ID No 286; 4-19, 27-68, 81-111, 121-160 and 60-79 of Seq ID No 287; 4-37, 40-46, 52-57, 199-205, 222-229, 236-244, 250-267, 269-282 and 27-197 of Seq ID No 288; 4-16, 24-30, 32-38, 63-75, 86-92, 98-111, 113-126, 160-165, 170-180, 198-204, 227-233, 239-245, 253-273, 308-314, 352-365, 382-387, 395-403, 423-429, 472-482, 484-493, 501-507, 518-526, 536-541, 543-550, 556-562, 586-600, 626-633, 649-661, 680-688 and 546-559 of Seq ID No 289; 16-33, 48-59, 63-71, 77-92, 94-109, 117-124, 139-151, 169-181, 184-227, 233-249, 251-261, 263-275, 282-294, 297-321, 326-332, 341-355, 383-399 and 258-272 of Seq ID No 290; 11-26, 31-39, 43-52, 55-62, 64-70, 80-94, 123-133, 135-141, 172-181, 185-206, 209-218, 224-230, 238-244, 251-262, 264-271, 290-301, 306-324, 333-340, 350-357, 367-375, 390-397, 434-441, 443-448, 77-226 and 350-429 of Seq ID No 291; 4-13, 22-27, 31-45, 50-59, 72-96, 99-114, 131-141, 143-150, 159-176, 180-186, 189-198, 208-214, 234-253, 271-287, 294-299, 310-366, 382-390, 398-416, 424-443 and 283-305 of Seq ID No 292; 9-26, 30-53, 62-72, 86-95, 112-122, 136-145, 153-160, 209-221, 227-237, 241-268, 281-288, 291-298, 308-314, 321-328, 336-346, 351-379, 388-397, 409-416, 423-433, 443-481, 511-519 and 213-232 of Seq ID No 293; 12-18, 25-31, 38-50, 59-67, 71-82, 96-126 and 76-88 of Seq ID No 294; 4-25, 39-44, 64-71, 74-88, 100-113, 128-138, 151-162, 164-177, 185-190, 204-213, 233-239, 246-254, 281-286, 293-306, 309-318, 333-347, 349-359, 385-398, 404-423, 458-465, 477-484, 490-499, 501-533, 554-566, 582-590, 596-616, 624-629, 631-639, 654-680, 694-720, 735-743 and 2-100 of Seq ID No 295; 4-16, 36-41, 52-75, 98-107, 109-117, 122-128, 133-139, 141-155, 159-165, 169-182, 187-193, 195-201, 211-224, 230-236, 247-269, 278-290 and 75-92 of Seq ID No 296; 7-21, 25-33, 37-43, 87-94, 103-120, 131-147, 168-174, 197-203, 207-212, 227-237, 247-257, 263-271, 279-287, 298-306, 320-325, 332-340, 363-374, 379-384, 390-401, 403-414, 428-433, 448-457, 462-475, 483-490, 513-519, 525-535, 543-554, 559-566, 571-620, 625-631, 636-642, 659-670, 688-706, 708-723, 770-779, 787-793, 796-807, 820-840, 848-854, 863-874, 895-905, 912-919, 934-942, 968-975, 983-1000, 1012-1019, 1026-1036, 1050-1060, 1064-1070, 1081-1091, 1094-1108, 1112-1118, 1140-1152, 1164-1169, 1172-1180, 1187-1192 and 732-748 of Seq ID No 297; 23-40, 42-59, 66-73, 78-97, 111-128, 130-141, 157-166, 178-183 and 53-71 of Seq ID No 298; 4-27, 38-44, 47-57, 59-85, 99-106, 114-121, 154-166, 181-186, 193-198, 238-244, 253-262, 272-278, 287-299, 314-320, 338-350, 358-368, 382-388, 407-416, 433-446, 456-461, 463-473 and 86-195 of Seq ID No 299; 5-24, 38-59, 64-80, 87-99, 105-126, 134-142, 149-163, 165-179, 181-202, 205-220, 227-233, 243-250, 257-263 and 87-245 of Seq ID No 300; 5-32, 47-53, 66-79, 81-97, 115-151, 155-174, 183-188, 196-210, 215-226, 230-238, 253-258, 263-270, 276-282, 295-301, 304-325, 334-344, 360-390, 397-412, 425-432, 434-462, 478-494, 508-526, 539-564, 571-579, 347-371 and 375-386 of Seq ID No 301; 4-15, 36-44, 49-56, 60-66, 68-82, 84-103, 109-115, 118-141, 147-154, 160-168, 176-185 and 26-39 of Seq ID No 302; 7-13, 23-33 and 13-21 of Seq ID No 303; 2-10 of Seq ID No 304; 4-9, 12-18, 35-42, 49-62 and 6-18 of Seq ID No 305; 19-25 and 1-13 of Seq ID No 306; 15-21, 27-45 and 12-25 of Seq ID No 307; 14-20 and 1-14 of Seq ID No 308; 4-18 and 13-26 of Seq ID No 309; 8-21 and 2-20 of Seq ID No 310; 4-14 and 4-16 of Seq ID No 311; 3-12 of Seq ID No 312; 6-14, 6-25, 35-57 and 2-14 of Seq ID No 313; 6-25, 35-57 and 17-31 of Seq ID No 314; 14-25, 32-46 and 5-19 of Seq ID No 315; 18-31 and 5-16 of Seq ID No 316; 19-24 and 4-26 of Seq ID No 317; 13-21, 29-34, 47-58, 61-73 and 36-47 of Seq ID No 318; 4-15 and 5-24 of Seq ID No 319; 6-18 of Seq ID No 320; 13-20 and 4-13 of Seq ID No 321; 15-23 of Seq ID No 322; 4-9 and 7-21 of Seq ID No 323; 1-10 of Seq ID No 324; 4-14 of Seq ID No 325; 4-17, 35-41, 46-89, 93-98 and 70-88 of Seq ID No 326; 1-13 of Seq ID No 327; 4-16, 26-32 and 25-38 of Seq ID No 328; 8-15, 23-28 and 4-17 of Seq ID No 329; 4-12 and 1-15 of Seq ID No 330; 4-29, 31-42, 52-58 and 6-16 of Seq ID No 331; 4-9, 24-32 and 9-19 of Seq ID No 332; 4-12, 18-27 and 5-18 of Seq ID No 333; 4-11, 37-56, 58-92 and 18-29 of Seq ID No 334; 8-28 and 20-35 of Seq ID No 335; 4-15 of Seq ID No 336; 4-23, 27-39, 55-63 and 35-58 of Seq ID No 337; 6-26, 28-54 and 28-47 of Seq ID No 338; 4-10, 38-52, 58-82 and 30-49 of Seq ID No 339; 4-22, 29-35, 44-50, 53-68, 70-80 and 20-33 of Seq ID No 340; 22-28, 30-36 and 18-33 of Seq ID No 341; 4-11, 13-21, 25-30 and 20-30 of Seq ID

No 342; 10-22 and 10-23 of Seq ID No 343; 4-11 and 9-20 of Seq ID No 344; 14-25, 32-46 and 6-19 of Seq ID No 345; 5-30 and 14-33 of Seq ID No 346; 4-15, 28-35, 46-55, 59-65, 76-84 and 9-24 of Seq ID No 347; 27-33 and 5-19 of Seq ID No 348; 5-13 and 8-18 of Seq ID No 349; 9-22, 24-34 and 21-40 of Seq ID No 350; 4-17, 35-41, 46-89, 93-98 and 71-89 of Seq ID No 351; 4-12, 14-24 and 2-17 of Seq ID No 352; 9-17 and 5-16 of Seq ID No 353; 7-41, 48-58, 63-75, 80-89 and 43-53 of Seq ID No 354; 4-22, 25-30 and 4-14 of Seq ID No 355; 4-55 and 18-33 of Seq ID No 356; 262-280 of Seq ID No 179; 131-146 of Seq ID No 186; 207-224 of Seq ID No 188; 27-50, 203-217 and 313-325 of Seq ID No 189; 110-129 of Seq ID No 192; 156-179, 174-197, 192-215, 210-233, 228-251 and 246-267 of Seq ID No 190; 377-400 of Seq ID No 196; 34-43, 234-257 and 350-367 of Seq ID No 203; 304-327 of Seq ID No 207; 25-48, 43-66 and 61-82 of Seq ID No 222; 398-421, 416-439, 434-457, 452-475, 470-493, 488-511, 506-529, 524-547, 621-644, 639-664, 707-730, 725-748, 743-766, 761-784, 779-802, 797-820, 984-1007, 1002-1025, 1020-1043, 1038-1061, 1056-1079, 1074-1097, 1092-1115, 1286-1309, 1304-1327, 1322-1345, 1340-1363, 1358-1381, 1376-1399, 1394-1417, 1412-1435, 1430-1453, 1448-1471, 1466-1489 and 1484-1507 of Seq ID No 226; 188-211, 206-229, 224-247, 242-265, 260-283 and 278-296 of Seq ID No 227; 56-79 and 122-132 of Seq ID No 229; 35-46 of Seq ID No 231; 178-201, 196-219, 214-237, 232-255, 250-273, 268-291, 379-402, 397-420, 415-438, 433-456, 451-474, 642-665, 660-683, 678-701, 696-719, 714-737, 732-755, 750-773, 768-791, 899-922, 917-940, 935-958, 1037-1060, 1055-1078, 1073-1096 and 1091-1114 of Seq ID No 232; 330-346 of Seq ID No 233; 571-594, 589-612, 607-630, 625-648, 643-666 and 661-684 of Seq ID No 242; 188-207 of Seq ID No 244; 61-84, 308-331, 326-349, 344-367, 362-385, 380-403 and 398-421 of Seq ID No 249; 79-98, 345-366, 844-867, 870-887 and 890-905 of Seq ID No 258; 94-109 of Seq ID No 268; 188-207 of Seq ID No 272; 290-306 of Seq ID No 276; 826-849 of Seq ID No 277; 228-252, 247-270, 265-288, 283-306, 301-324, 955-978, 973-996, 991-1014, 1009-1032, 1027-1050, 1045-1068, 2533-2556, 2551-2574, 2569-2592, 2587-2610, 2605-2628 and 2623-2646 of Seq ID No 279; 86-109 and 104-127 of Seq ID No 288; 546-560 of Seq ID No 289; 260-271 of Seq ID No 290; 106-129, 124-147, 142-165, 160-183, 178-201 and 375-398 of Seq ID No 291; 284-307 of Seq ID No 292; 362-385 of Seq ID No 301.

The present invention also provides a process for producing a *H. pylori* hyperimmune serum reactive antigen or a fragment thereof according to the present invention comprising expressing one or more of the nucleic acid molecules according to the present invention in a suitable expression system.

Moreover, the present invention provides a process for producing a cell, which expresses a *H. pylori* hyperimmune serum reactive antigen or a fragment thereof according to the present invention comprising transforming or transfecting a suitable host cell with the vector according to the present invention.

According to the present invention a pharmaceutical composition, especially a vaccine, comprising a hyperimmune serum-reactive antigen or a fragment thereof as defined in the present invention or a nucleic acid molecule as defined in the present invention is provided.

In a preferred embodiment the pharmaceutical composition further comprises an immunostimulatory substance, preferably selected from the group comprising polycationic polymers, especially polycationic peptides, immunostimulatory deoxynucleotides (ODNs), peptides containing at least two LysLeuLys motifs, especially KLKLSKLK, neuroactive compounds, especially human growth hormone, alumn, Freund's complete or incomplete adjuvants or combinations thereof.

In a more preferred embodiment the immunostimulatory substance is a combination of either a polycationic polymer and immunostimulatory deoxynucleotides or of a peptide containing at least two LysLeuLys motifs and immunostimulatory deoxynucleotides.

In a still more preferred embodiment the polycationic polymer is a polycationic peptide, especially polyarginine.

According to the present invention the use of a nucleic acid molecule according to the present invention or a hyperimmune serum-reactive antigen or fragment thereof according to the present invention for the manufacture of a pharmaceutical preparation, especially for the manufacture of a vaccine against *H. pylori* infection, is provided.

Also an antibody, or at least an effective part thereof, which binds at least to a selective part of the hyperimmune serum-reactive antigen or a fragment thereof according to the present invention is provided herewith.

In a preferred embodiment the antibody is a monoclonal antibody.

In another preferred embodiment the effective part of the antibody comprises Fab fragments.

In a further preferred embodiment the antibody is a chimeric antibody.

In a still preferred embodiment the antibody is a humanized antibody.

The present invention also provides a hybridoma cell line, which produces an antibody according to the present invention.

Moreover, the present invention provids a method for producing an antibody according to the present invention, characterized by the following steps:

- initiating an immune response in a non-human animal by administrating an hyperimmune serum-reactive antigen or a fragment thereof, as defined in the invention, to said animal,
- removing an antibody containing body fluid from said animal, and
- producing the antibody by subjecting said antibody containing body fluid to further purification steps.

Accordingly, the present invention also provides a method for producing an antibody according to the present invention, characterized by the following steps:

- initiating an immune response in a non-human animal by administrating an hyperimmune serum-reactive antigen or a fragment thereof, as defined in the present invention, to said animal,
- removing the spleen or spleen cells from said animal,
- producing hybridoma cells of said spleen or spleen cells,
- selecting and cloning hybridoma cells specific for said hyperimmune serum-reactive antigens or a fragment thereof,
- producing the antibody by cultivation of said cloned hybridoma cells and optionally further purification steps.

The antibodies provided or produced according to the above methods may be used for the preparation of a medicament for treating or preventing *H. pylori* infections.

According to another aspect the present invention provides an antagonist, which binds to a hyperimmune serum-reactive antigen or a fragment thereof according to the present invention.

Such an antagonist capable of binding to a hyperimmune serum-reactive antigen or fragment thereof according to the present invention may be identified by a method comprising the following steps:

a) contacting an isolated or immobilized hyperimmune serum-reactive antigen or a fragment thereof according to the present invention with a candidate antagonist under conditions to permit binding of said candidate antagonist to said hyperimmune serum-reactive antigen or fragment, in the presence of a component capable of providing a detectable signal in response to the binding of the candidate antagonist to said hyperimmune serum reactive antigen or fragment

thereof; and

b) detecting the presence or absence of a signal generated in response to the binding of the antagonist to the hyperimmune serum reactive antigen or the fragment thereof.

An antagonist capable of reducing or inhibiting the interaction activity of a hyperimmune serum-reactive antigen or a fragment thereof according to the present invention to its interaction partner may be identified by a method comprising the following steps:

a) providing a hyperimmune serum reactive antigen or a hyperimmune fragment thereof according to the present invention,
b) providing an interaction partner to said hyperimmune serum reactive antigen or a fragment thereof, especially an antibody according to the present invention,
c) allowing interaction of said hyperimmune serum reactive antigen or fragment thereof to said interaction partner to form an interaction complex,
d) providing a candidate antagonist,
e) allowing a competition reaction to occur between the candidate antagonist and the interaction complex,
f) determining whether the candidate antagonist inhibits or reduces the interaction activities of the hyperimmune serum reactive antigen or the fragment thereof with the interaction partner.

The hyperimmune serum reactive antigens or fragments thereof according to the present invention may be used for the isolation and/or purification and/or identification of an interaction partner of said hyperimmune serum reactive antigen or fragment thereof.

The present invention also provides a process for *in vitro* diagnosing a disease related to expression of a hyperimmune serum-reactive antigen or a fragment thereof according to the present invention comprising determining the presence of a nucleic acid sequence encoding said hyperimmune serum reactive antigen or fragment thereof according to the present invention or the presence of the hyperimmune serum reactive antigen or fragment thereof according to the present invention.

The present invention also provides a process for *in vitro* diagnosis of a bacterial infection, especially a *H. pylori* infection, comprising analyzing for the presence of a nucleic acid sequence encoding said hyperimmune serum reactive antigen or fragment thereof according to the present invention or the presence of the hyperimmune serum reactive antigen or fragment thereof according to the present invention.

Moreover, the present invention provides the use of a hyperimmune serum reactive antigen or fragment thereof according to the present invention for the generation of a peptide binding to said hyperimmune serum reactive antigen or fragment thereof, wherein the peptide is an anticaline.

The present invention also provides the use of a hyperimmune serum-reactive antigen or fragment thereof according to the present invention for the manufacture of a functional nucleic acid, wherein the functional nucleic acid is selected from the group comprising aptamers and spiegelmers.

The nucleic acid molecule according to the present invention may also be used for the manufacture of a functional ribonucleic acid, wherein the functional ribonucleic acid is selected from the group comprising ribozymes, antisense nucleic acids and siRNA.

The present invention advantageously provides an efficient, relevant and comprehensive set of isolated nucleic acid molecules and their encoded hyperimmune serum reactive antigens or fragments thereof identified from *H. pylori* using an antibody preparation from multiple human plasma pools and surface expression libraries derived from the genome of *H. pylori*. Thus, the present invention fulfils a widely felt demand for *H. pylori* antigens, vaccines, diagnostics and products useful in procedures for preparing

antibodies and for identifying compounds effective against *H. pylori* infection.

An effective vaccine should be composed of proteins or polypeptides, which are expressed by all strains and are able to induce high affinity, abundant antibodies against cell surface components of *H. pylori*. The antibodies should be IgG1 and/or IgG3 for opsonization, and any IgG subtype and IgA for neutralisation of adherence and toxin action. A chemically defined vaccine must be definitely superior compared to a whole cell vaccine (attenuated or killed), since components of *H. pylori*, which cross-react with human tissues or inhibit opsonization can be eliminated, and the individual proteins inducing protective antibodies and/or a protective immune response can be selected.

The approach, which has been employed for the present invention, is based on the interaction of *H. pylori* proteins or peptides with the antibodies present in human sera. The antibodies produced against *H. pylori* by the human immune system and present in human sera are indicative of the *in vivo* expression of the antigenic proteins and their immunogenicity. In addition, the antigenic proteins as identified by the bacterial surface display expression libraries using pools of pre-selected sera are processed in a second and third round of screening by individual selected or generated sera. Thus the present invention supplies an efficient, relevant, comprehensive set of *H. pylori* antigens as promising candidates for the development of a pharmaceutical composition, especially a vaccine preventing infection by *H. pylori*.

In the antigen identification program for identifying a comprehensive set of antigens according to the present invention, at least two different bacterial surface expression libraries are screened with several serum pools or plasma fractions or other pooled antibody containing body fluids (antibody pools). The antibody pools are derived from a serum collection, which has been tested against antigenic compounds of *H. pylori*, such as whole cell extracts and culture supernatant proteins. Preferably, 2 distinct serum collections are used: 1. With very stable antibody repertoire: normal adults, clinically healthy people, who are non-carriers and overcame previous encounters or currently carriers of *H. pylori* without acute disease and symptoms, 2. With antibodies induced acutely by the presence of the pathogenic organism: patients with manifest disease (e.g. *H. pylori* gastritis, peptic ulcer disease or gastric cancer). Sera have to react with multiple *H. pylori*-specific antigens in order to be considered hyperimmune and therefore relevant in the screening method applied for the present invention. The antibodies produced against *H. pylori* by the human immune system and present in human sera are indicative of the *in vivo* expression of the antigenic proteins and their immunogenicity.

The expression libraries as used in the present invention should allow expression of all potential antigens, e.g. derived from all surface proteins of *H. pylori*. Bacterial surface display libraries will be represented by a recombinant library of a bacterial host displaying a (total) set of expressed peptide sequences of *H. pylori* on a number of selected outer membrane proteins (LamB, FhuA) at the bacterial host membrane {Georgiou, G., 1997}; {Etz, H. et al., 2001}. One of the advantages of using recombinant expression libraries is that the identified hyperimmune serum-reactive antigens may be instantly produced by expression of the coding sequences of the screened and selected clones expressing the hyperimmune serum-reactive antigens without further recombinant DNA technology or cloning steps necessary.

The comprehensive set of antigens identified by the described program according to the present invention is analysed further by additional rounds of screening. Therefore individual antibody preparations or antibodies generated against selected peptides, which were identified as immunogenic are used. According to a preferred embodiment the individual antibody preparations for the second round of screening are derived from patients who have suffered from infection with *H. pylori*, especially from patients who show an antibody titer above a certain minimum level, for example an antibody titer being higher than 80 percentile, preferably higher than 90 percentile, especially higher than 95 percentile of the human (patient or healthy individual) sera tested. Using such high titer individual antibody preparations in the second screening round allows a very selective identification of the hyperimmune serum-reactive antigens and fragments thereof from *H. pylori*.

Following the high throughput screening procedure, the selected antigenic proteins, expressed as recombinant proteins or in vitro translated products, in case it can not be expressed in prokaryotic expression systems, or the identified antigenic peptides (produced synthetically) are tested in a second screening by a series of ELISA and Western blotting assays for the assessment of their immunogenicity with a large human serum collection (> 50 uninfected, > 100 patients sera).

It is important that the individual antibody preparations (which may also be the selected serum) allow a selective identification of the hyperimmune serum-reactive antigens from all the promising candidates from the first round. Therefore, preferably at least 10 individual antibody preparations (i.e. antibody preparations (e.g. sera) from at least 10 different individuals having suffered from an infection to the chosen pathogen) should be used in identifying these antigens in the second screening round. It is possible to use also less than 10 individual preparations, however, selectivity of the step may not be optimal with a low number of individual antibody preparations. Therefore, recognition of a given hyperimmune serum-reactive antigen (or an antigenic fragment thereof) by at least 10 individual antibody preparations, preferably at least 30, especially at least 50 individual antibody preparations confers proper selectivity in the identification process. Hyperimmune serum-reactivity may of course be tested with as many individual preparations as possible (e.g. with more than 100 or even with more than 1,000).

Therefore, the relevant portion of the hyperimmune serum-reactive antibody preparations according to the method of the present invention should preferably be at least 10, more preferred at least 30, especially at least 50 individual antibody preparations. Alternatively (or in combination) hyperimmune serum-reactive antigens may preferably be also identified with at least 20%, preferably at least 30%, especially at least 40% of all individual antibody preparations used in the second screening round.

According to a preferred embodiment of the present invention, the sera from which the individual antibody preparations for the second round of screening are prepared (or which are used as antibody preparations), are selected by their titer against *H. pylori* (e.g. against a preparation of this pathogen, such as a lysate, cell wall components and recombinant proteins). Preferably, some are selected with a total IgA titer above 4,000 U, especially above 6,000 U, and/or an IgG titer above 10,000 U, especially above 12,000 U (U = units, calculated from the OD_{405nm} reading at a given dilution) when the whole organism (total lysate or whole cells) is used as antigen in the ELISA.

The antibodies produced against Helicobacter by the human immune system and present in human sera are indicative of the in vivo expression of the antigenic proteins and their immunogenicity. The recognition of linear epitopes by antibodies can be based on sequences as short as 4-5 amino acids. It, however, does not necessarily mean that these short peptides are capable of inducing the given antibody in vivo. For that reason the defined epitopes, polypeptides and proteins are further to be tested in animals (mainly in mice) for their capacity to induce antibodies against the selected proteins in vivo.

The preferred antigens are located on the cell surface or secreted, and are therefore accessible extracellularly. Antibodies against cell wall proteins are expected to serve two purposes: to inhibit adhesion and to promote phagocytosis or complement mediated killing. Antibodies against secreted proteins are beneficial in neutralisation of their function as toxin or virulence component. It is also known that bacteria communicate with each other through secreted proteins. Neutralizing antibodies against these proteins will interrupt growth-promoting cross-talk between or within Helicobacter species. Bioinformatic analyses (signal sequences, cell wall localisation signals, transmembrane domains) proved to be very useful in assessing cell surface localisation or secretion. The experimental approach includes the isolation of antibodies with the corresponding epitopes and proteins from human serum, and the generation of immune sera in mice against (poly) peptides selected by the bacterial surface display screens. These sera are then used in a third round of screening as reagents in the following assays: cell

surface staining of Helicobacter grown under different conditions (FACS, microscopy), determination of neutralizing capacity (toxin, adherence), and promotion of opsonization and phagocytosis (in vitro phagocytosis assay).

For that purpose, bacterial *E. coli* clones are directly injected into mice and immune sera taken and tested in the relevant in vitro assay for functional opsonic or neutralizing antibodies. Alternatively, specific antibodies may be purified from human or mouse sera using peptides or proteins as substrate.

It is not clear as to what extend host defence against *H. pylori* relies on innate or adaptive immunological mechanisms. The mucous membranes and the gastric acidic environment are formidable barriers against invasion by Helicobacter. However, once the mucous membranes are breached the first line of non-adaptive cellular defence begins its co-ordinate action through complement and phagocytes, especially the polymorphonuclear leukocytes (PMNs) as indicated by the massive neutrophil infiltration of the gastric mucosa in response to the presence of *H. pylori*. Attachment of *H. pylori* induces strong pro-inflammatory cytokine release, including TNF-α, IL-1β and IL-8 that can mediate a local chemoattractant effect for immuno-effector cells, such as granulocytes {Prinz, C. et al., 2003}; {Sutton, P., 2001}. These cells can be regarded as the cornerstones in eliminating invading bacteria. As *H. pylori* is thought to be a exclusively extracellular pathogen, the major anti-Helicobacter adaptive response should come from the humoral arm of the immune system, and this seems to be in agreement with the high titers of primarily IgG and IgA antibodies that develop in patient upon *H. pylori* infection {Prinz, C. et al., 2003}; {Sutton, P., 2001}. The induction of high titer IgG and sectretory IgA type antibody response may reflect the importance of adaptive mechanisms in the immune response against this organism. In principle, the effect of these antibodies is mediated through three major mechanisms: promotion of opsonization, toxin neutralisation, and inhibition of adherence. It is believed that opsonization is especially important, because of its requirement for an effective phagocytosis. For efficient opsonization the microbial surface has to be coated with antibodies and complement factors for recognition by PMNs through receptors for the Fc fragment of IgG molecules or for activated C3b. After opsonization, the bacteria are phagocytosed and killed. Antibodies bound to specific antigens on the cell surface of bacteria serve as ligands for the attachment to PMNs and to promote phagocytosis. The very same antibodies bound to the adhesins and other cell surface proteins are expected to neutralize adhesion and prevent colonization.

Inducing high affinity antibodies of the opsonic and neutralizing type by vaccination helps the innate immune system to eliminate bacteria and toxins. This makes the method according to the present invention an optimal tool for the identification of *H. pylori* antigenic proteins. The selection of antigens as provided by the present invention is thus well suited to identify those that will lead to protection against infection in an animal model or in humans.

However, there is compelling evidence indicating that antibodies are not required for immunisation-induced effective immunity against gastric helicobacters. Indeed, *in vitro* studies have demonstrated that diminutive fraction of the colonizing *H. pylori* population might enter epithelial cells and this is in good agreement with the fact that *H. pylori* generally induces a predominantly T helper 1 (Th1) type immune response, normally associated with invasive bacteria. Gastric T cells isolated from infected animals and humans produce TNF-α and IFN-γ but not IL-4, typical for a Th1-biased response. This pro-inflammatory Th1 response is clearly not effective against infection {Prinz, C. et al., 2003}; {Sutton, P., 2001}. Current vaccination protocols, such as immunization with recombinant UreB, can drive the immune response to a polarized Th2 phenotype. Studies with knockout mice demonstrated that immunization with urease is possible when the Th2 response is absent. Therefore, vaccine development using new antigens as well as suitable adjuvants that are capable of inducing strong Th1-biased responses may be beneficial in disease protection caused by *H. pylori*.

According to the antigen identification method used herein, the present invention can surprisingly provide a set of comprehensive novel nucleic acids and novel hyperimmune serum reactive antigens and

fragments thereof of *H. pylori*, among other things, as described below. According to one aspect, the invention particularly relates to the nucleotide sequences encoding hyperimmune serum reactive antigens which sequences are set forth in the Sequence listing Seq ID No 1-178, and the corresponding encoded amino acid sequences representing hyperimmune serum reactive antigens are set forth in the Sequence Listing Seq ID No 179-356.

In a preferred embodiment of the present invention, a nucleic acid molecule is provided which exhibits 70% identity over their entire length to a nucleotide sequence set forth with Seq ID No 3-4, 16, 19-21, 28-29, 33-38, 41-42, 44, 48-52, 55, 57-58, 61, 63, 65, 67-68, 72, 74-75, 81, 84, 91, 94, 96-97, 101, 105-108, 112, 115-117, 119, 123-178. Most highly preferred are nucleic acids that comprise a region that is at least 80% or at least 85% identical over their entire length to a nucleic acid molecule set forth with Seq ID No 3-4, 16, 19-21, 28-29, 33-38, 41-42, 44, 48-52, 55, 57-58, 61, 63, 65, 67-68, 72, 74-75, 81, 84, 91, 94, 96-97, 101, 105-108, 112, 115-117, 119, 123-178. In this regard, nucleic acid molecules at least 90%, 91%, 92%, 93%, 94%, 95%, or 96% identical over their entire length to the same are particularly preferred. Furthermore, those with at least 97% are highly preferred, those with at least 98% and at least 99% are particularly highly preferred, with at least 99% or 99.5% being the more preferred, with 100% identity being especially preferred. Moreover, preferred embodiments in this respect are nucleic acids which encode hyperimmune serum reactive antigens or fragments thereof (polypeptides) which retain substantially the same biological function or activity as the mature polypeptide encoded by said nucleic acids set forth in the Seq ID No 3-4, 16, 19-21, 28-29, 33-38, 41-42, 44, 48-52, 55, 57-58, 61, 63, 65, 67-68, 72, 74-75, 81, 84, 91, 94, 96-97, 101, 105-108, 112, 115-117, 119, 123-178.

Identity, as known in the art and used herein, is the relationship between two or more polypeptide sequences or two or more polynucleotide sequences, as determined by comparing the sequences. In the art, identity also means the degree of sequence relatedness between polypeptide or polynucleotide sequences, as the case may be, as determined by the match between strings of such sequences. Identity can be readily calculated. While there exist a number of methods to measure identity between two polynucleotides or two polypeptide sequences, the term is well known to skilled artisans (e.g. *Sequence Analysis in Molecular Biology*, von Heinje, G., Academic Press, 1987). Preferred methods to determine identity are designed to give the largest match between the sequences tested. Methods to determine identity are codified in computer programs. Preferred computer program methods to determine identity between two sequences include, but are not limited to, GCG program package {Devereux, J. et al., 1984}, BLASTP, BLASTN, and FASTA {Altschul, S. et al., 1990}.

According to another aspect of the invention, nucleic acid molecules are provided which exhibit at least 96% identity to the nucleic acid sequence set forth with Seq ID No 8-10, 13-15, 17-18, 24, 27, 32, 39-40, 45-47, 56, 59, 62, 69-70, 73, 77, 79, 82, 85-86, 88, 90, 103, 109-110, 114, 121.

According to a further aspect of the present invention, nucleic acid molecules are provided which are identical to the nucleic acid sequences set forth with Seq ID No 5, 7, 30-31, 53, 60, 66, 76, 83, 87, 92, 99, 120.

The nucleic acid molecules according to the present invention can as a second alternative also be a nucleic acid molecule which is at least essentially complementary to the nucleic acid described as the first alternative above. As used herein complementary means that a nucleic acid strand is base pairing via Watson-Crick base pairing with a second nucleic acid strand. Essentially complementary as used herein means that the base pairing is not occurring for all of the bases of the respective strands but leaves a certain number or percentage of the bases unpaired or wrongly paired. The percentage of correctly pairing bases is preferably at least 70 %, more preferably 80 %, even more preferably 90 % and most preferably any percentage higher than 90 %. It is to be noted that a percentage of 70 % matching bases is considered as homology and the hybridization having this extent of matching base pairs is considered as stringent. Hybridization conditions for this kind of stringent hybridization may be taken from Current

Protocols in Molecular Biology (John Wiley and Sons, Inc., 1987). More particularly, the hybridization conditions can be as follows:

- Hybridization performed e.g. in 5 x SSPE, 5 x Denhardt's reagent, 0.1% SDS, 100 g/mL sheared DNA at 68°C
- Moderate stringency wash in 0.2xSSC, O.1% SDS at 42°C
- High stringency wash in 0.1xSSC, 0.1% SDS at 68°C

Genomic DNA with a GC content of 50% has an approximate T_M of 96°C. For 1% mismatch, the T_M is reduced by approximately 1°C.

In addition, any of the further hybridization conditions described herein is in principle applicable as well.

All nucleic acid sequence molecules which encode the same polypeptide molecule as those identified by the present invention are encompassed by any disclosure of a given coding sequence, since the degeneracy of the genetic code is directly applicable to unambiguously determine all possible nucleic acid molecules which encode a given polypeptide molecule, even if the number of such degenerated nucleic acid molecules may be high. This is also applicable for fragments of a given polypeptide, as long as the fragments encode a polypeptide being suitable to be used in a vaccination connection, e.g. as an active or passive vaccine.

The nucleic acid molecule according to the present invention can as a third alternative also be a nucleic acid which comprises a stretch of at least 15 bases of the nucleic acid molecule according to the first and second alternative of the nucleic acid molecules according to the present invention as outlined above. Preferably, the bases form a contiguous stretch of bases. However, it is also within the scope of the present invention that the stretch consists of two or more moieties, which are separated by a number of bases.

The present nucleic acids may preferably consist of at least 20, even more preferred at least 30, especially at least 50 contiguous bases from the sequences disclosed herein. The suitable length may easily be optimized due to the planned area of use (e.g. as (PCR) primers, probes, capture molecules (e.g. on a (DNA) chip), etc.). Preferred nucleic acid molecules contain at least a contiguous 15 base portion of one or more of the predicted immunogenic amino acid sequences listed in tables 1 and 2, especially the sequences of table 2 with scores of more than 10, preferably more than 20, especially with a score of more than 25. Specifically preferred are nucleic acids containing a contiguous portion of a DNA sequence of any sequence in the sequence protocol of the present application which shows 1 or more, preferably more than 2, especially more than 5, non-identical nucleic acid residues compared to the published *Helicobacter pylori strain 26695 and J99* genomes (Nature, 388: 539-547 (1997), 4658-4663; GenBank accession AE000511 and Nature, 397: 176-180 (1999), GenBank accession AE001439) and/or any other published *H. pylori* genome sequence or parts thereof. Specifically preferred non-identical nucleic acid residues are residues, which lead to a non-identical amino acid residue. Preferably, the nucleic acid sequences encode for polypeptides having at least 1, preferably at least 2, preferably at least three different amino acid residues compared to the published *H. pylori* counterparts mentioned above. Also such isolated polypeptides, being fragments of the proteins (or the whole protein) mentioned herein e.g. in the sequence listing, having at least 6, 7, or 8 amino acid residues and being encoded by these nucleic acids are preferred.

The nucleic acid molecule according to the present invention can as a fourth alternative also be a nucleic acid molecule which anneals under stringent hybridisation conditions to any of the nucleic acids of the present invention according to the above outlined first, second, and third alternative. Stringent hybridisation conditions are typically those described herein.

Finally, the nucleic acid molecule according to the present invention can as a fifth alternative also be a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to any of the nucleic acid molecules according to any nucleic acid molecule of the present invention according to the first, second, third, and fourth alternative as outlined above. This kind of nucleic acid molecule refers to the fact that preferably the nucleic acids according to the present invention code for the hyperimmune serum reactive antigens or fragments thereof according to the present invention. This kind of nucleic acid molecule is particularly useful in the detection of a nucleic acid molecule according to the present invention and thus the diagnosis of the respective microorganisms such as *H. pylori* and any disease or diseased condition where this kind of microorganim is involved. Preferably, the hybridisation would occur or be preformed under stringent conditions as described in connection with the fourth alternative described above.

Nucleic acid molecule as used herein generally refers to any ribonucleic acid molecule or deoxyribonucleic acid molecule, which may be unmodified RNA or DNA or modified RNA or DNA. Thus, for instance, nucleic acid molecule as used herein refers to, among other, single-and double-stranded DNA, DNA that is a mixture of single- and double-stranded RNA, and RNA that is a mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded, or triple-stranded, or a mixture of single- and double-stranded regions. In addition, nucleic acid molecule as used herein refers to triple-stranded regions comprising RNA or DNA or both RNA and DNA. The strands in such regions may be from the same molecule or from different molecules. The regions may include all of one or more of the molecules, but more typically involve only a region of some of the molecules. One of the molecules of a triple-helical region often is an oligonucleotide. As used herein, the term nucleic acid molecule includes DNAs or RNAs as described above that contain one or more modified bases. Thus, DNAs or RNAs with backbones modified for stability or for other reasons are "nucleic acid molecule" as that term is intended herein. Moreover, DNAs or RNAs comprising unusual bases, such as inosine, or modified bases, such as tritylated bases, to name just two examples, are nucleic acid molecule as the term is used herein. It will be appreciated that a great variety of modifications have been made to DNA and RNA that serve many useful purposes known to those of skill in the art. The term nucleic acid molecule as it is employed herein embraces such chemically, enzymatically or metabolically modified forms of nucleic acid molecule, as well as the chemical forms of DNA and RNA characteristic of viruses and cells, including simple and complex cells, *inter alia*. The term nucleic acid molecule also embraces short nucleic acid molecules often referred to as oligonucleotide(s). "Polynucleotide" and "nucleic acid" or "nucleic acid molecule" are often used interchangeably herein.

Nucleic acid molecules provided in the present invention also encompass numerous unique fragments, both longer and shorter than the nucleic acid molecule sequences set forth in the sequencing listing of the *H. pylori* coding regions, which can be generated by standard cloning methods. To be unique, a fragment must be of sufficient size to distinguish it from other known nucleic acid sequences, most readily determined by comparing any selected *H. pylori* fragment to the nucleotide sequences in computer databases such as GenBank.

Additionally, modifications can be made to the nucleic acid molecules and polypeptides that are encompassed by the present invention. For example, nucleotide substitutions can be made which do not affect the polypeptide encoded by the nucleic acid, and thus any nucleic acid molecule which encodes a hyperimmune serum reactive antigen or fragments thereof is encompassed by the present invention.

Furthermore, any of the nucleic acid molecules encoding hyperimmune serum reactive antigens or fragments thereof provided by the present invention can be functionally linked, using standard techniques such as standard cloning techniques, to any desired regulatory sequences, whether a *H. pylori* regulatory sequence or a heterologous regulatory sequence, heterologous leader sequence, heterologous marker sequence or a heterologous coding sequence to create a fusion protein.

Nucleic acid molecules of the present invention may be in the form of RNA, such as mRNA or cRNA, or in the form of DNA, including, for instance, cDNA and genomic DNA obtained by cloning or produced by chemical synthetic techniques or by a combination thereof. The DNA may be triple-stranded, double-stranded or single-stranded. Single-stranded DNA may be the coding strand, also known as the sense strand, or it may be the non-coding strand, also referred to as the anti-sense strand.

The present invention further relates to variants of the herein above described nucleic acid molecules which encode fragments, analogs and derivatives of the hyperimmune serum reactive antigens and fragments thereof having a deducted *H. pylori* amino acid sequence set forth in the Sequence Listing. A variant of the nucleic acid molecule may be a naturally occurring variant such as a naturally occurring allelic variant, or it may be a variant that is not known to occur naturally. Such non-naturally occurring variants of the nucleic acid molecule may be made by mutagenesis techniques, including those applied to nucleic acid molecules, cells or organisms.

Among variants in this regard are variants that differ from the aforementioned nucleic acid molecules by nucleotide substitutions, deletions or additions. The substitutions, deletions or additions may involve one or more nucleotides. The variants may be altered in coding or non-coding regions or both. Alterations in the coding regions may produce conservative or non-conservative amino acid substitutions, deletions or additions. Preferred are nucleic acid molecules encoding a variant, analog, derivative or fragment, or a variant, analogue or derivative of a fragment, which have a *H. pylori* sequence as set forth in the Sequence Listing, in which several, a few, 5 to 10, 1 to 5, 1 to 3, 2, 1 or no amino acid(s) is substituted, deleted or added, in any combination. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of the *H. pylori* polypeptides set forth in the Sequence Listing. Also especially preferred in this regard are conservative substitutions.

The peptides and fragments according to the present invention also include modified epitopes wherein preferably one or two of the amino acids of a given epitope are modified or replaced according to the rules disclosed in e.g. {Tourdot, S. et al., 2000}, as well as the nucleic acid sequences encoding such modified epitopes.

It is clear that also epitopes derived from the present epitopes by amino acid exchanges improving, conserving or at least not significantly impeding the T cell activating capability of the epitopes are covered by the epitopes according to the present invention. Therefore the present epitopes also cover epitopes, which do not contain the original sequence as derived from *H. pylori*, but trigger the same or preferably an improved T cell response. These epitope are referred to as "heteroclitic"; they need to have a similar or preferably greater affinity to MHC/HLA molecules, and the need the ability to stimulate the T cell receptors (TCR) directed to the original epitope in a similar or preferably stronger manner.

Heteroclitic epitopes can be obtained by rational design i.e. taking into account the contribution of individual residues to binding to MHC/HLA as for instance described by {Rammensee, H. et al., 1999}, combined with a systematic exchange of residues potentially interacting with the TCR and testing the resulting sequences with T cells directed against the original epitope. Such a design is possible for a skilled man in the art without much experimentation.

Another possibility includes the screening of peptide libraries with T cells directed against the original epitope. A preferred way is the positional scanning of synthetic peptide libraries. Such approaches have been described in detail for instance by {Hemmer, B. et al., 1999} and the references given therein.

As an alternative to epitopes represented by the present derived amino acid sequences or heteroclitic epitopes, also substances mimicking these epitopes e.g. "peptidemimetica" or "retro-inverso-peptides" can be applied.

Another aspect of the design of improved epitopes is their formulation or modification with substances increasing their capacity to stimulate T cells. These include T helper cell epitopes, lipids or liposomes or preferred modifications as described in WO 01/78767.

Another way to increase the T cell stimulating capacity of epitopes is their formulation with immune stimulating substances for instance cytokines or chemokines like interleukin-2, -7, -12, -18, class I and II interferons (IFN), especially IFN-gamma, GM-CSF, TNF-alpha, flt3-ligand and others.

As discussed additionally herein regarding nucleic acid molecule assays of the invention, for instance, nucleic acid molecules of the invention as discussed above, may be used as a hybridization probe for RNA, cDNA and genomic DNA to isolate full-length cDNAs and genomic clones encoding polypeptides of the present invention and to isolate cDNA and genomic clones of other genes that have a high sequence similarity to the nucleic acid molecules of the present invention. Such probes generally will comprise at least 15 bases. Preferably, such probes will have at least 20, at least 25 or at least 30 bases, and may have at least 50 bases. Particularly preferred probes will have at least 30 bases, and will have 50 bases or less, such as 30, 35, 40, 45, or 50 bases.

For example, the coding region of a nucleic acid molecule of the present invention may be isolated by screening a relevant library using the known DNA sequence to synthesize an oligonucleotide probe. A labeled oligonucleotide having a sequence complementary to that of a gene of the present invention is then used to screen a library of cDNA, genomic DNA or mRNA to determine to which members of the library the probe hybridizes.

The nucleic acid molecules and polypeptides of the present invention may be employed as reagents and materials for development of treatments of and diagnostics for disease, particularly human disease, as further discussed herein relating to nucleic acid molecule assays, *inter alia*.

The nucleic acid molecules of the present invention that are oligonucleotides can be used in the processes herein as described, but preferably for PCR, to determine whether or not the *H. pylori* genes identified herein in whole or in part are present and/or transcribed in infected tissue such as blood. It is recognized that such sequences will also have utility in diagnosis of the stage of infection and type of infection the pathogen has attained. For this and other purposes the arrays comprising at least one of the nucleic acids according to the present invention as described herein, may be used.

The nucleic acid molecules according to the present invention may be used for the detection of nucleic acid molecules and organisms or samples containing these nucleic acids. Preferably such detection is for diagnosis, more preferable for the diagnosis of a disease related or linked to the present or abundance of *H. pylori*.

Eukaryotes (herein also "individual(s)"), particularly mammals, and especially humans, infected with *H. pylori* may be identifiable by detecting any of the nucleic acid molecules according to the present invention detected at the DNA level by a variety of techniques. Preferred nucleic acid molecules candidates for distinguishing a *H. pylori* from other organisms can be obtained.

The invention provides a process for diagnosing disease, arising from infection with *H. pylori*, comprising determining from a sample isolated or derived from an individual an increased level of expression of a nucleic acid molecule having the sequence of a nucleic acid molecule set forth in the Sequence Listing. Expression of nucleic acid molecules can be measured using any one of the methods well known in the art for the quantitation of nucleic acid molecules, such as, for example, PCR, RT-PCR, Rnase protection, Northern blotting, other hybridisation methods and the arrays described herein.

Isolated as used herein means separated "by the hand of man" from its natural state; i.e., that, if it occurs in nature, it has been changed or removed from its original environment, or both. For example, a naturally occurring nucleic acid molecule or a polypeptide naturally present in a living organism in its natural state is not "isolated," but the same nucleic acid molecule or polypeptide separated from the coexisting materials of its natural state is "isolated", as the term is employed herein. As part of or following isolation, such nucleic acid molecules can be joined to other nucleic acid molecules, such as DNAs, for mutagenesis, to form fusion proteins, and for propagation or expression in a host, for instance. The isolated nucleic acid molecules, alone or joined to other nucleic acid molecules such as vectors, can be introduced into host cells, in culture or in whole organisms. Introduced into host cells in culture or in whole organisms, such DNAs still would be isolated, as the term is used herein, because they would not be in their naturally occurring form or environment. Similarly, the nucleic acid molecules and polypeptides may occur in a composition, such as a media formulations, solutions for introduction of nucleic acid molecules or polypeptides, for example, into cells, compositions or solutions for chemical or enzymatic reactions, for instance, which are not naturally occurring compositions, and, therein remain isolated nucleic acid molecules or polypeptides within the meaning of that term as it is employed herein.

The nucleic acids according to the present invention may be chemically synthesized. Alternatively, the nucleic acids can be isolated from *H. pylori* by methods known to the one skilled in the art.

According to another aspect of the present invention, a comprehensive set of novel hyperimmune serum reactive antigens and fragments thereof are provided by using the herein described antigen identification method. In a preferred embodiment of the invention, a hyperimmune serum-reactive antigen comprising an amino acid sequence being encoded by any one of the nucleic acids molecules herein described and fragments thereof are provided. In another preferred embodiment of the invention a novel set of hyperimmune serum-reactive antigens which comprises amino acid sequences selected from a group consisting of the polypeptide sequences as represented in **Seq ID No** 181-182, 194, 197-199, 206-207, 211-216, 219-220, 222, 226-230, 233, 235-236, 239, 241, 243, 245-246, 250, 252-253, 259, 262, 269, 272, 274-275, 279, 283-286, 290, 293-295, 297, 301-356 and fragments thereof are provided. In a further preferred embodiment of the invention hyperimmune serum-reactive antigens, which comprise amino acid sequences selected from a group consisting of the polypeptide sequences as represented in **Seq ID No** 186-188, 191-193, 195-196, 202, 205, 210, 217-218, 223-225, 234, 237, 240, 247-248, 251, 255, 257, 260, 263-264, 266, 268, 281, 287-288, 292, 299 and fragments thereof are provided. In a still preferred embodiment of the invention hyperimmune serum-reactive antigens which comprise amino acid sequences selected from a group consisting of the polypeptide sequences as represented in **Seq ID No** 183, 185, 208-209, 231, 238, 244, 254, 261, 265, 270, 277, 298 and fragments thereof are provided.

The hyperimmune serum reactive antigens and fragments thereof as provided in the invention include any polypeptide set forth in the Sequence Listing as well as polypeptides which have at least 70% identity to a polypeptide set forth in the Sequence Listing, preferably at least 80% or 85% identity to a polypeptide set forth in the Sequence Listing, and more preferably at least 90% similarity (more preferably at least 90% identity) to a polypeptide set forth in the Sequence Listing and still more preferably at least 95%, 96%, 97%, 98%, 99% or 99.5% similarity (still more preferably at least 95%, 96%, 97%, 98%, 99%, or 99.5% identity) to a polypeptide set forth in the Sequence Listing and also include portions of such polypeptides with such portion of the polypeptide generally containing at least 4 amino acids and more preferably at least 8, still more preferably at least 30, still more preferably at least 50 amino acids, such as 4, 8, 10, 20, 30, 35, 40, 45 or 50 amino acids.

The invention also relates to fragments, analogs, and derivatives of these hyperimmune serum reactive antigens and fragments thereof. The terms "fragment", "derivative" and "analog" when referring to an antigen whose amino acid sequence is set forth in the Sequence Listing, means a polypeptide which retains essentially the same or a similar biological function or activity as such hyperimmune serum reactive antigen and fragment thereof.

The fragment, derivative or analog of a hyperimmune serum reactive antigen and fragment thereof may be 1) one in which one or more of the amino acid residues are substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue) and such substituted amino acid residue may or may not be one encoded by the genetic code, or 2) one in which one or more of the amino acid residues includes a substituent group, or 3) one in which the mature hyperimmune serum reactive antigen or fragment thereof is fused with another compound, such as a compound to increase the half-life of the hyperimmune serum reactive antigen and fragment thereof (for example, polyethylene glycol), or 4) one in which the additional amino acids are fused to the mature hyperimmune serum reactive antigen or fragment thereof, such as a leader or secretory sequence or a sequence which is employed for purification of the mature hyperimmune serum reactive antigen or fragment thereof or a proprotein sequence. Such fragments, derivatives and analogs are deemed to be within the scope of those skilled in the art from the teachings herein.

Among the particularly preferred embodiments of the invention in this regard are the hyperimmune serum reactive antigens set forth in the Sequence Listing, variants, analogs, derivatives and fragments thereof, and variants, analogs and derivatives of fragments. Additionally, fusion polypeptides comprising such hyperimmune serum reactive antigens, variants, analogs, derivatives and fragments thereof, and variants, analogs and derivatives of the fragments are also encompassed by the present invention. Such fusion polypeptides and proteins, as well as nucleic acid molecules encoding them, can readily be made using standard techniques, including standard recombinant techniques for producing and expression of a recombinant polynucleic acid encoding a fusion protein.

Among preferred variants are those that vary from a reference by conservative amino acid substitutions. Such substitutions are those that substitute a given amino acid in a polypeptide by another amino acid of like characteristics. Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile; interchange of the hydroxyl residues Ser and Thr, exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln, exchange of the basic residues Lys and Arg and replacements among the aromatic residues Phe and Tyr.

Further particularly preferred in this regard are variants, analogs, derivatives and fragments, and variants, analogs and derivatives of the fragments, having the amino acid sequence of any polypeptide set forth in the Sequence Listing, in which several, a few, 5 to 10, 1 to 5, 1 to 3, 2, 1 or no amino acid residues are substituted, deleted or added, in any combination. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of the polypeptide of the present invention. Also especially preferred in this regard are conservative substitutions. Most highly preferred are polypeptides having an amino acid sequence set forth in the Sequence Listing without substitutions.

The hyperimmune serum reactive antigens and fragments thereof of the present invention are preferably provided in an isolated form, and preferably are purified to homogeneity.

Also among preferred embodiments of the present invention are polypeptides comprising fragments of the polypeptides having the amino acid sequence set forth in the Sequence Listing, and fragments of variants and derivatives of the polypeptides set forth in the Sequence Listing.

In this regard a fragment is a polypeptide having an amino acid sequence that entirely is the same as part but not all of the amino acid sequence of the afore mentioned hyperimmune serum reactive antigen and fragment thereof, and variants or derivative, analogs, fragments thereof. Such fragments may be "free-standing", i.e., not part of or fused to other amino acids or polypeptides, or they may be comprised within a larger polypeptide of which they form a part or region. Also preferred in this aspect of the

invention are fragments characterised by structural or functional attributes of the polypeptide of the present invention, i.e. fragments that comprise alpha-helix and alpha-helix forming regions, beta-sheet and beta-sheet forming regions, turn and turn-forming regions, coil and coil-forming regions, hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta-amphipathic regions, flexible regions, surface-forming regions, substrate binding regions, and high antigenic index regions of the polypeptide of the present invention, and combinations of such fragments. Preferred regions are those that mediate activities of the hyperimmune serum reactive antigens and fragments thereof of the present invention. Most highly preferred in this regard are fragments that have a chemical, biological or other activity of the hyperimmune serum reactive antigen and fragments thereof of the present invention, including those with a similar activity or an improved activity, or with a decreased undesirable activity. Particularly preferred are fragments comprising receptors or domains of enzymes that confer a function essential for viability of *H. pylori* or the ability to cause disease in humans. Further preferred polypeptide fragments are those that comprise or contain antigenic or immunogenic determinants in an animal, especially in a human.

An antigenic fragment is defined as a fragment of the identified antigen, which is for itself antigenic or may be made antigenic when provided as a hapten. Therefore, also antigens or antigenic fragments showing one or (for longer fragments) only a few amino acid exchanges are enabled with the present invention, provided that the antigenic capacities of such fragments with amino acid exchanges are not severely deteriorated on the exchange(s), i.e., suited for eliciting an appropriate immune response in an individual vaccinated with this antigen and identified by individual antibody preparations from individual sera.

Preferred examples of such fragments of a hyperimmune serum-reactive antigen are selected from the group consisting of peptides comprising amino acid sequences of column "predicted immunogenic aa", and "Location of identified immunogenic region" of Table 1, the serum reactive epitope of Table 3 especially peptides comprising amino acids 63-91, 95-101, 110-116, 134-148, 150-156, 158-164, 188-193, 197-209, 226-241, 247-254, 291-297, 312-319, 338-346, 351-358, 366-378, 404-410, 420-438, 448-454, 465-473, 482-488, 490-498, 503-510, 512-519, 531-543, 547-554, 568-575, 589-604, 610-631 and 239-308 of **Seq ID No** 179; 16-29, 35-47, 50-68, 70-79, 91-101, 143-149, 158-163, 185-191, 196-206, 215-224, 230-237, 244-251, 258-278, 290-311, 319-325, 338-351, 365-385, 396-429, 445-454, 458-466, 491-499, 501-521, 17-79 and 218-233 of **Seq ID No** 180; 4-10, 16-41, 46-66, 77-84, 91-97, 102-118, 125-144, 187-200, 202-214, 245-253, 255-261, 286-295, 300-330, 335-342, 350-361, 363-381, 385-392, 396-416, 435-450 and 460-470 of **Seq ID No** 181; 11-19, 27-48, 52-59, 77-82, 84-107, 118-125, 127-154, 178-183, 192-209, 215-221, 286-295, 302-313, 350-357, 402-415, 417-431, 453-463, 465-493 and 313-331 of **Seq ID No** 182; 19-26, 30-43, 47-55, 63-68, 72-80, 97-104, 107-119, 129-146, 160-175, 194-216, 231-251, 254-260 and 26-43 of **Seq ID No** 183; 7-13, 29-37, 65-81, 110-120, 123-131, 135-152, 230-249, 254-260, 284-290, 292-299, 317-326, 329-336, 403-444, 452-458, 466-477, 490-498, 510-519, 541-550, 557-566 and 533-567 of **Seq ID No** 184; 5-47, 71-77, 79-86, 89-95, 120-126, 137-144, 176-181, 184-196, 202-208, 211-232, 236-282, 301-313, 317-325, 341-347, 353-384, 394-400, 412-433, 436-443 and 59-75 of **Seq ID No** 185; 4-18, 22-38, 59-69, 106-112, 116-130, 138-149, 156-170, 175-197, 200-214, 216-223, 233-244, 255-261, 266-276, 279-286, 325-333, 342-348, 366-399, 402-420, 429-441, 1-104 and 130-147 of **Seq ID No** 186; 50-58, 69-95, 97-113, 131-136, 157-163, 170-175, 188-212, 220-226, 254-259, 265-277, 283-289, 297-308, 311-318, 347-358, 360-369, 378-401, 416-421, 440-450, 454-462, 470-476, 493-502, 506-514, 536-567, 585-590, 598-607, 613-618, 653-659 and 35-46 of **Seq ID No** 187; 16-29, 32-60, 65-87, 89-123, 128-134, 137-158, 162-173, 178-196, 210-216, 218-228 and 206-225 of **Seq ID No** 188; 10-20, 26-35, 51-64, 86-91, 94-100, 113-122, 154-160, 185-191, 193-201, 211-217, 225-230, 237-246, 251-257, 298-304, 306-312, 316-328, 340-348, 357-389, 391-397, 415-421, 449-456, 458-471, 488-495, 502-511, 24-55 and 236-341 of **Seq ID No** 189; 5-22, 41-51, 87-93, 114-122, 127-136, 150-156, 158-166, 223-233, 245-263, 291-296, 9-126 and 127-285 of **Seq ID No** 190; 30-43, 46-56, 61-70, 72-83, 85-93, 103-113, 119-125, 151-166, 179-191, 212-218, 225-231, 236-243, 262-267, 291-307, 331-344, 349-355, 366-372, 380-386, 414-422, 428-447, 459-464, 469-478, 507-519, 525-544, 563-569, 576-590, 620-626, 633-643, 654-659, 665-671, 684-707, 717-723, 725-733, 747-779, 782-801 and 347-361 of **Seq ID No** 191; 4-12, 14-26, 37-80, 107-115, 133-139, 144-150, 154-165, 173-180, 191-199, 205-211, 221-231, 237-244, 254-

284, 307-340, 342-353, 360-368, 370-380, 479-493, 495-503, 509-522, 525-536, 539-547, 554-560, 565-573, 578-583, 7-23 and 465-479 of Seq ID No 192; 4-17, 47-55, 76-83, 85-100, 104-112, 117-123, 126-135, 142-148, 156-167, 174-182, 267-273 and 258-283 of Seq ID No 193; 8-32, 36-42, 65-88, 102-108, 112-140, 147-163, 170-179, 183-193 and 117-124 of Seq ID No 194; 12-18, 45-50, 62-77, 82-95, 99-113, 115-123, 125-147, 155-177, 187-209, 211-223, 244-253, 259-270, 278-297, 302-307, 311-318, 329-334, 350-356, 359-365, 390-400, 402-413 and 333-350 of Seq ID No 195; 4-13, 15-27, 30-46, 53-58, 68-74, 82-95, 115-126, 134-139, 148-153, 159-176, 182-199, 201-217, 220-225, 227-235, 237-248, 253-266, 300-315, 322-336, 390-396, 412-426, 438-445, 448-459, 477-484, 502-508, 515-527, 529-537, 553-568, 643-651, 658-667, 690-703 and 376-400 of Seq ID No 196; 4-10, 24-32, 38-55, 59-67, 70-77, 80-87, 89-97, 123-129, 134-151, 166-172, 178-189, 191-216, 218-235, 245-259, 271-315, 326-339, 341-360 and 73-94 of Seq ID No 197; 13-25, 31-38, 43-57, 79-85, 92-99, 106-112, 117-128, 130-139, 146-158, 160-175, 194-204, 211-222, 225-232, 234-242, 263-270, 278-292, 299-320, 322-333 and 240-256 of Seq ID No 198; 4-17, 55-63, 66-101, 109-131, 135-143, 145-151, 155-161, 164-170, 177-185, 192-198, 213-218, 223-238, 246-256, 258-268, 273-283, 309-314, 322-328 and 195-221 of Seq ID No 199; 13-24, 31-39, 41-50, 63-69, 90-96, 104-109, 116-141, 148-153, 161-167, 173-178, 190-209, 253-258, 265-272, 279-289, 295-312, 317-343, 355-366, 376-389, 400-407, 430-451, 453-464, 466-472, 487-493, 499-505, 523-538, 554-559, 568-579, 584-601 and 344-363 of Seq ID No 200; 5-22, 30-36, 53-59, 61-70, 82-92, 99-106, 120-131, 135-148, 154-167, 169-183, 187-199, 204-212, 231-247 and 111-249 of Seq ID No 201; 17-36, 40-66, 71-144, 148-171, 173-191, 199-214, 220-252, 265-272, 278-288, 298-333, 342-385 and 287-307 of Seq ID No 202; 4-16, 22-28, 30-36, 42-48, 95-116, 154-162, 164-174, 239-252, 258-263, 273-285, 306-313, 323-333, 341-357, 363-369, 372-379, 395-401, 430-436, 438-453, 464-480, 33-44, 233-258 and 349-369 of Seq ID No 203; 4-21, 30-37, 46-53, 59-68, 80-92, 98-104, 118-143, 150-160, 165-185, 187-200, 204-211, 224-236, 241-246, 252-258, 271-280, 288-294, 311-320, 335-341 and 191-350 of Seq ID No 204; 4-16, 37-59, 64-70, 79-87, 93-102, 107-127, 143-165, 172-188, 197-204, 207-218, 221-227, 242-248, 258-277, 289-296, 298-316, 332-338, 344-365, 367-373, 375-382, 400-408, 415-425, 438-446 and 235-250 of Seq ID No 205; 4-37, 39-66, 84-98, 101-127, 140-149, 157-163, 166-172, 175-182, 184-193, 203-208, 215-232, 234-247, 250-299, 303-345 and 183-204 of Seq ID No 206; 10-20, 41-61, 73-87, 112-141, 176-192, 194-201, 205-222, 230-237, 257-264, 276-282, 284-310, 312-318, 330-337, 349-357 and 304-328 of Seq ID No 207; 4-31, 42-103, 105-113, 121-153, 160-181, 188-196, 210-226, 231-264, 272-287, 297-304, 328-336 and 304-318 of Seq ID No 208; 21-43, 46-52, 54-70, 72-79, 94-107, 133-141, 160-166, 217-253, 311-317, 359-365, 374-381, 390-395, 434-440, 488-494, 497-502, 511-522, 554-563, 565-574, 577-585, 591-598, 601-606, 617-625, 633-643, 658-664, 676-682, 694-702, 710-719, 754-760, 782-788, 802-808, 916-921, 942-948, 955-964, 973-979, 992-998, 1006-1011, 1016-1023, 1030-1038, 1046-1053, 1059-1066, 1088-1098, 1119-1126, 1129-1135, 1156-1171, 1173-1181, 1202-1210, 1255-1261, 1268-1280, 1295-1310, 1312-1320, 1375-1381, 1406-1417, 1450-1471, 1478-1492, 1498-1506, 1569-1578, 1603-1608, 1611-1624, 1648-1655, 1663-1670, 1680-1698, 1702-1707, 1713-1719, 1737-1742, 1747-1753, 1762-1769, 1771-1785, 1790-1804, 1811-1818, 1830-1836, 1838-1852, 1874-1886, 1893-1899, 1902-1909, 1942-1948, 1952-1962, 1980-1986, 2001-2017, 2020-2028, 2042-2050, 2052-2068, 2074-2079, 2083-2095, 2107-2113, 2147-2155, 2177-2194, 2203-2211, 2236-2241, 2251-2258, 2267-2274, 2285-2292, 2314-2328, 2330-2340, 2358-2365, 2390-2401, 2408-2418, 2432-2453, 2463-2476, 2486-2507, 2528-2537, 2540-2548, 2552-2558, 2568-2576, 2596-2601, 2610-2622, 2629-2638, 2653-2669, 2718-2727, 2749-2767, 2777-2784, 2789-2795, 2806-2815, 2817-2824, 2835-2843, 2847-2854, 2860-2881, 511-523, 612-630 and 1790-1803 of Seq ID No 209; 4-54, 61-68, 72-82, 86-93, 100-108, 115-130, 147-154, 187-194, 196-207, 224-229, 236-251, 275-287 and 96-109 of Seq ID No 210; 31-39, 62-69, 91-101, 158-172, 175-180, 186-193, 201-208, 210-223, 243-250, 273-286, 293-299, 319-325, 343-354, 356-365, 368-384, 414-435, 471-491, 512-518, 550-556, 567-581, 584-589, 633-639, 680-692, 697-708, 716-721, 747-754, 779-786, 810-816 and 366-503 of Seq ID No 211; 5-20, 22-48, 57-65, 96-101, 111-122, 130-145, 154-164, 170-181, 193-199, 201-216, 224-241, 244-262, 281-323, 342-351, 359-367, 369-396, 406-416, 424-433, 450-456, 485-491, 493-499, 501-515, 517-535 and 289-305 of Seq ID No 212; 4-17, 22-44, 53-60, 66-83, 87-94, 101-106, 110-116, 131-137, 148-183, 189-207, 209-215, 233-242, 251-262, 264-272, 290-296, 308-327, 359-373, 375-380, 397-405, 415-420, 426-433, 444-475, 478-484, 529-536, 548-558 and 106-126 of Seq ID No 213; 4-38, 42-50, 58-64, 72-81, 92-118, 140-146, 157-165, 172-192, 198-204, 208-216, 227-234, 238-258, 271-278, 288-293, 311-322, 327-346, 357-370, 375-383, 395-409, 411-417, 425-432, 436-445, 109-129 and 370-380 of Seq ID No 214; 23-30, 36-49, 52-64, 86-94, 97-104, 121-129, 257-272, 279-286, 288-294, 307-327, 334-340, 369-375, 377-386, 406-412, 418-423, 430-438, 441-447, 459-465, 469-476, 482-488, 510-546, 550-580, 584-622, 638-645, 653-659, 675-683, 692-705, 723-731, 752-761, 788-795 and 54-72 of Seq ID No 215; 11-33,

36-46, 88-104, 116-126, 134-170, 189-195, 199-217, 225-250, 255-261, 266-273, 280-291, 296-313, 334-341, 343-349, 354-360, 362-369, 373-380, 387-401, 406-420 and 259-273 of Seq ID No 216; 9-14, 28-44, 57-64, 72-79, 86-93, 104-111, 116-126, 142-150, 159-164 and 61-86 of Seq ID No 217; 10-17, 26-33, 43-61, 69-95, 101-107, 109-125, 129-135, 137-144, 147-153, 158-169, 177-187, 209-219, 221-232, 235-247, 261-268, 271-282, 296-302, 306-347, 355-362, 364-379, 386-399, 409-418, 424-442, 451-460, 467-479, 490-498 and 60-74 of Seq ID No 218; 8-14, 20-31, 65-84, 94-99, 154-179, 193-207, 238-253 and 96-118 of Seq ID No 219; 4-24, 30-44, 47-62, 84-93, 108-116, 124-133, 136-141, 201-209, 217-223, 228-235, 238-245, 247-270, 275-285, 290-314, 328-338, 342-349, 353-365, 375-383, 386-392, 394-402, 417-427, 443-459, 465-481, 492-514, 516-524, 550-566, 602-617, 630-639, 666-676, 687-693, 719-730, 747-753, 783-790, 799-816, 824-831, 837-842 and 167-189 of Seq ID No 220; 6-15, 18-28, 58-66, 84-101, 106-129, 136-151, 154-165, 182-203, 205-211, 214-220, 222-228, 233-240, 251-260, 270-277, 284-291, 306-315, 322-328, 363-369, 378-388, 392-405, 443-452, 495-501, 512-523, 574-583 and 362-375 of Seq ID No 221; 5-25, 27-34, 47-59, 64-70, 76-86, 145-158, 166-183, 189-202, 217-231, 235-242, 260-270, 278-309 and 1-102 of Seq ID No 222; 4-19, 24-76, 78-83, 90-99, 102-109, 114-122, 137-147, 154-174, 177-188, 203-212, 217-223, 227-239 and 226-325 of Seq ID No 223; 7-37, 71-90, 94-109, 117-128, 141-153, 179-192, 199-206, 225-231, 237-243, 258-264 and 40-51 of Seq ID No224; 13-19, 25-30, 46-59, 75-91, 101-107, 114-124, 129-135, 137-145, 160-167, 171-179, 187-194, 209-215, 217-222, 229-239, 243-249, 257-265, 269-275, 299-308, 310-327 and 282-300 of Seq ID No 225; 86-100, 216-230, 342-369, 382-388, 424-430, 438-445, 452-458, 488-494, 501-518, 554-560, 568-574, 584-592, 603-609, 611-629, 639-645, 652-661, 669-699, 708-714, 726-738, 747-753, 763-775, 785-791, 794-807, 815-824, 826-845, 854-860, 863-868, 870-883, 892-898, 901-906, 909-921, 930-937, 946-959, 968-974, 977-990, 998-1007, 1009-1027, 1037-1043, 1046-1051, 1053-1066, 1075-1081, 1084-1089, 1092-1103, 1113-1119, 1122-1135, 1143-1152, 1154-1172, 1182-1188, 1191-1196, 1200-1210, 1220-1226, 1229-1235, 1237-1249, 1259-1265, 1268-1281, 1289-1298, 1305-1318, 1328-1334, 1337-1343, 1345-1357, 1367-1373, 1390-1396, 1405-1411, 1418-1423, 1426-1435, 1445-1455, 1474-1483, 1493-1500, 1505-1512, 1517-1524, 1538-1544, 1568-1578, 1595-1601, 1674-1682, 1687-1720, 1728-1736, 1738-1744, 1754-1761, 1764-1774, 1798-1824, 1836-1842, 1886-1893, 1895-1903, 366-781, 782-1518 and 1731-1747 of Seq ID No 226; 4-17, 20-39, 46-55, 60-66, 102-110, 114-122, 125-131, 161-167, 172-178, 185-190, 195-202, 218-232, 236-252, 264-291, 293-302, 309-315, 324-339 and 169-381 of Seq ID No 227; 5-10, 13-40, 42-53, 69-75, 83-89, 120-135, 150-161, 174-190, 203-225, 229-247, 257-287, 318-348 and 30-200 of Seq ID No 228; 7-19, 43-53, 64-72, 124-139, 52-84 and 120-131 of Seq ID No 229; 12-19, 39-48, 58-100, 117-123, 154-162, 164-187, 189-195, 202-216, 218-235, 241-246, 262-278, 315-328, 333-347, 354-366, 372-379, 391-405, 422-429, 431-442, 444-450, 458-466, 478-485, 494-501, 504-510, 520-535, 573-580, 589-598, 615-625, 666-676, 686-698, 722-729, 737-746, 756-767, 787-796, 805-816, 824-829, 833-848, 856-864, 866-876, 879-886, 898-904, 918-924, 927-934, 941-960, 967-978 and 561-575 of Seq ID No 230; 11-29, 49-55, 70-77, 84-100, 102-112, 148-155, 160-177, 181-204 and 1-104 of Seq ID No 231; 27-44, 64-71, 122-133, 151-156, 164-178, 214-220, 226-232, 235-244, 253-262, 282-288, 294-310, 317-325, 350-356, 362-368, 376-383, 438-443, 449-454, 459-464, 492-498, 500-511, 529-535, 538-546, 567-573, 597-603, 660-665, 674-679, 724-734, 763-769, 773-784, 791-801, 807-815, 821-826, 840-848, 863-868, 897-902, 908-928, 932-953, 956-975, 980-987, 990-996, 1012-1018, 1042-1063, 1095-1116, 1149-1157, 1160-1167, 110-357, 358-501 and 502-1161 of Seq ID No 232; 4-21, 64-71, 73-84, 128-138, 144-162, 203-217, 240-263, 288-298, 300-308, 310-317, 325-351, 369-380, 391-411 and 330-345 of Seq ID No 233; 5-11, 25-31, 39-48, 51-79, 89-98, 100-122, 135-148, 166-201, 203-227, 230-250, 254-260, 266-272, 274-282, 299-305, 328-337 and 31-45 of Seq ID No 234; 12-23, 29-48, 51-60, 66-72, 75-81, 83-93, 103-115, 133-148, 168-174, 195-204, 222-229, 231-240, 242-251, 270-280, 286-305, 322-344, 349-360, 364-370, 378-400, 421-441, 448-484, 486-493, 495-501, 504-534, 547-561, 567-590, 597-607, 621-635, 643-649, 658-685, 688-694, 702-711, 717-731, 737-742, 759-765, 767-772, 776-786, 803-809, 815-825, 854-908, 910-919, 923-930, 942-948, 961-975, 994-1014 and 915-940 of Seq ID No 235; 4-9, 32-47, 51-61, 75-96, 139-191 and 1-124 of Seq ID No 236; 4-13, 17-38, 43-49, 55-76, 88-95, 110-121, 128-146, 151-157, 162-214, 222-240, 243-249, 251-273, 275-281, 292-298, 300-309, 312-320, 322-331, 355-369, 376-408, 446-460, 471-482, 485-509 and 191-203 of Seq ID No 237; 4-21, 72-82, 89-103, 106-115, 118-124, 140-146, 174-184, 191-200, 204-213, 218-224, 261-266, 282-293, 299-309, 311-340, 342-358, 362-372, 381-389, 391-402, 413-421, 438-447, 457-464, 470-478, 501-507, 545-560, 578-624, 631-641, 658-670, 680-689, 717-738, 753-759, 795-805, 816-822, 830-838, 842-848, 869-881, 892-898, 33-51 and 818-835 of Seq ID No 238; 4-21, 79-85, 156-177, 183-188, 206-214, 243-249, 261-269, 287-292, 315-322, 334-345, 360-366, 374-390, 402-411, 37-97 and 260-399 of Seq ID No 239; 4-9, 19-54, 58-78, 97-104, 111-120, 126-134, 137-145, 163-173, 178-188, 193-203, 211-224, 246-286, 288-

324, 337-346, 355-362, 374-390, 392-398, 409-417 and 240-249 of Seq ID No 240; 5-12, 14-31, 35-41, 43-61, 82-92, 97-105, 134-145, 155-166, 184-203, 215-223, 225-251, 272-279, 281-306, 310-345, 358-418, 435-473, 482-490, 525-532, 538-547, 549-563, 578-604, 613-639 and 144-154 of Seq ID No 241; 53-59, 64-72, 74-100, 133-152, 154-172, 176-181, 207-214, 225-238, 275-297, 304-310, 331-340, 362-367, 384-395, 403-410, 437-443, 448-456, 482-490, 579-597, 602-610, 625-630, 633-651, 699-707, 709-715, 734-743, 750-762 and 544-685 of Seq ID No 242; 12-18, 22-40, 45-83, 89-97, 103-109, 147-153, 159-173, 195-204, 210-219, 243-253, 259-265, 273-282, 303-309, 315-325, 332-340, 346-358, 362-367, 377-390, 393-402, 418-426, 447-455, 467-480, 505-512, 514-525, 548-561, 566-576, 584-596, 619-626, 638-645, 649-659, 661-680, 699-708, 714-720, 753-759, 766-772, 775-781, 801-808, 202-218, 282-299, 339-350 and 617-628 of Seq ID No 243; 5-33, 52-62, 87-101, 111-135, 137-143, 145-152, 190-202, 209-221, 233-245, 253-270 and 151-215 of Seq ID No 244; 19-29, 32-39, 42-48, 75-94, 124-135, 137-145, 152-160, 176-182, 193-203, 215-236, 266-273, 275-291, 297-306, 311-319, 322-342, 348-360, 369-378, 394-401 and 48-64 of Seq ID No 245; 4-11, 13-33, 36-43, 53-63, 65-80, 112-129, 134-141, 143-155, 157-168, 178-188, 191-199, 201-207, 215-229, 242-255, 263-270, 283-315, 320-329, 333-338, 340-349, 412-426, 465-478, 485-490, 498-512, 540-554 and 390-516 of Seq ID No 246; 4-18, 23-32, 41-47, 54-70, 88-99, 104-111, 118-138, 143-148, 150-162, 168-175, 181-188, 203-211, 214-220, 227-245, 251-268, 275-281, 287-296, 323-333 and 1-90 of Seq ID No 247; 8-34, 38-49, 72-83, 85-91, 94-104, 112-125, 134-142, 148-168, 181-189, 191-198, 202-214, 222-233, 242-254, 256-262, 273-278, 287-294, 314-325 and 141-159 of Seq ID No 248; 4-24, 30-36, 47-75, 82-105, 124-134, 151-157, 192-202, 208-214, 219-226, 234-247, 285-290, 318-324, 332-340, 343-349, 380-386, 453-462, 472-478, 484-501, 531-540, 550-557, 604-612, 620-625, 642-648, 652-671, 64-84, 93-180 and 181-446 of Seq ID No 249; 12-18, 24-32, 68-75, 77-83, 96-101, 109-116, 129-136, 152-164, 175-184, 190-199, 206-215, 224-233, 241-250, 258-264, 273-292, 302-312, 319-331, 334-346, 348-368, 387-395, 408-416, 420-429, 437-452 and 364-374 of Seq ID No 250; 11-28, 36-52, 60-67, 74-79, 108-116 and 61-76 of Seq ID No 251; 20-27, 38-49, 69-74, 84-107, 138-145, 161-168, 179-195, 210-226, 228-252, 267-281, 283-296, 305-311, 333-340, 342-356, 361-372, 380-399, 401-414, 458-466, 475-481, 492-507, 515-520 and 146-160 of Seq ID No 252; 43-61, 68-74, 76-90, 120-128, 130-149, 156-161, 164-182, 206-234, 242-252, 269-274, 291-304, 332-345, 349-355, 360-371, 374-388, 434-440, 447-453, 459-465, 469-496, 504-522 and 261-285 of Seq ID No 253; 4-17, 24-30, 37-49, 87-98, 118-124, 126-136, 144-171, 176-188, 206-214, 216-228, 233-240, 246-252, 262-271, 277-297, 307-330, 333-342, 346-352, 355-361, 368-386, 391-400, 413-420, 474-480 and 401-427 of Seq ID No 254; 15-26, 31-46, 51-72, 80-93, 96-109, 131-137, 150-158, 179-185, 189-209, 211-219, 221-234, 241-247, 255-262, 265-271, 283-288 and 173-190 of Seq ID No 255; 28-37, 39-45, 51-58, 77-84, 89-97, 132-148, 171-180, 199-205, 212-218, 220-226, 257-265, 273-300, 307-327, 334-340, 344-365, 385-390, 402-408, 426-436, 450-468, 476-485 and 425-497 of Seq ID No 256; 4-25, 70-76, 80-88, 90-100, 120-128, 162-169, 183-203, 261-277, 279-289, 291-297, 302-308, 321-327, 339-353, 358-377, 392-401, 404-410, 414-422, 443-450, 456-461, 470-488, 490-497, 510-535, 570-611, 618-630, 639-647, 649-660, 668-690, 702-716, 718-724, 737-747, 750-764 and 497-509 of Seq ID No 257; 12-48, 50-64, 99-108, 216-223, 235-241, 244-254, 262-274, 287-293, 310-316, 320-326, 361-366, 377-383, 390-395, 408-414, 418-425, 438-444, 462-469, 494-505, 524-530, 536-547, 551-566, 592-598, 601-613, 678-685, 687-695, 709-717, 727-737, 751-757, 760-765, 772-778, 782-788, 801-807, 822-830, 859-868, 870-878, 884-890, 898-903, 909-919, 953-969, 973-980, 990-1000, 1002-1019, 1041-1047, 1059-1065, 1090-1095, 1116-1127, 1130-1139, 1143-1149, 1151-1168, 1178-1183, 1188-1195, 1197-1209, 1213-1220, 1226-1234, 1236-1247, 1255-1274, 1276-1282, 76-100, 270-284, 309-438, 493-505, 786-942 and 947-967 of Seq ID No 258; 4-9, 24-34, 46-95, 97-109, 119-130 and 138-156 of Seq ID No 259; 9-26, 28-35, 43-53, 55-68, 83-92, 99-105, 110-135, 139-149, 157-162, 164-170, 173-183, 193-208, 210-230, 239-245, 253-259, 263-271, 293-305, 310-320, 322-331, 336-343, 351-364, 367-376, 92-107 and 154-173 of Seq ID No 260; 19-39, 52-62, 108-117, 145-152, 160-168, 194-203, 229-240, 252-268, 280-287, 308-316, 333-339, 383-390, 403-412, 414-424, 438-445, 464-472, 479-484, 489-505, 510-526 and 247-260 of Seq ID No 261; 5-17, 25-52, 60-77, 105-113, 118-125, 162-167, 228-234, 272-279, 328-334, 341-357, 381-395, 400-406, 512-518, 557-569, 586-592, 645-651, 690-695, 701-709, 720-726, 733-743, 751-758, 781-786, 879-886, 929-934, 939-944, 952-960, 965-975, 994-1001, 1039-1045, 1102-1109, 1164-1181, 1198-1206, 1223-1229, 1253-1259, 1283-1292, 1312-1317, 1339-1349, 1360-1370, 1389-1398, 1400-1412, 1452-1465, 1470-1484, 1490-1497, 1519-1525, 1554-1564, 1578-1591, 1623-1636, 1638-1646, 1669-1679, 1685-1697, 1704-1711, 1713-1720, 1730-1736, 1738-1749, 1756-1764, 1778-1786, 1796-1803, 1817-1826, 1849-1866, 1975-1993, 2017-2032, 2044-2053, 2070-2086, 2091-2109, 2116-2127, 2156-2167, 2182-2188, 2197-2202, 2244-2252, 2281-2287, 2290-2307, 2350-2361, 2383-2404, 2425-2433, 2445-2455, 2495-2505 and 394-549 of Seq ID No 262; 9-24, 31-53, 57-67, 69-79, 84-114,

133-141, 144-172, 178-186 and 13-46 of Seq ID No 263; 4-25, 27-35, 43-52, 59-70, 79-91, 115-130, 136-152, 154-163, 170-179 and 1-58 of Seq ID No 264; 4-30, 49-55, 71-80, 96-105, 111-126, 139-146, 149-162, 239-245, 279-285, 290-296, 300-307, 331-337, 343-350 and 250-351 of Seq ID No 265; 9-27, 34-41, 43-51, 92-111, 114-120, 123-131, 139-150, 156-171, 176-186, 188-204, 229-241, 252-258, 266-279, 288-297, 319-334, 338-348, 373-379, 389-398, 431-439, 479-484 and 214-398 of Seq ID No 266; 4-15, 18-27, 47-52, 68-83, 91-97, 104-110, 115-121, 139-147, 157-164, 198-206, 227-236, 241-254, 264-273, 278-289, 311-320, 353-361, 372-383, 405-420, 426-434 and 232-386 of Seq ID No 267; 4-10, 24-34, 91-97, 129-141, 156-163, 184-190, 205-219, 229-235, 256-273, 278-285 and 93-116 of Seq ID No 268; 7-29, 35-54, 71-83, 85-91, 104-111, 122-134, 138-144, 146-154, 158-174, 177-183, 186-201, 207-215, 223-235, 240-247, 262-273, 275-283, 287-292 and 48-66 of Seq ID No 269; 7-27, 31-47, 49-70, 75-102, 110-149, 157-171, 217-223, 235-251, 294-302, 358-364, 367-375, 387-393, 395-412, 423-430, 441-451, 456-470, 472-486, 488-495, 499-509, 515-529, 536-549, 556-570, 574-603, 607-615, 625-633, 642-658, 670-676, 683-702, 708-716, 720-726, 747-756, 763-784, 803-812, 815-826 and 475-490 of Seq ID No 270; 7-22, 30-38, 53-59, 64-75, 83-95, 97-112, 120-131, 133-142, 145-151, 154-166, 172-180, 189-203, 227-238, 277-287, 9-156 and 174-287 of Seq ID No 271; 13-23, 25-32, 111-117, 150-164, 185-193, 207-212, 216-224, 230-236, 263-272, 304-311, 342-348, 374-385, 391-407, 444-458, 480-487, 489-499, 523-542, 544-558, 572-579, 620-640, 686-696, 703-710, 742-755, 765-772, 817-822, 830-837, 865-872, 931-937 and 66-86 of Seq ID No 272; 4-27, 49-56, 62-70, 86-92, 121-127, 151-163, 170-182, 195-202, 212-226, 237-243 and 234-254 of Seq ID No 273; 4-10, 13-24, 39-51, 62-78, 92-104, 107-117, 134-141, 156-161, 166-181, 210-216, 222-229, 256-266, 273-280, 297-304, 313-330, 336-349, 371-376, 433-439, 443-448, 488-493, 506-515, 527-534, 560-572, 575-583, 587-593 and 252-483 of Seq ID No 274; 4-15, 21-38, 45-56, 81-95, 102-108, 118-130, 133-147, 152-162, 166-171, 199-204, 211-218, 230-240, 253-261, 274-283, 288-294, 312-317, 325-336, 344-357, 391-414 and 24-146 of Seq ID No 275; 26-31, 38-56, 65-82, 90-101, 112-119, 123-153, 175-188, 197-216, 234-242, 249-265, 273-286, 290-305, 327-335, 338-346, 361-372, 394-404 and 290-306 of Seq ID No 276; 17-26, 43-48, 50-73, 81-93, 95-107, 139-146, 158-168, 171-176, 190-196, 202-212, 216-223, 243-266, 274-282, 308-313, 324-330, 344-378, 380-387, 403-422, 427-443, 448-455, 457-465, 491-515, 517-528, 553-567, 589-599, 610-617, 642-648, 670-697, 709-717, 726-743, 745-759, 769-803, 807-823, 840-849 and 820-851 of Seq ID No 277; 4-18, 39-48, 53-63, 66-90, 102-117, 125-134, 137-145, 156-162, 169-197, 26-40 and 56-80 of Seq ID No 278; 21-33, 36-42, 49-60, 68-76, 91-105, 123-130, 141-161, 169-178, 185-190, 192-199, 205-214, 223-233, 239-247, 260-269, 284-293, 300-314, 324-352, 357-364, 373-382, 389-403, 420-432, 438-446, 466-471, 477-484, 503-509, 549-556, 558-576, 600-623, 625-635, 654-661, 663-669, 671-687, 702-716, 735-741, 744-750, 757-766, 776-786, 807-815, 824-832, 854-860, 863-897, 909-915, 920-946, 952-959, 982-997, 1024-1038, 1049-1055, 1071-1085, 1104-1113, 1121-1132, 1138-1150, 1187-1196, 1212-1221, 1227-1236, 1257-1262, 1264-1278, 1282-1294, 1307-1318, 1353-1370, 1382-1388, 1396-1409, 1434-1440, 1446-1454, 1465-1478, 1485-1513, 1516-1529, 1540-1545, 1563-1568, 1575-1593, 1607-1616, 1628-1645, 1648-1661, 1676-1682, 1689-1697, 1713-1719, 1739-1749, 1753-1758, 1763-1774, 1797-1803, 1807-1846, 1855-1874, 1877-1891, 1893-1907, 1912-1925, 1931-1943, 1955-1965, 1976-1990, 2032-2043, 2045-2051, 2099-2105, 2131-2138, 2161-2179, 2188-2199, 2205-2216, 2219-2227, 2235-2245, 2247-2267, 2277-2288, 2294-2304, 2314-2326, 2346-2358, 2365-2377, 2383-2402, 2407-2423, 2437-2450, 2454-2473, 2489-2497, 2525-2531, 2557-2570, 2580-2587, 2589-2599, 2621-2641, 2647-2653, 2661-2677, 2685-2690, 2697-2717, 2722-2733, 2739-2777, 2786-2793, 2801-2808, 2811-2822, 2825-2835, 2838-2845, 2859-2871, 2877-2883, 213-344, 954-1080 and 2524-2733 of Seq ID No 279; 10-16, 18-23, 28-41, 63-69, 77-91, 101-109, 118-136, 146-153, 155-162, 168-179, 192-207, 217-226, 229-235, 239-254, 279-286, 294-307, 313-319, 334-341, 344-353, 363-377, 390-396 and 178-328 of Seq ID No 280; 18-42, 68-84, 89-95, 100-105, 107-115, 125-135, 154-177, 189-195, 205-228, 236-243, 252-259, 279-300, 309-316, 323-331, 340-351, 353-364, 377-402 and 85-97 of Seq ID No 281; 4-18, 26-32, 66-76, 100-126, 151-159, 178-186, 188-194, 200-210, 241-248, 253-259, 262-279, 284-291, 307-313, 315-322, 327-337, 376-386, 399-407, 432-441, 467-473, 487-497, 499-505, 543-549, 560-568, 585-593, 598-604, 608-614, 630-642, 647-653, 690-703, 717-730, 21-200 and 468-480 of Seq ID No 282; 17-49, 52-58, 62-73, 78-97, 100-117, 122-172, 185-190, 193-217, 225-236 and 33-42 of Seq ID No 283; 7-39, 50-58, 73-89, 96-107, 109-120, 126-142, 152-170, 178-202, 205-211, 224-244, 249-259, 261-270, 300-310, 312-325 and 158-169 of Seq ID No 284; 4-31, 40-64, 71-82, 85-92, 102-124, 126-139, 147-152, 159-173, 176-188, 195-207, 210-216, 234-241, 249-256, 258-276, 279-293, 296-302, 310-315, 349-356, 363-378, 380-403, 411-426, 435-441, 448-459, 463-476, 488-494 and 201-221 of Seq ID No 285; 5-13, 15-74, 87-104, 107-120, 123-129, 136-145, 150-191, 193-206, 227-248, 250-264, 278-302, 304-323, 332-378, 384-407, 409-419, 425-457, 462-471, 474-497, 511-545, 555-564, 571-578, 585-598, 640-647,

669-675, 682-691, 693-705, 729-743, 752-761, 772-780, 786-804, 808-818, 822-846, 858-880, 884-900, 910-939, 941-947, 962-971, 973-988, 998-1003, 1007-1027 and 236-259 of Seq ID No 286; 4-19, 27-68, 81-111, 121-160 and 60-79 of Seq ID No 287; 4-37, 40-46, 52-57, 199-205, 222-229, 236-244, 250-267, 269-282 and 27-197 of Seq ID No 288; 4-16, 24-30, 32-38, 63-75, 86-92, 98-111, 113-126, 160-165, 170-180, 198-204, 227-233, 239-245, 253-273, 308-314, 352-365, 382-387, 395-403, 423-429, 472-482, 484-493, 501-507, 518-526, 536-541, 543-550, 556-562, 586-600, 626-633, 649-661, 680-688 and 546-559 of Seq ID No 289; 16-33, 48-59, 63-71, 77-92, 94-109, 117-124, 139-151, 169-181, 184-227, 233-249, 251-261, 263-275, 282-294, 297-321, 326-332, 341-355, 383-399 and 258-272 of Seq ID No 290; 11-26, 31-39, 43-52, 55-62, 64-70, 80-94, 123-133, 135-141, 172-181, 185-206, 209-218, 224-230, 238-244, 251-262, 264-271, 290-301, 306-324, 333-340, 350-357, 367-375, 390-397, 434-441, 443-448, 77-226 and 350-429 of Seq ID No 291; 4-13, 22-27, 31-45, 50-59, 72-96, 99-114, 131-141, 143-150, 159-176, 180-186, 189-198, 208-214, 234-253, 271-287, 294-299, 310-366, 382-390, 398-416, 424-443 and 283-305 of Seq ID No 292; 9-26, 30-53, 62-72, 86-95, 112-122, 136-145, 153-160, 209-221, 227-237, 241-268, 281-288, 291-298, 308-314, 321-328, 336-346, 351-379, 388-397, 409-416, 423-433, 443-481, 511-519 and 213-232 of Seq ID No 293; 12-18, 25-31, 38-50, 59-67, 71-82, 96-126 and 76-88 of Seq ID No 294; 4-25, 39-44, 64-71, 74-88, 100-113, 128-138, 151-162, 164-177, 185-190, 204-213, 233-239, 246-254, 281-286, 293-306, 309-318, 333-347, 349-359, 385-398, 404-423, 458-465, 477-484, 490-499, 501-533, 554-566, 582-590, 596-616, 624-629, 631-639, 654-680, 694-720, 735-743 and 2-100 of Seq ID No 295; 4-16, 36-41, 52-75, 98-107, 109-117, 122-128, 133-139, 141-155, 159-165, 169-182, 187-193, 195-201, 211-224, 230-236, 247-269, 278-290 and 75-92 of Seq ID No 296; 7-21, 25-33, 37-43, 87-94, 103-120, 131-147, 168-174, 197-203, 207-212, 227-237, 247-257, 263-271, 279-287, 298-306, 320-325, 332-340, 363-374, 379-384, 390-401, 403-414, 428-433, 448-457, 462-475, 483-490, 513-519, 525-535, 543-554, 559-566, 571-620, 625-631, 636-642, 659-670, 688-706, 708-723, 770-779, 787-793, 796-807, 820-840, 848-854, 863-874, 895-905, 912-919, 934-942, 968-975, 983-1000, 1012-1019, 1026-1036, 1050-1060, 1064-1070, 1081-1091, 1094-1108, 1112-1118, 1140-1152, 1164-1169, 1172-1180, 1187-1192 and 732-748 of Seq ID No 297; 23-40, 42-59, 66-73, 78-97, 111-128, 130-141, 157-166, 178-183 and 53-71 of Seq ID No 298; 4-27, 38-44, 47-57, 59-85, 99-106, 114-121, 154-166, 181-186, 193-198, 238-244, 253-262, 272-278, 287-299, 314-320, 338-350, 358-368, 382-388, 407-416, 433-446, 456-461, 463-473 and 86-195 of Seq ID No 299; 5-24, 38-59, 64-80, 87-99, 105-126, 134-142, 149-163, 165-179, 181-202, 205-220, 227-233, 243-250, 257-263 and 87-245 of Seq ID No 300; 5-32, 47-53, 66-79, 81-97, 115-151, 155-174, 183-188, 196-210, 215-226, 230-238, 253-258, 263-270, 276-282, 295-301, 304-325, 334-344, 360-390, 397-412, 425-432, 434-462, 478-494, 508-526, 539-564, 571-579, 347-371 and 375-386 of Seq ID No 301; 4-15, 36-44, 49-56, 60-66, 68-82, 84-103, 109-115, 118-141, 147-154, 160-168, 176-185 and 26-39 of Seq ID No 302; 7-13, 23-33 and 13-21 of Seq ID No 303; 2-10 of Seq ID No 304; 4-9, 12-18, 35-42, 49-62 and 6-18 of Seq ID No 305; 19-25 and 1-13 of Seq ID No 306; 15-21, 27-45 and 12-25 of Seq ID No 307; 14-20 and 1-14 of Seq ID No 308; 4-18 and 13-26 of Seq ID No 309; 8-21 and 2-20 of Seq ID No 310; 4-14 and 4-16 of Seq ID No 311; 3-12 of Seq ID No 312; 6-14, 6-25, 35-57 and 2-14 of Seq ID No 313; 6-25, 35-57 and 17-31 of Seq ID No 314; 14-25, 32-46 and 5-19 of Seq ID No 315; 18-31 and 5-16 of Seq ID No 316; 19-24 and 4-26 of Seq ID No 317; 13-21, 29-34, 47-58, 61-73 and 36-47 of Seq ID No 318; 4-15 and 5-24 of Seq ID No 319; 6-18 of Seq ID No 320; 13-20 and 4-13 of Seq ID No 321; 15-23 of Seq ID No 322; 4-9 and 7-21 of Seq ID No 323; 1-10 of Seq ID No 324; 4-14 of Seq ID No 325; 4-17, 35-41, 46-89, 93-98 and 70-88 of Seq ID No 326; 1-13 of Seq ID No 327; 4-16, 26-32 and 25-38 of Seq ID No 328; 8-15, 23-28 and 4-17 of Seq ID No 329; 4-12 and 1-15 of Seq ID No 330; 4-29, 31-42, 52-58 and 6-16 of Seq ID No 331; 4-9, 24-32 and 9-19 of Seq ID No 332; 4-12, 18-27 and 5-18 of Seq ID No 333; 4-11, 37-56, 58-92 and 18-29 of Seq ID No 334; 8-28 and 20-35 of Seq ID No 335; 4-15 of Seq ID No 336; 4-23, 27-39, 55-63 and 35-58 of Seq ID No 337; 6-26, 28-54 and 28-47 of Seq ID No 338; 4-10, 38-52, 58-82 and 30-49 of Seq ID No 339; 4-22, 29-35, 44-50, 53-68, 70-80 and 20-33 of Seq ID No 340; 22-28, 30-36 and 18-33 of Seq ID No 341; 4-11, 13-21, 25-30 and 20-30 of Seq ID No 342; 10-22 and 10-23 of Seq ID No 343; 4-11 and 9-20 of Seq ID No 344; 14-25, 32-46 and 6-19 of Seq ID No 345; 5-30 and 14-33 of Seq ID No 346; 4-15, 28-35, 46-55, 59-65, 76-84 and 9-24 of Seq ID No 347; 27-33 and 5-19 of Seq ID No 348; 5-13 and 8-18 of Seq ID No 349; 9-22, 24-34 and 21-40 of Seq ID No 350; 4-17, 35-41, 46-89, 93-98 and 71-89 of Seq ID No 351; 4-12, 14-24 and 2-17 of Seq ID No 352; 9-17 and 5-16 of Seq ID No 353; 7-41, 48-58, 63-75, 80-89 and 43-53 of Seq ID No 354; 4-22, 25-30 and 4-14 of Seq ID No 355; 4-55 and 18-33 of Seq ID No 356; ; 262-280 of Seq ID No 179; 131-146 of Seq ID No 186; 207-224 of Seq ID No 188; 27-50, 203-217 and 313-325 of Seq ID No 189; 110-129 of Seq ID No 192; 156-179, 174-197, 192-215, 210-233, 228-

251 and 246-267 of Seq ID No 190; 377-400 of Seq ID No 196; 34-43, 234-257 and 350-367 of Seq ID No 203; 304-327 of Seq ID No 207; 25-48, 43-66 and 61-82 of Seq ID No 222; 398-421, 416-439, 434-457, 452-475, 470-493, 488-511, 506-529, 524-547, 621-644, 639-664, 707-730, 725-748, 743-766, 761-784, 779-802, 797-820, 984-1007, 1002-1025, 1020-1043, 1038-1061, 1056-1079, 1074-1097, 1092-1115, 1286-1309, 1304-1327, 1322-1345, 1340-1363, 1358-1381, 1376-1399, 1394-1417, 1412-1435, 1430-1453, 1448-1471, 1466-1489 and 1484-1507 of Seq ID No 226; 188-211, 206-229, 224-247, 242-265, 260-283 and 278-296 of Seq ID No 227; 56-79 and 122-132 of Seq ID No 229; 35-46 of Seq ID No 231; 178-201, 196-219, 214-237, 232-255, 250-273, 268-291, 379-402, 397-420, 415-438, 433-456, 451-474, 642-665, 660-683, 678-701, 696-719, 714-737, 732-755, 750-773, 768-791, 899-922, 917-940, 935-958, 1037-1060, 1055-1078, 1073-1096 and 1091-1114 of Seq ID No 232; 330-346 of Seq ID No 233; 571-594, 589-612, 607-630, 625-648, 643-666 and 661-684 of Seq ID No 242; 188-207 of Seq ID No 244; 61-84, 308-331, 326-349, 344-367, 362-385, 380-403 and 398-421 of Seq ID No 249; 79-98, 345-366, 844-867, 870-887 and 890-905 of Seq ID No 258; 94-109 of Seq ID No 268; 188-207 of Seq ID No 272; 290-306 of Seq ID No 276; 826-849 of Seq ID No 277; 228-252, 247-270, 265-288, 283-306, 301-324, 955-978, 973-996, 991-1014, 1009-1032, 1027-1050, 1045-1068, 2533-2556, 2551-2574, 2569-2592, 2587-2610, 2605-2628 and 2623-2646 of Seq ID No 279; 86-109 and 104-127 of Seq ID No 288; 546-560 of Seq ID No 289; 260-271 of Seq ID No 290; 106-129, 124-147, 142-165, 160-183, 178-201 and 375-398 of Seq ID No 291; 284-307 of Seq ID No 292; 362-385 of Seq ID No 301, and fragments comprising at least 6, preferably more than 8, especially more than 10 aa of said sequences. All these fragments individually and each independently form a preferred selected aspect of the present invention.

All linear hyperimmune serum reactive fragments of a particular antigen may be identified by analysing the entire sequence of the protein antigen by a set of peptides overlapping by 1 amino acid with a length of at least 10 amino acids. Subsequently, non-linear epitopes can be identified by analysis of the protein antigen with hyperimmune sera using the expressed full-length protein or domain polypeptides thereof. Assuming that a distinct domain of a protein is sufficient to form the 3D structure independent from the native protein, the analysis of the respective recombinant or synthetically produced domain polypeptide with hyperimmune serum would allow the identification of conformational epitopes within the individual domains of multi-domain proteins. For those antigens where a domain possesses linear as well as conformational epitopes, competition experiments with peptides corresponding to the linear epitopes may be used to confirm the presence of conformational epitopes.

It will be appreciated that the invention also relates to, among others, nucleic acid molecules encoding the aforementioned fragments, nucleic acid molecules that hybridise to nucleic acid molecules encoding the fragments, particularly those that hybridise under stringent conditions, and nucleic acid molecules, such as PCR primers, for amplifying nucleic acid molecules that encode the fragments. In these regards, preferred nucleic acid molecules are those that correspond to the preferred fragments, as discussed above.

The present invention also relates to vectors, which comprise a nucleic acid molecule or nucleic acid molecules of the present invention, host cells which are genetically engineered with vectors of the invention and the production of hyperimmune serum reactive antigens and fragments thereof by recombinant techniques.

A great variety of expression vectors can be used to express a hyperimmune serum reactive antigen or fragment thereof according to the present invention. Generally, any vector suitable to maintain, propagate or express nucleic acids to express a polypeptide in a host may be used for expression in this regard. In accordance with this aspect of the invention the vector may be, for example, a plasmid vector, a single or double-stranded phage vector, a single or double-stranded RNA or DNA viral vector. Starting plasmids disclosed herein are either commercially available, publicly available, or can be constructed from available plasmids by routine application of well-known, published procedures. Preferred among vectors, in certain respects, are those for expression of nucleic acid molecules and hyperimmune serum reactive antigens or fragments thereof of the present invention. Nucleic acid constructs in host cells can

be used in a conventional manner to produce the gene product encoded by the recombinant sequence. Alternatively, the hyperimmune serum reactive antigens and fragments thereof of the invention can be synthetically produced by conventional peptide synthesizers. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA construct of the present invention.

Host cells can be genetically engineered to incorporate nucleic acid molecules and express nucleic acid molecules of the present invention. Representative examples of appropriate hosts include bacterial cells, such as streptococci, staphylococci, *E. coli, Streptomyces* and *Bacillus subtillis* cells; fungal cells, such as yeast cells and *Aspergillus* cells; insect cells such as Drosophila S2 and Spodoptera Sf9 cells; animal cells such as CHO, COS, Hela, C127, 3T3, BHK, 293 and Bowes melanoma cells; and plant cells.

The invention also provides a process for producing a *H. pylori* hyperimmune serum reactive antigen and a fragment thereof comprising expressing from the host cell a hyperimmune serum reactive antigen or fragment thereof encoded by the nucleic acid molecules provided by the present invention. The invention further provides a process for producing a cell, which expresses a *H. pylori* hyperimmune serum reactive antigen or a fragment thereof comprising transforming or transfecting a suitable host cell with the vector according to the present invention such that the transformed or transfected cell expresses the polypeptide encoded by the nucleic acid contained in the vector.

The polypeptide may be expressed in a modified form, such as a fusion protein, and may include not only secretion signals but also additional heterologous functional regions. Thus, for instance, a region of additional amino acids, particularly charged amino acids, may be added to the N- or C-terminus of the polypeptide to improve stability and persistence in the host cell, during purification or during subsequent handling and storage. Also, regions may be added to the polypeptide to facilitate purification. Such regions may be removed prior to final preparation of the polypeptide. The addition of peptide moieties to polypeptides to engender secretion or excretion, to improve stability or to facilitate purification, among others, are familiar and routine techniques in the art. A preferred fusion protein comprises a heterologous region from immunoglobulin that is useful to solubilize or purify polypeptides. For example, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobin molecules together with another protein or part thereof. In drug discovery, for example, proteins have been fused with antibody Fc portions for the purpose of high-throughout screening assays to identify antagonists. See for example, {Bennett, D. et al., 1995} and {Johanson, K. et al., 1995}.

The *H. pylori* hyperimmune serum reactive antigen or a fragment thereof can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, hydroxylapatite chromatography and lectin chromatography.

The hyperimmune serum reactive antigens and fragments thereof according to the present invention can be produced by chemical synthesis as well as by biotechnological means. The latter comprise the transfection or transformation of a host cell with a vector containing a nucleic acid according to the present invention and the cultivation of the transfected or transformed host cell under conditions, which are known to the ones skilled in the art. The production method may also comprise a purification step in order to purify or isolate the polypeptide to be manufactured. In a preferred embodiment the vector is a vector according to the present invention.

The hyperimmune serum reactive antigens and fragments thereof according to the present invention may be used for the detection of the organism or organisms in a sample containing these organisms or

polypeptides derived thereof. Preferably such detection is for diagnosis, more preferable for the diagnosis of a disease, most preferably for the diagnosis of diseases related or linked to the presence or abundance of Gram-negative bacteria, especially bacteria selected from the group comprising Helicobacter, Campylobacter and Arcobacter. More preferably, the microorganisms are selected from the group comprising *Helicobacter cinaedi* and *Helicobacter fanneliae*, especially the microorganism is *Helicobacter pylori*.

The present invention also relates to diagnostic assays such as quantitative and diagnostic assays for detecting levels of the hyperimmune serum reactive antigens and fragments thereof of the present invention in cells and tissues, including determination of normal and abnormal levels. Thus, for instance, a diagnostic assay in accordance with the invention for detecting over-expression of the polypeptide compared to normal control tissue samples may be used to detect the presence of an infection, for example, and to identify the infecting organism. Assay techniques that can be used to determine levels of a polypeptide, in a sample derived from a host are well-known to those of skill in the art. Such assay methods include radioimmunoassays, competitive-binding assays, Western Blot analysis and ELISA assays. Among these, ELISAs frequently are preferred. An ELISA assay initially comprises preparing an antibody specific to the polypeptide, preferably a monoclonal antibody. In addition, a reporter antibody generally is prepared which binds to the monoclonal antibody. The reporter antibody is attached to a detectable reagent such as radioactive, fluorescent or enzymatic reagent, such as horseradish peroxidase enzyme.

The hyperimmune serum reactive antigens and fragments thereof according to the present invention may also be used for the purpose of or in connection with an array. More particularly, at least one of the hyperimmune serum reactive antigens and fragments thereof according to the present invention may be immobilized on a support. Said support typically comprises a variety of hyperimmune serum reactive antigens and fragments thereof whereby the variety may be created by using one or several of the hyperimmune serum reactive antigens and fragments thereof according to the present invention and/or hyperimmune serum reactive antigens and fragments thereof being different. The characterizing feature of such array as well as of any array in general is the fact that at a distinct or predefined region or position on said support or a surface thereof, a distinct polypeptide is immobilized. Because of this any activity at a distinct position or region of an array can be correlated with a specific polypeptide. The number of different hyperimmune serum reactive antigens and fragments thereof immobilized on a support may range from as little as 10 to several 1000 different hyperimmune serum reactive antigens and fragments thereof. The density of hyperimmune serum reactive antigens and fragments thereof per cm^2 is in a preferred embodiment as little as 10 peptides/polypeptides per cm^2 to at least 400 different peptides/polypeptides per cm^2 and more particularly at least 1000 different hyperimmune serum reactive antigens and fragments thereof per cm^2.

The manufacture of such arrays is known to the one skilled in the art and, for example, described in US patent 5,744,309. The array preferably comprises a planar, porous or non-porous solid support having at least a first surface. The hyperimmune serum reactive antigens and fragments thereof as disclosed herein, are immobilized on said surface. Preferred support materials are, among others, glass or cellulose. It is also within the present invention that the array is used for any of the diagnostic applications described herein. Apart from the hyperimmune serum reactive antigens and fragments thereof according to the present invention also the nucleic acid molecules according to the present invention may be used for the generation of an array as described above. This applies as well to an array made of antibodies, preferably monoclonal antibodies as, among others, described herein.

In a further aspect the present invention relates to an antibody directed to any of the hyperimmune serum reactive antigens and fragments thereof, derivatives or fragments thereof according to the present invention. The present invention includes, for example, monoclonal and polyclonal antibodies, chimeric, single chain, and humanized antibodies, as well as Fab fragments, or the product of a Fab expression

library. It is within the present invention that the antibody may be chimeric, i. e. that different parts thereof stem from different species or at least the respective sequences are taken from different species.

Antibodies generated against the hyperimmune serum reactive antigens and fragments thereof corresponding to a sequence of the present invention can be obtained by direct injection of the hyperimmune serum reactive antigens and fragments thereof into an animal or by administering the hyperimmune serum reactive antigens and fragments thereof to an animal, preferably a non-human. The antibody so obtained will then bind the hyperimmune serum reactive antigens and fragments thereof itself. In this manner, even a sequence encoding only a fragment of a hyperimmune serum reactive antigen and fragments thereof can be used to generate antibodies binding the whole native hyperimmune serum reactive antigen and fragments thereof. Such antibodies can then be used to isolate the hyperimmune serum reactive antigens and fragments thereof from tissue expressing those hyperimmune serum reactive antigens and fragments thereof.

For preparation of monoclonal antibodies, any technique known in the art, which provides antibodies produced by continuous cell line cultures can be used. (as described originally in {Kohler, G. et al., 1975}.

Techniques described for the production of single chain antibodies (U.S. Patent No. 4,946,778) can be adapted to produce single chain antibodies to immunogenic hyperimmune serum reactive antigens and fragments thereof according to this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies to immunogenic hyperimmune serum reactive antigens and fragments thereof according to this invention.

Alternatively, phage display technology or ribosomal display could be utilized to select antibody genes with binding activities towards the hyperimmune serum reactive antigens and fragments thereof either from repertoires of PCR amplified v-genes of lymphocytes from humans screened for possessing respective target antigens or from naïve libraries {McCafferty, J. et al., 1990}; {Marks, J. et al., 1992}. The affinity of these antibodies can also be improved by chain shuffling {Clackson, T. et al., 1991}.

If two antigen binding domains are present, each domain may be directed against a different epitope – termed 'bispecific' antibodies.

The above-described antibodies may be employed to isolate or to identify clones expressing the hyperimmune serum reactive antigens and fragments thereof or purify the hyperimmune serum reactive antigens and fragments thereof of the present invention by attachment of the antibody to a solid support for isolation and/or purification by affinity chromatography.

Thus, among others, antibodies against the hyperimmune serum reactive antigens and fragments thereof of the present invention may be employed to inhibit and/or treat infections, particularly bacterial infections and especially infections arising from *H. pylori*.

Hyperimmune serum reactive antigens and fragments thereof include antigenically, epitopically or immunologically equivalent derivatives, which form a particular aspect of this invention. The term "antigenically equivalent derivative" as used herein encompasses a hyperimmune serum reactive antigen and fragments thereof or its equivalent which will be specifically recognized by certain antibodies which, when raised to the protein or hyperimmune serum reactive antigen and fragments thereof according to the present invention, interfere with the interaction between pathogen and mammalian host. The term "immunologically equivalent derivative" as used herein encompasses a peptide or its equivalent which when used in a suitable formulation to raise antibodies in a vertebrate, the antibodies act to interfere with the interaction between pathogen and mammalian host.

The hyperimmune serum reactive antigens and fragments thereof, such as an antigenically or

immunologically equivalent derivative or a fusion protein thereof can be used as an antigen to immunize a mouse or other animal such as a rat or chicken. The fusion protein may provide stability to the hyperimmune serum reactive antigens and fragments thereof. The antigen may be associated, for example by conjugation, with an immunogenic carrier protein, for example bovine serum albumin (BSA) or keyhole limpet haemocyanin (KLH). Alternatively, an antigenic peptide comprising multiple copies of the protein or hyperimmune serum reactive antigen and fragments thereof, or an antigenically or immunologically equivalent hyperimmune serum reactive antigen and fragments thereof, may be sufficiently antigenic to improve immunogenicity so as to obviate the use of a carrier.

Preferably the antibody or derivative thereof is modified to make it less immunogenic in the individual. For example, if the individual is human the antibody may most preferably be "humanized", wherein the complimentarity determining region(s) of the hybridoma-derived antibody has been transplanted into a human monoclonal antibody, for example as described in {Jones, P. et al., 1986} or {Tempest, P. et al., 1991}.

The use of a polynucleotide of the invention in genetic immunization will preferably employ a suitable delivery method such as direct injection of plasmid DNA into muscle, delivery of DNA complexed with specific protein carriers, coprecipitation of DNA with calcium phosphate, encapsulation of DNA in various forms of liposomes, particle bombardment {Tang, D. et al., 1992}, {Eisenbraun, M. et al., 1993} and *in vivo* infection using cloned retroviral vectors {Seeger, C. et al., 1984}.

In a further aspect the present invention relates to a peptide binding to any of the hyperimmune serum reactive antigens and fragments thereof according to the present invention, and a method for the manufacture of such peptides whereby the method is characterized by the use of the hyperimmune serum reactive antigens and fragments thereof according to the present invention and the basic steps are known to the one skilled in the art.

Such peptides may be generated by using methods according to the state of the art such as phage display or ribosome display. In case of phage display, basically a library of peptides is generated, in form of phages, and this kind of library is contacted with the target molecule, in the present case a hyperimmune serum reactive antigen and fragments thereof according to the present invention. Those peptides binding to the target molecule are subsequently removed, preferably as a complex with the target molecule, from the respective reaction. It is known to the one skilled in the art that the binding characteristics, at least to a certain extent, depend on the particularly realized experimental set-up such as the salt concentration and the like. After separating those peptides binding to the target molecule with a higher affinity or a bigger force, from the non-binding members of the library, and optionally also after removal of the target molecule from the complex of target molecule and peptide, the respective peptide(s) may subsequently be characterised. Prior to the characterisation optionally an amplification step is realized such as, e. g. by propagating the peptide encoding phages. The characterisation preferably comprises the sequencing of the target binding peptides. Basically, the peptides are not limited in their lengths, however, preferably peptides having a lengths from about 8 to 20 amino acids are preferably obtained in the respective methods. The size of the libraries may be about 10^2 to 10^{18}, preferably 10^8 to 10^{15} different peptides, however, is not limited thereto.

A particular form of target binding hyperimmune serum reactive antigens and fragments thereof are the so-called "anticalines" which are, among others, described in the German patent application DE 197 42 706.

In a further aspect the present invention relates to functional nucleic acids interacting with any of the hyperimmune serum reactive antigens and fragments thereof according to the present invention, and a method for the manufacture of such functional nucleic acids whereby the method is characterized by the use of the hyperimmune serum reactive antigens and fragments thereof according to the present

invention and the basic steps are known to the one skilled in the art. The functional nucleic acids are preferably aptamers and spiegelmers.

Aptamers are D-nucleic acids, which are either single stranded or double stranded and which specifically interact with a target molecule. The manufacture or selection of aptamers is, e. g., described in European patent EP 0 533 838. Basically the following steps are realized. First, a mixture of nucleic acids, i. e. potential aptamers, is provided whereby each nucleic acid typically comprises a segment of several, preferably at least eight subsequent randomised nucleotides. This mixture is subsequently contacted with the target molecule whereby the nucleic acid(s) bind to the target molecule, such as based on an increased affinity towards the target or with a bigger force thereto, compared to the candidate mixture. The binding nucleic acid(s) are/is subsequently separated from the remainder of the mixture. Optionally, the thus obtained nucleic acid(s) is amplified using, e.g. polymerase chain reaction. These steps may be repeated several times giving at the end a mixture having an increased ratio of nucleic acids specifically binding to the target from which the final binding nucleic acid is then optionally selected. These specifically binding nucleic acid(s) are referred to as aptamers. It is obvious that at any stage of the method for the generation or identification of the aptamers samples of the mixture of individual nucleic acids may be taken to determine the sequence thereof using standard techniques. It is within the present invention that the aptamers may be stabilized such as, e. g., by introducing defined chemical groups which are known to the one skilled in the art of generating aptamers. Such modification may for example reside in the introduction of an amino group at the 2'-position of the sugar moiety of the nucleotides. Aptamers are currently used as therapeutical agents. However, it is also within the present invention that the thus selected or generated aptamers may be used for target validation and/or as lead substance for the development of medicaments, preferably of medicaments based on small molecules. This is actually done by a competition assay whereby the specific interaction between the target molecule and the aptamer is inhibited by a candidate drug whereby upon replacement of the aptamer from the complex of target and aptamer it may be assumed that the respective drug candidate allows a specific inhibition of the interaction between target and aptamer, and if the interaction is specific, said candidate drug will, at least in principle, be suitable to block the target and thus decrease its biological availability or activity in a respective system comprising such target. The thus obtained small molecule may then be subject to further derivatisation and modification to optimise its physical, chemical, biological and/or medical characteristics such as toxicity, specificity, biodegradability and bioavailability.

Spiegelmers and their generation or manufacture is based on a similar principle. The manufacture of spiegelmers is described in international patent application WO 98/08856. Spiegelmers are L-nucleic acids, which means that they are composed of L-nucleotides rather than D-nucleotides as aptamers are. Spiegelmers are characterized by the fact that they have a very high stability in biological systems and, comparable to aptamers, specifically interact with the target molecule against which they are directed. In the process of generating spiegelmers, a heterogeonous population of D-nucleic acids is created and this population is contacted with the optical antipode of the target molecule, in the present case for example with the D-enantiomer of the naturally occurring L-enantiomer of the hyperimmune serum reactive antigens and fragments thereof according to the present invention. Subsequently, those D-nucleic acids are separated which do not interact with the optical antipode of the target molecule. But those D-nucleic acids interacting with the optical antipode of the target molecule are separated, optionally identified and/or sequenced and subsequently the corresponding L-nucleic acids are synthesized based on the nucleic acid sequence information obtained from the D-nucleic acids. These L-nucleic acids which are identical in terms of sequence with the aforementioned D-nucleic acids interacting with the optical antipode of the target molecule, will specifically interact with the naturally occurring target molecule rather than with the optical antipode thereof. Similar to the method for the generation of aptamers it is also possible to repeat the various steps several times and thus to enrich those nucleic acids specifically interacting with the optical antipode of the target molecule.

In a further aspect the present invention relates to functional nucleic acids interacting with any of the nucleic acid molecules according to the present invention, and a method for the manufacture of such functional nucleic acids whereby the method is characterized by the use of the nucleic acid molecules and their respective sequences according to the present invention and the basic steps are known to the one skilled in the art. The functional nucleic acids are preferably ribozymes, antisense oligonucleotides and siRNA.

Ribozymes are catalytically active nucleic acids, which preferably consist of RNA which basically comprises two moieties. The first moiety shows a catalytic activity whereas the second moiety is responsible for the specific interaction with the target nucleic acid, in the present case the nucleic acid coding for the hyperimmune serum reactive antigens and fragments thereof according to the present invention. Upon interaction between the target nucleic acid and the second moiety of the ribozyme, typically by hybridisation and Watson-Crick base pairing of essentially complementary stretches of bases on the two hybridising strands, the catalytically active moiety may become active which means that it catalyses, either intramolecularly or intermolecularly, the target nucleic acid in case the catalytic activity of the ribozyme is a phosphodiesterase activity. Subsequently, there may be a further degradation of the target nucleic acid, which in the end results in the degradation of the target nucleic acid as well as the protein derived from the said target nucleic acid. Ribozymes, their use and design principles are known to the one skilled in the art, and, for example described in {Doherty, E. et al., 2001} and {Lewin, A. et al., 2001}.

The activity and design of antisense oligonucleotides for the manufacture of a medicament and as a diagnostic agent, respectively, is based on a similar mode of action. Basically, antisense oligonucleotides hybridise based on base complementarity, with a target RNA, preferably with a mRNA, thereby activating RNase H. RNase H is activated by both phosphodiester and phosphorothioate-coupled DNA. Phosphodiester-coupled DNA, however, is rapidly degraded by cellular nucleases with the exception of phosphorothioate-coupled DNA. These resistant, non-naturally occurring DNA derivatives do not inhibit RNase H upon hybridisation with RNA. In other words, antisense polynucleotides are only effective as DNA RNA hybride complexes. Examples for this kind of antisense oligonucleotides are described, among others, in US-patent US 5,849,902 and US 5,989,912. In other words, based on the nucleic acid sequence of the target molecule which in the present case are the nucleic acid molecules for the hyperimmune serum reactive antigens and fragments thereof according to the present invention, either from the target protein from which a respective nucleic acid sequence may in principle be deduced, or by knowing the nucleic acid sequence as such, particularly the mRNA, suitable antisense oligonucleotides may be designed base on the principle of base complementarity.

Particularly preferred are antisense-oligonucleotides, which have a short stretch of phosphorothioate DNA (3 to 9 bases). A minimum of 3 DNA bases is required for activation of bacterial RNase H and a minimum of 5 bases is required for mammalian RNase H activation. In these chimeric oligonucleotides there is a central region that forms a substrate for RNase H that is flanked by hybridising "arms" comprised of modified nucleotides that do not form substrates for RNase H. The hybridising arms of the chimeric oligonucleotides may be modified such as by 2'-O-methyl or 2'-fluoro. Alternative approaches used methylphosphonate or phosphoramidate linkages in said arms. Further embodiments of the antisense oligonucleotide useful in the practice of the present invention are P-methoxyoligonucleotides, partial P-methoxyoligodeoxyribonucleotides or P-methoxyoligonucleotides.

Of particular relevance and usefulness for the present invention are those antisense oligonucleotides as more particularly described in the above two mentioned US patents. These oligonucleotides contain no naturally occurring 5'→3'-linked nucleotides. Rather the oligonucleotides have two types of nucleotides: 2'-deoxyphosphorothioate, which activate RNase H, and 2'-modified nucleotides, which do not. The linkages between the 2'-modified nucleotides can be phosphodiesters, phosphorothioate or P-ethoxyphosphodiester. Activation of RNase H is accomplished by a contiguous RNase H-activating

region, which contains between 3 and 5 2′-deoxyphosphorothioate nucleotides to activate bacterial RNase H and between 5 and 10 2′- deoxyphosphorothioate nucleotides to activate eucaryotic and, particularly, mammalian RNase H. Protection from degradation is accomplished by making the 5′ and 3′ terminal bases highly nuclease resistant and, optionally, by placing a 3′ terminal blocking group.

More particularly, the antisense oligonucleotide comprises a 5′ terminus and a 3′ terminus; and from position 11 to 59 5′→3′-linked nucleotides independently selected from the group consisting of 2′-modified phosphodiester nucleotides and 2′-modified P-alkyloxyphosphotriester nucleotides; and wherein the 5′-terminal nucleoside is attached to an RNase H-activating region of between three and ten contiguous phosphorothioate-linked deoxyribonucleotides, and wherein the 3′-terminus of said oligonucleotide is selected from the group consisting of an inverted deoxyribonucleotide, a contiguous stretch of one to three phosphorothioate 2′-modified ribonucleotides, a biotin group and a P-alkyloxyphosphotriester nucleotide.

Also an antisense oligonucleotide may be used wherein not the 5′ terminal nucleoside is attached to an RNase H-activating region but the 3′ terminal nucleoside as specified above. Also, the 5′ terminus is selected from the particular group rather than the 3′ terminus of said oligonucleotide.

The nucleic acids as well as the hyperimmune serum reactive antigens and fragments thereof according to the present invention may be used as or for the manufacture of pharmaceutical compositions, especially vaccines. Preferably such pharmaceutical composition, preferably vaccine is for the prevention or treatment of diseases caused by, related to or associated with *H. pylori*. In so far another aspect of the invention relates to a method for inducing an immunological response in an individual, particularly a mammal, which comprises inoculating the individual with the hyperimmune serum reactive antigens and fragments thereof of the invention, or a fragment or variant thereof, adequate to produce antibodies to protect said individual from infection, particularly *Helicobacter* infection and most particularly *H. pylori* infections.

Yet another aspect of the invention relates to a method of inducing an immunological response in an individual which comprises, through gene therapy or otherwise, delivering a nucleic acid functionally encoding hyperimmune serum reactive antigens and fragments thereof, or a fragment or a variant thereof, for expressing the hyperimmune serum reactive antigens and fragments thereof, or a fragment or a variant thereof *in vivo* in order to induce an immunological response to produce antibodies or a cell mediated T cell response, either cytokine-producing T cells or cytotoxic T cells, to protect said individual from disease, whether that disease is already established within the individual or not. One way of administering the gene is by accelerating it into the desired cells as a coating on particles or otherwise.

A further aspect of the invention relates to an immunological composition which, when introduced into a host capable of having induced within it an immunological response, induces an immunological response in such host, wherein the composition comprises recombinant DNA which codes for and expresses an antigen of the hyperimmune serum reactive antigens and fragments thereof of the present invention. The immunological response may be used therapeutically or prophylactically and may take the form of antibody immunity or cellular immunity such as that arising from CTL or CD4+ T cells.

The hyperimmune serum reactive antigens and fragments thereof of the invention or a fragment thereof may be fused with a co-protein which may not by itself produce antibodies, but is capable of stabilizing the first protein and producing a fused protein which will have immunogenic and protective properties. This fused recombinant protein preferably further comprises an antigenic co-protein, such as Glutathione-S-transferase (GST) or beta-galactosidase, relatively large co-proteins which solubilise the protein and facilitate production and purification thereof. Moreover, the co-protein may act as an adjuvant in the sense of providing a generalized stimulation of the immune system. The co-protein may be attached to either the amino or carboxy terminus of the first protein.

Also, provided by this invention are methods using the described nucleic acid molecule or particular fragments thereof in such genetic immunization experiments in animal models of infection with *H. pylori*. Such fragments will be particularly useful for identifying protein epitopes able to provoke a prophylactic or therapeutic immune response. This approach can allow for the subsequent preparation of monoclonal antibodies of particular value from the requisite organ of the animal successfully resisting or clearing infection for the development of prophylactic agents or therapeutic treatments of *H. pylori* infection in mammals, particularly humans.

The hyperimmune serum reactive antigens and fragments thereof may be used as an antigen for vaccination of a host to produce specific antibodies which protect against invasion of bacteria, for example by blocking adherence of bacteria to damaged tissue. Examples of tissue damage include wounds in skin or connective tissue caused e.g. by mechanical, chemical or thermal damage or by implantation of indwelling devices, or wounds in the mucous membranes, such as the mouth, mammary glands, urethra or vagina.

The present invention also includes a vaccine formulation, which comprises the immunogenic recombinant protein together with a suitable carrier. Since the protein may be broken down in the stomach, it is preferably administered parenterally, including, for example, administration that is subcutaneous, intramuscular, intravenous, intradermal intranasal or tramsdermal. Formulations suitable for parenteral administration include aqueous and non-aqueous sterile injection solutions which may contain anti-oxidants, buffers, bacteriostats and solutes which render the formulation isotonic with the bodily fluid, preferably the blood, of the individual; and aqueous and non-aqueous sterile suspensions which may include suspending agents or thickening agents. The formulations may be presented in unit-dose or multi-dose containers, for example, sealed ampoules and vials, and may be stored in a freeze-dried condition requiring only the addition of the sterile liquid carrier immediately prior to use. The vaccine formulation may also include adjuvant systems for enhancing the immunogenicity of the formulation, such as oil-in-water systems and other systems known in the art. The dosage will depend on the specific activity of the vaccine and can be readily determined by routine experimentation.

According to another aspect, the present invention relates to a pharmaceutical composition comprising such a hyperimmune serum-reactive antigen or a fragment thereof as provided in the present invention for *H. pylori*. Such a pharmaceutical composition may comprise one, preferably at least two or more hyperimmune serum reactive antigens or fragments thereof against *H. pylori*. Optionally, such *H. pylori* hyperimmune serum reactive antigens or fragments thereof may also be combined with antigens against other pathogens in a combination pharmaceutical composition. Preferably, said pharmaceutical composition is a vaccine for preventing or treating an infection caused by *H. pylori* and/or other pathogens against which the antigens have been included in the vaccine.

According to a further aspect, the present invention relates to a pharmaceutical composition comprising a nucleic acid molecule encoding a hyperimmune serum-reactive antigen or a fragment thereof as identified above for *H. pylori*. Such a pharmaceutical composition may comprise one or more nucleic acid molecules encoding hyperimmune serum reactive antigens or fragments thereof against *H. pylori*. Optionally, such *H. pylori* nucleic acid molecules encoding hyperimmune serum reactive antigens or fragments thereof may also be combined with nucleic acid molecules encoding antigens against other pathogens in a combination pharmaceutical composition. Preferably, said pharmaceutical composition is a vaccine for preventing or treating an infection caused by *H. pylori* and/or other pathogens against which the antigens have been included in the vaccine.

The pharmaceutical composition may contain any suitable auxiliary substances, such as buffer substances, stabilisers or further active ingredients, especially ingredients known in connection of pharmaceutical composition and/or vaccine production.

A preferable carrier/or excipient for the hyperimmune serum-reactive antigens, fragments thereof or a coding nucleic acid molecule thereof according to the present invention is an immunostimulatory compound for further stimulating the immune response to the given hyperimmune serum-reactive antigen, fragment thereof or a coding nucleic acid molecule thereof. Preferably the immunostimulatory compound in the pharmaceutical preparation according to the present invention is selected from the group of polycationic substances, especially polycationic peptides, immunostimulatory nucleic acids molecules, preferably immunostimulatory deoxynucleotides, alum, Freund's complete adjuvants, Freund's incomplete adjuvants, neuroactive compounds, especially human growth hormone, or combinations thereof.

It is also within the scope of the present invention that the pharmaceutical composition, especially vaccine, comprises apart from the hyperimmune serum reactive antigens, fragments thereof and/or coding nucleic acid molecules thereof according to the present invention other compounds which are biologically or pharmaceutically active. Preferably, the vaccine composition comprises at least one polycationic peptide. The polycationic compound(s) to be used according to the present invention may be any polycationic compound, which shows the characteristic effects according to the WO 97/30721. Preferred polycationic compounds are selected from basic polyppetides, organic polycations, basic polyamino acids or mixtures thereof. These polyamino acids should have a chain length of at least 4 amino acid residues (WO 97/30721). Especially preferred are substances like polylysine, polyarginine and polypeptides containing more than 20 %, especially more than 50 % of basic amino acids in a range of more than 8, especially more than 20, amino acid residues or mixtures thereof. Other preferred polycations and their pharmaceutical compositions are described in WO 97/30721 (e.g. polyethyleneimine) and WO 99/38528. Preferably these polypeptides contain between 20 and 500 amino acid residues, especially between 30 and 200 residues.

These polycationic compounds may be produced chemically or recombinantly or may be derived from natural sources.

Cationic (poly)peptides may also be anti-microbial with properties as reviewed in {Ganz, T., 1999}. These (poly)peptides may be of prokaryotic or animal or plant origin or may be produced chemically or recombinantly (WO 02/13857). Peptides may also belong to the class of defensins (WO 02/13857). Sequences of such peptides can be, for example, found in the Antimicrobial Sequences Database under the following internet address:

http://www.bbcm.univ.trieste.it/~tossi/pag2.html

Such host defence peptides or defensives are also a preferred form of the polycationic polymer according to the present invention. Generally, a compound allowing as an end product activation (or down-regulation) of the adaptive immune system, preferably mediated by APCs (including dendritic cells) is used as polycationic polymer.

Especially preferred for use as polycationic substances in the present invention are cathelicidin derived antimicrobial peptides or derivatives thereof (International patent application WO 02/13857, incorporated herein by reference), especially antimicrobial peptides derived from mammalian cathelicidin, preferably from human, bovine or mouse.

Polycationic compounds derived from natural sources include HIV-REV or HIV-TAT (derived cationic peptides, antennapedia peptides, chitosan or other derivatives of chitin) or other peptides derived from these peptides or proteins by biochemical or recombinant production. Other preferred polycationic compounds are cathelin or related or derived substances from cathelin. For example, mouse cathelin is a peptide, which has the amino acid sequence NH_2-RLAGLLRKGGEKIGEKLKKIGQKIKNFFQKLVPQPE-

COOH. Related or derived cathelin substances contain the whole or parts of the cathelin sequence with at least 15-20 amino acid residues. Derivations may include the substitution or modification of the natural amino acids by amino acids, which are not among the 20 standard amino acids. Moreover, further cationic residues may be introduced into such cathelin molecules. These cathelin molecules are preferred to be combined with the antigen. These cathelin molecules surprisingly have turned out to be also effective as an adjuvant for an antigen without the addition of further adjuvants. It is therefore possible to use such cathelin molecules as efficient adjuvants in vaccine formulations with or without further immunactivating substances.

Another preferred polycationic substance to be used according to the present invention is a synthetic peptide containing at least 2 KLK-motifs separated by a linker of 3 to 7 hydrophobic amino acids (International patent application WO 02/32451, incorporated herein by reference).

The pharmaceutical composition of the present invention may further comprise immunostimulatory nucleic acid(s). Immunostimulatory nucleic acids are e. g. neutral or artificial CpG containing nucleic acids, short stretches of nucleic acids derived from non-vertebrates or in form of short oligonucleotides (ODNs) containing non-methylated cytosine-guanine di-nucleotides (CpG) in a certain base context (e.g. described in WO 96/02555). Alternatively, also nucleic acids based on inosine and cytidine as e.g. described in the WO 01/93903, or deoxynucleic acids containing deoxy-inosine and/or deoxyuridine residues (described in WO 01/93905 and PCT/EP 02/05448, incorporated herein by reference) may preferably be used as immunostimulatory nucleic acids for the present invention. Preferablly, the mixtures of different immunostimulatory nucleic acids may be used according to the present invention.

It is also within the present invention that any of the aforementioned polycationic compounds is combined with any of the immunostimulatory nucleic acids as aforementioned. Preferably, such combinations are according to the ones as described in WO 01/93905, WO 02/32451, WO 01/54720, WO 01/93903, WO 02/13857 and PCT/EP 02/05448 and the Austrian patent application A 1924/2001, incorporated herein by reference.

In addition or alternatively such vaccine composition may comprise apart from the hyperimmune serum reactive antigens and fragments thereof, and the coding nucleic acid molecules thereof according to the present invention a neuroactive compound. Preferably, the neuroactive compound is human growth factor as, e.g. described in WO 01/24822. Also preferably, the neuroactive compound is combined with any of the polycationic compounds and/or immunostimulatory nucleic acids as afore-mentioned.

In a further aspect the present invention is related to a pharmaceutical composition. Such pharmaceutical composition is, for example, the vaccine described herein. Also a pharmaceutical composition is a pharmaceutical composition which comprises any of the following compounds or combinations thereof: the nucleic acid molecules according to the present invention, the hyperimmune serum reactive antigens and fragments thereof according to the present invention, the vector according to the present invention, the cells according to the present invention, the antibody according to the present invention, the functional nucleic acids according to the present invention and the binding peptides such as the anticalines according to the present invention, any agonists and antagonists screened as described herein. In connection therewith any of these compounds may be employed in combination with a non-sterile or sterile carrier or carriers for use with cells, tissues or organisms, such as a pharmaceutical carrier suitable for administration to a subject. Such compositions comprise, for instance, a media additive or a therapeutically effective amount of a hyperimmune serum reactive antigen and fragments thereof of the invention and a pharmaceutically acceptable carrier or excipient. Such carriers may include, but are not limited to, saline, buffered saline, dextrose, water, glycerol, ethanol and combinations thereof. The formulation should suit the mode of administration.

The pharmaceutical compositions may be administered in any effective, convenient manner including, for instance, administration by topical, oral, anal, vaginal, intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal or intradermal routes among others.

In therapy or as a prophylactic, the active agent may be administered to an individual as an injectable composition, for example as a sterile aqueous dispersion, preferably isotonic.

Alternatively the composition may be formulated for topical application, for example in the form of ointments, creams, lotions, eye ointments, eye drops, ear drops, mouthwash, impregnated dressings and sutures and aerosols, and may contain appropriate conventional additives, including, for example, preservatives, solvents to assist drug penetration, and emollients in ointments and creams. Such topical formulations may also contain compatible conventional carriers, for example cream or ointment bases, and ethanol or oleyl alcohol for lotions. Such carriers may constitute from about 1 % to about 98 % by weight of the formulation; more usually they will constitute up to about 80 % by weight of the formulation.

In addition to the therapy described above, the compositions of this invention may be used generally as a wound treatment agent to prevent adhesion of bacteria to matrix proteins exposed in wound tissue and for prophylactic use in dental treatment as an alternative to, or in conjunction with, antibiotic prophylaxis.

A vaccine composition is conveniently in injectable form. Conventional adjuvants may be employed to enhance the immune response. A suitable unit dose for vaccination is 0.05-5 μg antigen / per kg of body weight, and such dose is preferably administered 1-3 times and with an interval of 1-3 weeks.

With the indicated dose range, no adverse toxicological effects should be observed with the compounds of the invention, which would preclude their administration to suitable individuals.

In a further embodiment the present invention relates to diagnostic and pharmaceutical packs and kits comprising one or more containers filled with one or more of the ingredients of the aforementioned compositions of the invention. The ingredient(s) can be present in a useful amount, dosage, formulation or combination. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, reflecting approval by the agency of the manufacture, use or sale of the product for human administration.

In connection with the present invention any disease related use as disclosed herein such as, e. g. use of the pharmaceutical composition or vaccine, is particularly a disease or diseased condition which is caused by, linked or associated with Helicobacter, more preferably, *H. pylori*. In connection therewith it is to be noted that *H. pylori* comprises several strains including those disclosed herein. A disease related, caused or associated with the bacterial infection to be prevented and/or treated according to the present invention includes besides others peptic ulcer and assoziated cancer in humans.

In a still further embodiment the present invention is related to a screening method using any of the hyperimmune serum reactive antigens or nucleic acids according to the present invention. Screening methods as such are known to the one skilled in the art and can be designed such that an agonist or an antagonist is screened. Preferably an antagonist is screened which in the present case inhibits or prevents the binding of any hyperimmune serum reactive antigen and fragment thereof according to the present invention to an interaction partner. Such interaction partner can be a naturally occurring interaction partner or a non-naturally occurring interaction partner.

The invention also provides a method of screening compounds to identify those, which enhance (agonist)

or block (antagonist) the function of hyperimmune serum reactive antigens and fragments thereof or nucleic acid molecules of the present invention, such as its interaction with a binding molecule. The method of screening may involve high-throughput.

For example, to screen for agonists or antagonists, the interaction partner of the nucleic acid molecule and nucleic acid, respectively, according to the present invention, maybe a synthetic reaction mix, a cellular compartment, such as a membrane, cell envelope or cell wall, or a preparation of any thereof, may be prepared from a cell that expresses a molecule that binds to the hyperimmune serum reactive antigens and fragments thereof of the present invention. The preparation is incubated with labelled hyperimmune serum reactive antigens and fragments thereof in the absence or the presence of a candidate molecule, which may be an agonist or antagonist. The ability of the candidate molecule to bind the binding molecule is reflected in decreased binding of the labelled ligand. Molecules which bind gratuitously, i. e., without inducing the functional effects of the hyperimmune serum reactive antigens and fragments thereof, are most likely to be good antagonists. Molecules that bind well and elicit functional effects that are the same as or closely related to the hyperimmune serum reactive antigens and fragments thereof are good agonists.

The functional effects of potential agonists and antagonists may be measured, for instance, by determining the activity of a reporter system following interaction of the candidate molecule with a cell or appropriate cell preparation, and comparing the effect with that of the hyperimmune serum reactive antigens and fragments thereof of the present invention or molecules that elicit the same effects as the hyperimmune serum reactive antigens and fragments thereof. Reporter systems that may be useful in this regard include but are not limited to colorimetric labelled substrate converted into product, a reporter gene that is responsive to changes in the functional activity of the hyperimmune serum reactive antigens and fragments thereof, and binding assays known in the art.

Another example of an assay for antagonists is a competitive assay that combines the hyperimmune serum reactive antigens and fragments thereof of the present invention and a potential antagonist with membrane-bound binding molecules, recombinant binding molecules, natural substrates or ligands, or substrate or ligand mimetics, under appropriate conditions for a competitive inhibition assay. The hyperimmune serum reactive antigens and fragments thereof can be labelled such as by radioactivity or a colorimetric compound, such that the molecule number of hyperimmune serum reactive antigens and fragments thereof bound to a binding molecule or converted to product can be determined accurately to assess the effectiveness of the potential antagonist.

Potential antagonists include small organic molecules, peptides, polypeptides and antibodies that bind to a hyperimmune serum reactive antigen and fragments thereof of the invention and thereby inhibit or extinguish its acitivity. Potential antagonists also may be small organic molecules, a peptide, a polypeptide such as a closely related protein or antibody that binds to the same sites on a binding molecule without inducing functional activity of the hyperimmune serum reactive antigens and fragments thereof of the invention.

Potential antagonists include a small molecule, which binds to and occupies the binding site of the hyperimmune serum reactive antigens and fragments thereof thereby preventing binding to cellular binding molecules, such that normal biological activity is prevented. Examples of small molecules include but are not limited to small organic molecules, peptides or peptide-like molecules.

Other potential antagonists include antisense molecules (see (Okano, H. et al., 1991); OLIGODEOXYNUCLEOTIDES AS ANTISENSE INHIBITORS OF GENE EXPRESSION; CRC Press, Boca Ration, FL (1988), for a description of these molecules).

Preferred potential antagonists include derivatives of the hyperimmune serum reactive antigens and

fragments thereof of the invention.

As used herein the activity of a hyperimmune serum reactive antigen and fragment thereof according to the present invention is its capability to bind to any of its interaction partner or the extent of such capability to bind to its or any interaction partner.

In a particular aspect, the invention provides the use of the hyperimmune serum reactive antigens and fragments thereof, nucleic acid molecules or inhibitors of the invention to interfere with the initial physical interaction between a pathogen and mammalian host responsible for sequelae of infection. In particular the molecules of the invention may be used: i) in the prevention of adhesion of *H. pylori* to mammalian extracellular matrix proteins on in-dwelling devices or to extracellular matrix proteins in mucosal wounds; ii) to block protein mediated mammalian cell invasion by, for example, initiating phosphorylation of mammalian tyrosine kinases (Rosenshine, I. et al., 1992) to block bacterial adhesion between mammalian extracellular matrix proteins and bacterial proteins which mediate tissue damage; iv) to block the normal progression of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or by other surgical techniques.

Each of the DNA coding sequences provided herein may be used in the discovery and development of antibacterial compounds. The encoded protein upon expression can be used as a target for the screening of antibacterial drugs. Additionally, the DNA sequences encoding the amino terminal regions of the encoded protein or Shine-Delgarno or other translation facilitating sequences of the respective mRNA can be used to construct antisense sequences to control the expression of the coding sequence of interest.

The antagonists and agonists may be employed, for instance, to inhibit diseases arising from infection with Helicobacter, especially *H. pylori*, such as peptic ulcer disease and gastric cancer.

In a still further aspect the present invention is related to an affinity device such affinity device comprises as least a support material and any of the hyperimmune serum reactive antigens and fragments thereof according to the present invention, which is attached to the support material. Because of the specificity of the hyperimmune serum reactive antigens and fragments thereof according to the present invention for their target cells or target molecules or their interaction partners, the hyperimmune serum reactive antigens and fragments thereof allow a selective removal of their interaction partner(s) from any kind of sample applied to the support material provided that the conditions for binding are met. The sample may be a biological or medical sample, including but not limited to, fermentation broth, cell debris, cell preparation, tissue preparation, organ preparation, blood, urine, lymph liquid, liquor and the like.

The hyperimmune serum reactive antigens and fragments thereof may be attached to the matrix in a covalent or non-covalent manner. Suitable support material is known to the one skilled in the art and can be selected from the group comprising cellulose, silicon, glass, aluminium, paramagnetic beads, starch and dextrane.

The present invention is further illustrated by the following figures, examples and the sequence listing from which further features, embodiments and advantages may be taken. It is to be understood that the present examples are given by way of illustration only and not by way of limitation of the disclosure.

In connection with the present invention

Figure 1 shows the characterization of *H. pylori* specific human sera.

Figure 2 shows the characterization of the small fragment genomic library LHP1-50 from *H. pylori* isolate KTH-Ca1.

Figure 3 shows the characterization of the small fragment genomic library LHP2-50 from *H. pylori* isolate KTH-Du.

Figure 4 shows the selection of bacterial cells by MACS using biotinylated human IgGs.

Table 1 shows the summary of all screens performed with genomic *H. pylori* libraries and human serum.

Table 2 shows the summary of all gene distribution experiments performed with genomic *H. pylori* DNA from individual isolates and gene specific oligonucleotides.

Table 3 shows the summary of epitope serology analysis with human sera.

The figures to which it might be referred to in the specification are described in the following in more details.

Figure 1 shows the characterization of human sera for anti-*H. pylori* antibodies as measured by immune assays. Total anti- *H. pylori* IgG and IgA antibody levels were measured by standard ELISA using total bacterial lysate prepared from *H. pylori* KTH Ca1 strain as coating antigen. **(A)** Serum samples from randomly selected 54 adults were analysed for antibody levels and afterwards interviewed for symptoms (gasctric pain) and previous history of *H. pylori* infections. Four individuals were identified with high antibody titers without symptoms or disease (S-) and four with acute symptoms or known clinical disease (S+). **(B)** Sera from patients presenting themselves with typical symptoms of *H. pylori* diseases were analysed for IgG and IgA levels and grouped based on negative or positive results in the Urease test performed by clinicians. ELISA units are calculated from absorbance readings at two serum dilutions (10.000X and 50.000X). Averages for the two different groups are given. **(C)** Immunoblot analysis was performed on sera pre-selected by ELISA in order to ensure multiple immune reactivity with protein antigens. Results of a representative experiment using total bacterial lysate prepared from *H. pylori* KTH Ca1 strain and selected sera at 5.000X dilution are shown. Serum samples are from; Lane 1: a high titer S- individual, Lane 2: a high titer urease -patient, Lane 3 and 4: a high titer urease + patient. Lane 1-3 was developed with anti-human IgG secondary antibody and Lane 4 with anti-human IgA secondary antibody. Mw: molecular weigth markers.

Figure 2 shows the fragment size distribution of the KTH-Ca1 *H. pylori* strain small fragment genomic library, LHP1-50. After sequencing 576 randomly selected clones sequences were trimmed to eliminate vector residues and the number of clones with various genomic fragment sizes were plotted. **(B)** Graphic illustration of the distribution of the same set of randomly sequenced clones of LHP1-50 over the *H. pylori* chromosome. Blue circles indicate matching sequences to annotated ORFs in both +/+ and +/- orientations. Red rectangles represent fully matched clones to non-coding chromosomal sequences in both +/+ and +/- orientations. Green diamonds positions all clones with chimeric sequences. Numeric distances in base pairs are indicated over each circular genome for orientation. Partitioning of various clone sets within the library is given in numbers and percentage at the bottom of the figure.

Figure 3 shows the fragment size distribution of the KTH-Du *H. pylori* strain small fragment genomic library, LHP2-50. After sequencing 576 randomly selected clones sequences were trimmed to eliminate vector residues and the number of clones with various genomic fragment sizes were plotted. **(B)** Graphic illustration of the distribution of the same set of randomly sequenced clones of LHP2-50 over the *H. pylori* chromosome. Blue circles indicate matching sequences to annotated ORFs in both +/+ and +/- orientations. Red rectangles represent fully matched clones to non-coding chromosomal sequences in both +/+ and +/- orientations. Green diamonds positions all clones with chimeric sequences. Numeric distances in base pairs are indicated over each circular genome for orientation. Partitioning of various clone sets within the library is given in numbers and percentage at the bottom of the figure.

Figure 4A shows the MACS selection with biotinylated human IgGs. The LHP1-50 library in pMAL9.1 was screened with 10 µg biotinylated, human serum (P6-IgG) in the first and with 10 µg in the second selection round. As negative control, no serum was added to the library cells for screening. Number of cells selected after the 1st and 2nd elution are shown for each selection round. Figure 4B shows the reactivity of specific clones (1-26) isolated by bacterial surface display as analysed by Western blot analysis with the human serum (P6-IgG) used for selection by MACS at a dilution of 1:3,000. As a loading control the same blot was also analysed with antibodies directed against the platform protein LamB at a dilution of 1:5,000. LB, Extract from a clone expressing LamB without foreign peptide insert.

Table 1: Immunogenic proteins identified by bacterial surface display.
A, 300bp library of *H. pylori* KTH Ca1 in fhuA with IC7-IgG (757), B, 300bp library of *H. pylori* KTH Ca1 in fhuA with P5-IgG (729), C, 300bp library of *H. pylori* KTH Ca1 in fhuA with P9-IgG (441), D, 50bp library of *H. pylori* KTH Ca1 in lamB with IC7-IgG (448), E, 50bp library of *H. pylori* KTH Ca1 in lamB with P5-IgA (1130), F, 50bp library of *H. pylori* KTH Ca1 in lamB with P5-IgG (911), G, 50bp library of *H. pylori* KTH Ca1 in lamB with P6-IgA (1135), H, 50bp library of *H. pylori* KTH Ca1 in lamB with P6-IgG (844), I, 50bp library of *H. pylori* KTH Ca1 in lamB with P9-IgG (1121), J, 300bp library of *H. pylori* KTH Du in fhuA with P6-IgG (433), K, 300bp library of *H. pylori* KTH Du in fhuA with P8-IgG (550), L, 50bp library of *H. pylori* KTH Du in lamB with P6-IgG (1077), M, 50bp library of *H. pylori* KTH Du in lamB with P8-IgG (740); *, prediction of antigenic sequences longer than 5 amino acids was performed with the program ANTIGENIC {Kolaskar, A. et al., 1990}.

Table 2: Gene distribution in *H. pylori* strains.
28 *H. pylori* strains (including *H. pylori* KTH-Ca1 and KTH-Du, see example 2) and were tested by PCR with oligonucleotides specific for the genes encoding relevant antigens. The PCR fragment of one selected PCR fragment was sequenced in order to confirm the amplification of the correct DNA fragment. *, number of amino acid substitutions in a *H. pylori* strain derived from a cancer patient as compared to *H. pylori* strain KE26695 (aa, amino acids). #, an alternative strain was used for sequencing.

Table 3: Epitope serology with human sera.
Immune reactivity of individual synthetic peptides representing selected epitopes with individual human sera is shown. Extent of reactivity is colour coded; white: neg (<500), light grey: + (500-650), dark grey: ++ (650-800), and black: +++ (>800). Numbers represent ELISA readings generated by measuring OD_{405nm} at serum dilution 200X. S stands for score, calculated as the sum of all reactivities (addition of the number of all +); P1 to P18 sera are from patients with definitive clinical diagnosis of duodenal or gastric ulcer, N1-4 sera are from healthy adults with high anti-*H. pylori* antibody titers without clinical symptomes of *H. pylori* disease. Location of synthetic peptides within the antigenic ORFs according to the genome annotation of *H. pylori* strain 26695 are given in columns from and to indicating the first and last amino acid residues, respectively. Peptide names: HP0009.1 present in annotated ORF HP0009.

EXAMPLES

Example 1: Characterization and selection of human sera based anti-*H.pylori* antibodies, preparation of antibody screening reagents

Experimental procedures

Enzyme linked immune assay (ELISA).
ELISA plates (Maxisorb, Millipore) were coated with 5-10 µg/ml total protein diluted in coating buffer

(0.1M sodium carbonate pH 9.2). Three dilutions of sera (2,000X, 10,000X, 50,000X) were made in PBS-BSA. Highly specific Horse Radish Peroxidase (HRP)-conjugated anti-human IgG or anti-human IgA secondary antibodies (Southern Biotech) were used according to the manufacturers' recommendations (dilution: 1,000x). Antigen-antibody complexes were quantified by measuring the conversion of the substrate (ABTS) to colored product based on OD_{405nm} readings by automatic ELIAS reader (TECAN SUNRISE).

Preparation of bacterial antigen extracts
H. pylori KTH DU or KTH Ca1 strains were grown for 48 hours on agar plates, cells collected and lysed by repeated freeze-thaw cycles: incubation on dry ice/ethanol-mixture until frozen (1 min), then thawed at 37°C (5 min): repeated 3 times. This was followed by sonication and collection of supernatant by centrifugation (3,500 rpm, 15 min, 4°C).

Immunoblotting
Total bacterial lysate preparations were prepared from *in vitro* grown *H. pylori* KTH DU or KTH Ca1 strains. 10 to 25µg total protein/lane was separated by SDS-PAGE using the BioRad Mini-Protean 3 Cell electrophoresis system and proteins transferred to nitrocellulose membrane (ECL, Amersham Pharmacia). After overnight blocking in 5% milk, human sera were added at 2,000x dilution, and HRPO labeled anti-human IgG was used for detection.

Purification of antibodies for genomic screening. Five sera from both the patient and the healthy group were selected based on the overall anti-streptococcal titers for a serum pool used in the screening procedure. Antibodies against *E. coli* proteins were removed by incubating the heat-inactivated sera with whole cell *E. coli* cells (DH5alpha, transformed with pHIE11, grown under the same condition as used for bacterial surface display). Highly enriched preparations of IgGs from the pooled, depleted sera were generated by protein G affinity chromatography, according to the manufacturer's instructions (UltraLink Immobilized Protein G, Pierce). IgA antibodies were purified also by affinity chromatography using biotin-labeled anti-human IgA (Southern Biotech) immobilized on Streptavidin-agarose (GIBCO BRL). The efficiency of depletion and purification was checked by SDS-PAGE, Western blotting, ELISA and protein concentration measurements.

Results

The antibodies produced against *H. pylori* by the human immune system and present in human sera are indicative of the *in vivo* expression of the antigenic proteins and their immunogenicity. These molecules are essential for the identification of individual antigens in the approach as described in the present invention, which is based on the interaction of the specific antibodies and the corresponding *H. pylori* peptides or proteins. To gain access to relevant antibody repertoires, human sera were collected from

I. 54 randomly selected healthy adults. Individuals were interviewed for the presence or absence of clinical symptoms and previously diagnosed *H. pylori* infection.
II. patients with duodenal ulcer.
III. patients with gastric ulcer and cancer.
For the patient groups *H. pylori* infection was confirmed and medical diagnosis was based on medical microbiological tests, Urease test, biopsy or gastroscopy. A total of 191 sera from patients were included in the analysis.

The sera were characterized for anti-*H. pylori* antibodies by a series of ELISA and immunoblotting assays. For that purpose two different antigen preparation were used: whole cell extracts prepared from *H. pylori* strains KTH-Ca1 and KTH-Du and both IgG and IgA antibody levels were determined. Antibody titers were expressed as units calculated from absorbance readings at two different dilutions - 10.000X and 50.000X for IgG and 1.000X and 5.000X for IgA - where the response was linear (Fig 1A and B). Among

the high titer randomly taken individuals eigth out of the 54 included (15%) showed significant IgG and IgA antibody levels. Half of these individuals were known *H. pylori* 'patients' acutely or before, the other half had no medical history or any complains. Sera of these four individuals were pooled and prepared for antigen identification. Since *H. pylori* infections are common, antibodies are present as a consequence of natural immunization from previous encounters with *Helicobacter* even without consequent carriage. The value of the ELISA assay imployed were further proved by analyzing patients' sera with or without active disease. Comparing the antibody levels in urease test positive and urease test negative individuals, significantly higher antibody levels were measured in the Urease + group (Fig. 1B). According to literature data, the false negative cases (~ 10%) are much more prevalent then the false positives in this test, suggesting that the ELIAS assays is likely to be even more powerful predicting active *H. pylori* infections. Sera were ranked based on the reactivity against total lysate preparation in both antibody classes, and the highest ones from all three serum donor groups were selected for further analysis by immunoblotting. This latter assay confirmed immune reactivity against multiple *H. pylori* proteins, as it is examplified on Fig. 1C.

This extensive antibody characterization approach has led to the unambiguous identification of anti-*Helicobacter* hyperimmune sera and allowed the preparation of 5 donor pools.

Example 2: Generation of highly random, frame-selected, small-fragment, genomic DNA libraries of *Helicobacter pylori*

Experimental procedures

Preparation of helicobacter genomic DNA. Sufficient amounts of bacterial pellets from the KTH-Ca1 and KTH-Du clinical isolates of *H. pylori* were obtained from Dr. Lars Engstrand. Bacterial pellets were washed 3 x with PBS and carefully re-suspended in 0.5 ml of Lysozyme solution (100 mg/ml). 0.1 ml of 10 mg/ml heat treated RNase A and 20 U of RNase T1 were added, mixed carefully and the solution was incubated for 1 h at 37°C. Following the addition of 0.2 ml of 20 % SDS solution and 0.1 ml of Proteinase K (10 mg/ml) the tube was incubated overnight at 55 °C. 1/3 volume of saturated NaCl was then added and the solution was incubated for 20 min at 4°C. The extract was pelleted in a microfuge (13,000 rpm) and the supernatant transferred into a new tube. The solution was extracted with PhOH/$CHCl_3$/IAA (25:24:1) and with $CHCl_3$/IAA (24:1). DNA was precipitated at room temperature by adding 0.6x volume of Isopropanol, spooled from the solution with a sterile Pasteur pipette and transferred into tubes containing 80% ice-cold ethanol. DNA was recovered by centrifuging the precipitates with 10-12,000x g, then dried on air and dissolved in ddH_2O.

Preparation of small genomic DNA fragments. Genomic DNA was mechanically sheared into fragments ranging in size between 150 and 300 bp using a cup-horn sonicator (Bandelin Sonoplus UV 2200 sonicator equipped with a BB5 cup horn, 10 sec. pulses at 100 % power output) or into fragments of size between 50 and 70 bp by mild DN*ase* I treatment (Novagen). It was observed that sonication yielded a much tighter fragment size distribution when breaking the DNA into fragments of the 150-300 bp size range. However, despite extensive exposure of the DNA to ultrasonic wave-induced hydromechanical shearing force, subsequent decrease in fragment size could not be efficiently and reproducibly achieved. Therefore, fragments of 50 to 70 bp in size were obtained by mild DN*ase* I treatment using Novagen's shotgun cleavage kit. A 1:20 dilution of DN*ase* I provided with the kit was prepared and the digestion was performed in the presence of $MnCl_2$ in a 60 µl volume at 20°C for 5 min to ensure double-stranded cleavage by the enzyme. Reactions were stopped with 2 µl of 0.5 M EDTA and the fragmentation efficiency was evaluated on a 2% TAE-agarose gel. This treatment resulted in total fragmentation of genomic DNA into near 50-70 bp fragments. Fragments were then blunt-ended twice using T4 DNA Polymerase in the presence of 100 µM each of dNTPs to ensure efficient flushing of the ends. Fragments

were used immediately in ligation reactions or frozen at -20°C for subsequent use.

Description of the vectors. The vector pMAL4.31 was constructed on a pASK-IBA backbone {Skerra, A., 1994} with the beta-lactamase (*bla*) gene exchanged with the Kanamycin resistance gene. In addition, the *bla* gene was cloned into the multiple cloning site. The sequence encoding mature beta-lactamase is preceded by the leader peptide sequence of *ompA* to allow efficient secretion across the cytoplasmic membrane. Furthermore a sequence encoding the first 12 amino acids (spacer sequence) of mature beta-lactamase follows the *ompA* leader peptide sequence to avoid fusion of sequences immediately after the leader peptidase cleavage site, since e.g. clusters of positive charged amino acids in this region would decrease or abolish translocation across the cytoplasmic membrane {Kajava, A. et al., 2000}. A *Sma*I restriction site serves for library insertion. An upstream FseI site and a downstream NotI site, which were used for recovery of the selected fragment, flank the *Sma*I site. The three restriction sites are inserted after the sequence encoding the 12 amino acid spacer sequence in such a way that the *bla* gene is transcribed in the -1 reading frame resulting in a stop codon 15 bp after the *Not*I site. A +1 bp insertion restores the *bla* ORF so that beta-lactamase protein is produced with a consequent gain of Ampicillin resistance.

The vector pMAL9.1 was constructed by cloning the *lamB* gene into the multiple cloning site of pEH1 {Hashemzadeh-Bonehi, L. et al., 1998}. Subsequently, a sequence was inserted in *lamB* after amino acid 154, containing the restriction sites *Fse*I, *Sma*I and *Not*I. The reading frame for this insertion was constructed in such a way that transfer of frame-selected DNA fragments excised by digestion with *Fse*I and *Not*I from plasmid pMAL4.31 yields a continuous reading frame of *lamB* and the respective insert.

The vector pHIE11 was constructed by cloning the *fhuA* gene into the multiple cloning site of pEH1. Thereafter, a sequence was inserted in *fhuA* after amino acid 405, containing the restriction site *Fse*I, *Xba*I and *Not*I. The reading frame for this insertion was chosen in a way that transfer of frame-selected DNA fragments excised by digestion with *Fse*I and *Not*I from plasmid pMAL4.31 yields a continuous reading frame of *fhuA* and the respective insert.

Cloning and evaluation of the library for frame selection. Genomic fragments of *H.pylori* DNA were ligated into the *Sma*I site of the vector pMAL4.31. Recombinant DNA was electroporated into DH10B electrocompetent *E. coli* cells (GIBCO BRL) and transformants plated on LB-agar supplemented with Kanamycin (50 µg/ml) and Ampicillin (50 µg/ml). Plates were incubated over night at 37°C and colonies collected for large scale DNA extraction. A representative plate was stored and saved for collecting colonies for colony PCR analysis and large-scale sequencing. A simple colony PCR assay was used to initially determine the rough fragment size distribution as well as insertion efficiency. From sequencing data the precise fragment size was evaluated, junction intactness at the insertion site as well as the frame selection accuracy (*3n+1 rule*).

Cloning and evaluation of the library for bacterial surface display. Genomic DNA fragments were excised from the pMAL4.31 vector, containing the *H. pylori* libraries with the restriction enzymes *Fse*I and *Not*I. The entire population of fragments was then transferred into plasmids pMAL9.1 (LamB) or pHIE11 (FhuA), which have been digested with *Fse*I and *Not*I. Using these two restriction enzymes, which recognise an 8 bp GC rich sequence, the reading frame that was selected in the pMAL4.31 vector is maintained in each of the platform vectors. The plasmid library was then transformed into *E. coli* DH5alpha cells by electroporation. Cells were plated onto large LB-agar plates supplemented with 50 µg/ml Kanamycin and grown over night at 37°C at a density yielding clearly visible single colonies. Cells were then scraped off the surface of these plates, washed with fresh LB medium and stored in aliquots for library screening at -80°C.

Results

Libraries for frame selection. Four libraries (LHP1-50, LHP2-50, LHP1-300 and LHP2-300) were generated in the pMAL4.31 vector with sizes of approximately 50 and 300 bp, respectively. For each library, ligation and subsequent transformation of approximately 1 µg of pMAL4.31 plasmid DNA and 50 ng of fragmented genomic *H. pylori* DNA yielded 4x 10^5 to 2x 10^6 clones after frame selection. To assess the randomness of the libraries, approximately 600 randomly chosen clones of LHP1-50 and LHP2-50 were sequenced. The bioinformatic analysis showed that of these clones only very few were present more than once. Furthermore, it was shown for example for LHP2-50 that 90% of the clones fell in the size range between 19 and 64 bp with an average size of 28 bp (Figure 2, 3). All sequences followed the *"3n+1 rule"*, showing that all clones were properly frame selected.

Bacterial surface display libraries. The display of peptides on the surface of *E. coli* required the transfer of the inserts from the LHP libraries from the frame selection vector pMAL4.31 to the display plasmids pMAL9.1 (LamB) or pHIE11 (FhuA). Genomic DNA fragments were excised by *Fse*I and *Not*I restriction and ligation of 5ng inserts with 0.1µg plasmid DNA and subsequent transformation into DH5alpha cells resulted in 2-5x 10^6 clones. The clones were scraped off the LB plates and frozen without further amplification.

Example 3: Identification of highly immunogenic peptide sequences from *H. pylori* using bacterial surface displayed genomic libraries and human serum

Experimental procedures

MACS screening. Approximately 2.5x 10^8 cells from a given library were grown in 5 ml LB-medium supplemented with 50 µg/ml Kanamycin for 2 h at 37°C. Expression was induced by the addition of 1 mM IPTG for 30 min. Cells were washed twice with fresh LB medium and approximately 2x 10^7 cells re-suspended in 100 µl LB medium and transferred to an Eppendorf tube.

10 µg of biotinylated, human IgGs purified from serum was added to the cells and the suspension incubated over night at 4°C with gentle shaking. 900 µl of LB medium was added, the suspension mixed and subsequently centrifuged for 10 min at 6,000 rpm at 4°C (for IgA screens, 10 µg of purified IgAs were used and these captured with biotinylated anti-human-IgA secondary antibodies). Cells were washed once with 1 ml LB and then re-suspended in 100 µl LB medium. 10 µl of MACS microbeads coupled to streptavidin (Miltenyi Biotech, Germany) were added and the incubation continued for 20 min at 4°C. Thereafter 900 µl of LB medium was added and the MACS microbead cell suspension was loaded onto the equilibrated MS column (Miltenyi Biotech, Germany) which was fixed to the magnet. (The MS columns were equilibrated by washing once with 1 ml 70% EtOH and twice with 2 ml LB medium.)

The column was then washed three times with 3 ml LB medium. After removal of the magnet, cells were eluted by washing with 2 ml LB medium. After washing the column with 3 ml LB medium, the 2 ml eluate was loaded a second time on the same column and the washing and elution process repeated. The loading, washing and elution process was performed a third time, resulting in a final eluate of 2 ml.

A second round of screening was performed as follows. The cells from the final eluate were collected by centrifugation and re-suspended in 1 ml LB medium supplemented with 50 µg/ml Kanamycin. The culture was incubated at 37°C for 90 min and then induced with 1 mM IPTG for 30 min. Cells were subsequently collected, washed once with 1 ml LB medium and suspended in 10 µl LB medium. Since the volume was reduced, 10 µg of human, biotinylated IgGs was added and the suspension incubated over night at 4°C with gentle shaking. All further steps were exactly the same as in the first selection round. Cells selected after two rounds of selection were plated onto LB-agar plates supplemented with 50 µg/ml Kanamycin and grown over night at 37°C.

Evaluation of selected clones by sequencing and Western blot analysis. Selected clones were grown over night at 37°C in 3 ml LB medium supplemented with 50 µg/ml Kanamycin to prepare plasmid DNA using standard procedures. Sequencing was performed at MWG (Germany).

For Western blot analysis approximately 10 to 20 µg of total cellular protein was separated by 10% SDS-PAGE and blotted onto HybondC membrane (Amersham Pharmacia Biotech, England). The LamB or FhuA fusion proteins were detected using human serum as the primary antibody at a dilution of approximately 1:5,000 and anti-human IgG or IgA antibodies coupled to HRP at a dilution of 1:5,000 as secondary antibodies. Detection was performed using the ECL detection kit (Amersham Pharmacia Biotech, England). Alternatively, rabbit anti FhuA or mouse anti LamB antibodies were used as primary antibodies in combination with the respective secondary antibodies coupled to HRP for the detection of the fusion proteins.

Results

Screening of bacterial surface display libraries by magnetic activated cell sorting (MACS) using biotinylated Igs. The libraries LHP1-50 and LHP2-50 in pMAL9.1 and LHP1-300 and LHP2-300 in pHIE11 were screened with pools of biotinylated, human IgGs and IgAs from patient sera or sera from healthy individuals (see Example 1: *Preparation of antibodies from human serum*). The selection procedure was performed as described under Experimental procedures. Figure 4A shows a representative example of a screen with the LHP1-50 library and P6-IgGs. As can be seen from the colony count after the first selection cycle from MACS screening, the total number of cells recovered at the end is reduced from app. 1 to 2x 10^7 cells to approximately 10^4 cells, whereby the selection in the presence of serum yielded a slightly higher number of cells than in the absence of antibodies (Figure 4A). After the second round of screening however, a similar number of cells was recovered with P6-IgG, while only a few hundred cells were recovered when no IgGs from human serum were added, clearly showing that selection was dependent on *H. pylori* specific antibodies. To evaluate the performance of the screen, approximately 50 selected clones were picked randomly and subjected to Western blot analysis with the same, pooled serum (Figure 4B). This analysis revealed that 70% of the selected clones showed reactivity with antibodies present in the relevant serum whereas the control strain expressing LamB without a *H. pylori* specific insert did not react with the same serum. In general, the rate of reactivity was observed to lie within the range of 35 to 75%. Colony PCR analysis confirmed that all selected clones contained an insert in the expected size range.

Subsequent sequencing of a larger number of randomly picked clones (600 to 1200 per screen) led to the identification of the gene and the corresponding peptide or protein sequence that was specifically recognized by the human serum used for screening. The frequency with which a specific clone is selected reflects at least in part the abundance and/or affinity of the specific antibodies in the serum used for selection and recognizing the epitope presented by this clone. In that regard it is striking that clones derived from some ORFs (e.g. HP0527, HP0547 and HP1341) were picked more than 100 times, indicating their highly immunogenic property. Table 1 summarizes the data obtained for all 13 performed screens. All clones in Table 1 have been verified by Western blot analysis with whole cellular extracts from single clones to show the indicated reactivity with the pool of human serum used in the respective screen. As seen in Table 1, distinct regions of the identified ORF are identified as immunogenic, since variably sized fragments of the proteins are displayed on the surface by the platform proteins.

It is further worth noticing that most of the genes identified by the bacterial surface display screen encode proteins that are either attached to the surface of *H. pylori* and/or are secreted. This is in accordance with the expected role of surface attached or secreted proteins in virulence of *H. pylori*.

Example 4: Gene distribution studies with highly immunogenic proteins identified from *H. pylori*.

Experimental procedures

Gene distribution of H. pylori antigens by PCR. In order to establish whether the genes encoding the identified *Helicobacter pylori* antigens occur ubiquitously in *H. pylori* strains, PCR was performed on a series of independent *H. pylori* isolates with primers specific for the gene of interest. *H. pylori* isolates were obtained from patients covering various disease conditions associated with *H. pylori* infection (cancer patients: 11 strains, duodenal ulcer: 6, atrophic gastritis: 5, gastritis: 3, Hiatus hernia: 1, normal controls: 2). Oligonucleotide sequences as primers were designed for all identified ORFs yielding products of approximately 1,000 bp, if possible covering all identified immunogenic epitopes. Genomic DNA of all *H. pylori* strains was prepared as described under Example 2. PCR was performed in a reaction volume of 25 µl using Taq polymerase (1U), 200 nM dNTPs, 10 pMol of each oligonucleotide and the kit according to the manufacturers instructions (Invitrogen, The Netherlands). As standard, 30 cycles (1x: 5min. 95°C, 30x: 30sec. 95°C, 30sec. 56°C, 30sec. 72°C, 1x 4min. 72°C) were performed, unless conditions had to be adapted for individual primer pairs.

Results

Identified genes encoding immunogenic proteins were tested by PCR for their presence in 28 different strains of *H. pylori* (Table 2). An ideal vaccine antigen would be an antigen that is present in all, or the vast majority of strains of the target organism to which the vaccine is directed. For a large number of antigens, the PCR reaction amplified a DNA fragment of the correct size with all 28 chosen *H. pylori* strains (e.g. HP0563, HP0887, HP1341). The sequencing of one PCR fragment from one individual strain showed that the amplified DNA fragment corresponds to the correct gene, but it also allows an estimation of the level of variation within this particular gene. While some genes possess a completely identical amino acid sequence in the two compared strains (e.g. HP0121, HP0413, HP1374), most antigens showed some degree of variation as listed in Table 2. The sequencing revealed that the amino acid sequences of approximately 80% of all antigens were to more than 95% identical in the two analysed strains, with only 1 strain showing a level of identity below 85%.
From a total of 106 genes analysed, 76 were present in all strains tested, 14 were present in more than 80% of the strains, while only 16 genes were absent in more than 20% of the tested 28 strains (Table 2). In addition, only 9 genes (e.g. HP115, HP717, HP887, HP913 and HP1119) showed a clear variation in size but were present in all or most *H. pylori* isolates. Importantly, many of the identified antigens are well conserved in all strains in sequence and size and are therefore novel vaccine candidates to prevent infections by *H. pylori.*

Example 5: Assessment of the reactivity of highly immunogenic peptide sequences from *H. pylori* with individual human sera.

Experimental procedures

Peptide synthesis
Peptides were synthesized in small scale (4 mg resin; up to 288 in parallel) using standard F-moc chemistry on a Rink amide resin (PepChem, Tübingen, Germany) using a SyroII synthesizer (Multisyntech, Witten, Germany). After the sequence was assembled, peptides were elongated with Fmoc-epsilon-aminohexanoic acid (as a linker) and biotin (Sigma, St. Louis, MO; activated like a normal amino acid). Peptides were cleaved off the resin with 93%TFA, 5% triethylsilane, and 2% water for one hour. Peptides were dried under vacuum and freeze dried three times from acetonitrile/water (1:1). The presence of the correct mass was verified by mass spectrometry on a Reflex III MALDI-TOF (Bruker, Bremen Germany). The peptides were used without further purification.

Enzyme linked immune assay (ELISA).
Biotin-labeled peptides (at the N-terminus) were coated on Streptavidin ELISA plates (EXICON) at 10 µg/ml concentration according to the manufacturer's instructions. Highly specific Horse Radish

Peroxidase (HRP)-conjugated anti-human IgG secondary antibodies (Southern Biotech) were used according to the manufacturers' recommendations (dilution: 1,000x). Sera were tested at two serum dilutions, 200X and 1,000X. Following manual coating, peptide plates were processed and analyzed by the Gemini 160 ELISA robot (TECAN) with a built-in ELISA reader (GENIOS, TECAN).

Results

Following the bioinformatic analysis of selected clones, corresponding peptides were designed and synthesized. In case of epitopes with more than 26 amino acid residues, overlapping peptides were made. All peptides were synthesized with a N-terminal biotin-tag and used as coating reagents on Streptavidin-coated ELISA plates.

The analysis was performed with 144 peptides and 22 individual human serum samples which were included in the serum pools used for preparations of IgG and IgA screening reagents for bacterial surface display. A summary for serum reactivity of peptides representing *H. pylori* epitopes from the genomic screen analysed with human sera is shown in Table 3. The peptides were compared by the score calculated for each peptide based on the number of positive sera and the extent of reactivity. Peptides range from highly and widely reactive to weakly positive ones. Among the most reactive ones there are known antigens, some of them are also protective in animal challenge models, such as the CagA (HP0547) and vacuolating cytotoxin (HP0887). Besides the known antigens several novel highly immunogenic proteins and epitopes within those have been identified, such as the siderophore-mediated iron transport protein (HP1341), fumarate reductase flavoprotein subunit (frdA) (HP0192) and HP0087 hypothetical protein among others.

References

Altschul, S., et al. (1990). Journal of Molecular Biology 215: 403-10.
Bennett, D., et al. (1995). J Mol Recognit 8: 52-8.
Bjorkholm, B., et al. (2003). J Intern Med 253: 102-19.
Blaser, M. (2000). Nat Med 6: 376-7.
Censini, S., et al. (1996). Proc Natl Acad Sci U S A 93: 14648-53.
Clackson, T., et al. (1991). Nature 352: 624-8.
Devereux, J., et al. (1984). Nucleic acids research 12: 387-95.
Doherty, E., et al. (2001). Annu Rev Biophys Biomol Struct 30: 457-475.
Dubreuil, J., et al. (2002). Microbiol Mol Biol Rev 66: 617-29.
Eisenbraun, M., et al. (1993). DNA Cell Biol 12: 791-7.
Etz, H., et al. (2001). J Bacteriol 183: 6924-35.
Ferrero, R., et al. (2001). Scand J Immunol 53: 443-8.
Fujikawa, A., et al. (2003). Nat Genet 33: 375-81.
Ganz, T. (1999). Science 286: 420-421.
Georgiou, G. (1997). Nature Biotechnology 15: 29-34.
Hancock, R. E., et al. (1999). Drugs 57: 469-473
Hashemzadeh-Bonehi, L., et al. (1998). Mol Microbiol 30: 676-678.
Heinje, von G (1987) e.g Sequence Analysis in Molecular Biology, Academic Press
Hemmer, B., et al. (1999). Nat Med 5: 1375-82.
Johanson, K., et al. (1995). J Biol Chem 270: 9459-71.
John Wiley & Sons (1987) Current Protocols in Molecular Biology
Jones, P., et al. (1986). Nature 321: 522-5.
Kajava, A., et al. (2000). J Bacteriol 182: 2163-9.
Kersulyte, D., et al. (2000). J Bacteriol 182: 3210-8.
Kohler, G., et al. (1975). Nature 256: 495-7.
Kolaskar, A., et al. (1990). FEBS Lett 276: 172-4.
Lewin, A., et al. (2001). Trends Mol Med 7: 221-8.
Loughlin, M., et al. (2003). Infect Immun 71: 2022-31.
Marks, J., et al. (1992). Biotechnology (N Y) 10: 779-83.
McCafferty, J., et al. (1990). Nature 348: 552-4.
Okano, H., et al. (1991). J Neurochem 56: 560-7.
Oliaro, J., et al. (2000). J Med Microbiol 49: 643-50.
Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression; CRC Press, Boca Ration, FL (1988) for a description of these molecules.
Prinz, C., et al. (2003). Trends Microbiol 11: 134-8.
Rammensee, H., et al. (1999). Immunogenetics 50: 213-9.
Rosenshine, I., et al. (1992). Infect Immun 60: 2211-7.
Sabarth, N., et al. (2002). Infect Immun 70: 6499-5303.
Seeger, C., et al. (1984). Proc Natl Acad Sci U S A 81: 5849-52.
Shibuya, A., et al. (2000) Nature Immunology 1: 441-446
Skerra, A. (1994). Gene 151: 131-5.
Sutton, P. (2001). Vaccine 19: 2286-90.
Svennerholm, A. (2003). Vaccine 21: 347-53.
Tang, D., et al. (1992). Nature 356: 152-4.
Tempest, P., et al. (1991). Biotechnology (N Y) 9: 266-71.
Tourdot, S., et al. (2000). Eur J Immunol 30: 3411-21.

Table 1: Immunogenic proteins identified by bacterial surface display.

A, 300bp library of *H. pylori* KTH Ca1 in fhuA with IC7-IgG (757), B, 300bp library of *H. pylori* KTH Ca1 in fhuA with P5-IgG (729), C, 300bp library of *H. pylori* KTH Ca1 in fhuA with P9-IgG (441), D, 50bp library of *H. pylori* KTH Ca1 in lamB with IC7-IgG (448), E, 50bp library of *H. pylori* KTH Ca1 in lamB with P5-IgA (1130), F, 50bp library of *H. pylori* KTH Ca1 in lamB with P5-IgG (911), G, 50bp library of *H. pylori* KTH Ca1 in lamB with P6-IgA (1135), H, 50bp library of *H. pylori* KTH Ca1 in lamB with P6-IgG (844), I, 50bp library of *H. pylori* KTH Ca1 in lamB with P9-IgG (1121), J, 300bp library of *H. pylori* KTH Du in fhuA with P6-IgG (433), K, 300bp library of *H. pylori* KTH Du in fhuA with P8-IgG (550), L, 50bp library of *H. pylori* KTH Du in lamB with P6-IgG (1077), M, 50bp library of *H. pylori* KTH Du in lamB with P8-IgG (740); *, prediction of antigenic sequences longer than 5 amino acids was performed with the program ANTIGENIC (Kolaskar and Tongaonkar, 1990).

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
HP0009	outer membrane protein (omp1)	63-91,95-101,110-116,134-148,150-156,158-164,188-193,197-209,226-241,247-254,291-297,312-319,338-346,351-358,366-378,404-410,420-438,448-454,465-473,482-488,490-498,503-510,512-519,531-543,547-554,568-575,589-604,610-631	G: 1, H: 2, K: 2, M: 38	239-308	1, 179
HP0010	chaperone and heat shock protein (groEL)	16-29,35-47,50-68,70-79,91-101,143-149,158-163,185-191,196-206,215-224,230-237,244-251,258-278,290-311,319-325,338-351,365-385,396-429,445-454,458-466,491-499,501-521	K: 1	17-79, 218-233	2, 180
HP0043	mannose-6-phosphate isomerase (pmi)	4-10,16-41,46-66,77-84,91-97,102-118,125-144,187-200,202-214,245-253,255-261,286-295,300-330,335-342,350-361,363-381,385-392,396-416,435-450	G: 1	460-470	3, 181
HP0063	hypothetical protein	11-19,27-48,52-59,77-82,84-107,118-125,127-154,178-183,192-209,215-221,286-295,302-313,350-357,402-415,417-431,453-463,465-493	D: 4, E: 1, G: 2	313-331	4, 182
HP0067	urease accessory protein (ureH)	19-26,30-43,47-55,63-68,72-80,97-104,107-119,129-146,160-175,194-216,231-251,254-260	H: 1	26-43	5, 183
HP0072	urease beta subunit (urea amidohydrolase) (ureB)	7-13,29-37,65-81,110-120,123-131,135-152,230-249,254-260,284-290,292-299,317-326,329-336,403-444,452-458,466-477,490-498,510-519,541-550,557-566	E: 2, G: 3, H: 1, M: 2	533-567	6, 184
HP0086	Conserved hypothetical protein	5-47,71-77,79-86,89-95,120-126,137-144,176-181,184-196,202-208,211-232,236-282,301-313,317-325,341-347,353-384,394-400,412-433,436-443	B: 3, C: 1, I: 4	59-75	7, 185
HP0087	hypothetical protein	4-18,22-38,59-69,106-112,116-130,138-149,156-	A: 2, B: 2,	1-104, 130-147	8, 186

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
		170,175-197,200-214,216-223,233-244,255-261,266-276,279-286,325-333,342-348,366-399,402-420,429-441	E: 2, F: 1, G: 2, I: 1, L: 2		
HP0088	RNA polymerase sigma-70 factor (rpoD)	50-58,69-95,97-113,131-136,157-163,170-175,188-212,220-226,254-259,265-277,283-289,297-308,311-318,347-358,360-369,378-401,416-421,440-450,454-462,470-476,493-502,506-514,536-567,585-590,598-607,613-618,653-659	A: 2, B: 9, D: 2, F: 3, H: 4	35-46	9, 187
HP0089	pfs protein (pfs)	16-29,32-60,65-87,89-123,128-134,137-158,162-173,178-196,210-216,218-228	E: 11, G: 2	206-225	10, 188
HP0115	flagellin B (flaB)	10-20,26-35,51-64,86-91,94-100,113-122,154-160,185-191,193-201,211-217,225-230,237-246,251-257,298-304,306-312,316-328,340-348,357-389,391-397,415-421,449-456,458-471,488-495,502-511	F: 2, H: 1, K: 1, L: 52	24-55, 236-341	11, 189
HP0175	cell binding factor 2	5-22,41-51,87-93,114-122,127-136,150-156,158-166,223-233,245-263,291-296	A: 11, C: 7, K: 2	9-126, 127-285	12, 190
HP0121	phosphoenolpyruvate synthase (ppsA)	30-43,46-56,61-70,72-83,85-93,103-113,119-125,151-166,179-191,212-218,225-231,236-243,262-267,291-307,331-344,349-355,366-372,380-386,414-422,428-447,459-464,469-478,507-519,525-544,563-569,576-590,620-626,633-643,654-659,665-671,684-707,717-723,725-733,747-779,782-801	H: 3, I: 4, K: 3	347-361	13, 191
HP0123	threonyl-tRNA synthetase (thrS)	4-12,14-26,37-80,107-115,133-139,144-150,154-165,173-180,191-199,205-211,221-231,237-244,254-284,307-340,342-353,360-368,370-380,479-493,495-503,509-522,525-536,539-547,554-560,565-573,578-583	D: 6, F: 1, H: 2, M: 1	7-23, 465-479	14, 192
HP0130	hypothetical protein	4-17,47-55,76-83,85-100,104-112,117-123,126-135,142-148,156-167,174-182,267-273	A: 1, C: 1, I: 1, K: 1, M: 3	258-283	15, 193
HP0150	hypothetical protein	3-32,36-42,65-88,102-108,112-140,147-163,170-179,183-193	A: 1, B: 1, D: 1, J: 1, L: 2	117-124	16, 194
HP0183	serine hydroxymethyltransferase (glyA)	12-18,45-50,62-77,82-95,99-113,115-123,125-147,155-177,187-209,211-223,244-253,259-270,278-297,302-307,311-318,329-334,350-356,359-365,390-400,402-413	I: 5	333-350	17, 195
HP0192	fumarate reductase,	4-13,15-27,30-46,53-58,68-74,82-95,115-126,134-	H : 1, I : 4,	376-400	18, 196

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
	flavoprotein subunit (frdA)	139,148-153,159-176,182-199,201-217,220-225,227-235,237-248,253-266,300-315,322-336,390-396,412-426,438-445,448-459,477-484,502-508,515-527,529-537,553-568,643-651,658-667,690-703	L: 20		
HP0197	S-adenosylmethionine synthetase 2 (metX)	4-10,24-32,38-55,59-67,70-77,80-87,89-97,123-129,134-151,166-172,178-189,191-216,218-235,245-259,271-315,326-339,341-360	F: 1, H: 1, L: 8	73-94	19, 197
HP0201	fatty acid/phospholipid synthesis protein (plsX)	13-25,31-38,43-57,79-85,92-99,106-112,117-128,130-139,146-158,160-175,194-204,211-222,225-232,234-242,263-270,278-292,299-320,322-333	L: 5	240-256	20, 198
HP0202	beta-ketoacyl-acyl carrier protein synthase III	4-17,55-63,66-101,109-131,135-143,145-151,155-161,164-170,177-185,192-198,213-218,223-238,246-256,258-268,273-283,309-314,322-328	F: 1, I: 3	195-221	21, 199
HP0210	chaperone and heat shock protein C62.5 (htpG)	13-24,31-39,41-50,63-69,90-96,104-109,116-141,148-153,161-167,173-178,190-209,253-258,265-272,279-289,295-312,317-343,355-366,376-389,400-407,430-451,453-464,466-472,487-493,499-505,523-538,554-559,568-579,584-601	F: 1, M: 2	344-363	22, 200
HP0211	conserved hypothetical secreted protein	5-22,30-36,53-59,61-70,82-92,99-106,120-131,135-148,154-167,169-183,187-199,204-212,231-247	A: 1, C: 1, K: 1	111-249	23, 201
HP0228	conserved hypothetical integral membrane protein	17-36,40-66,71-144,148-171,173-191,199-214,220-252,265-272,278-288,298-333,342-385	A: 1, E: 6, F: 1	287-307	24, 202
HP0229	outer membrane protein (omp6)	4-16,22-28,30-36,42-48,95-116,154-162,164-174,239-252,258-263,273-285,306-313,323-333,341-357,363-369,372-379,395-401,430-436,438-453,464-480	E: 1, F: 1, L: 14	33-44, 233-258, 349-369	25, 203
HP0235	conserved hypothetical secreted protein	4-21,30-37,46-53,59-68,80-92,98-104,118-143,150-160,165-185,187-200,204-211,224-236,241-246,252-258,271-280,288-294,311-320,335-341	B: 5	191-350	26, 204
HP0239	glutamyl-tRNA reductase (hemA)	4-16,37-59,64-70,79-87,93-102,107-127,143-165,172-188,197-204,207-218,221-227,242-248,258-277,289-296,298-316,332-338,344-365,367-373,375-382,400-408,415-425,438-446	H: 2	235-250	27, 205

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
HP0258	conserved hypothetical integral membrane protein	4-37,39-66,84-98,101-127,140-149,157-163,166-172,175-182,184-193,203-208,215-232,234-247,250-299,303-345	H: 1, L: 1	183-204	28, 206
HP0266	dihydroorotase (pyrC)	10-20,41-61,73-87,112-141,176-192,194-201,205-222,230-237,257-264,276-282,284-310,312-318,330-337,349-357	M: 21	304-328	29, 207
HP0279	lipopolysaccharide heptosyltransferase-1 (rfaC)	4-31,42-103,105-113,121-153,160-181,188-196,210-226,231-264,272-287,297-304,328-336	G: 1, L: 6	304-318	30, 208
HP0289	toxin-like outer membrane protein	21-43,46-52,54-70,72-79,94-107,133-141,160-166,217-253,311-317,359-365,374-381,390-395,434-440,488-494,497-502,511-522,554-563,565-574,577-585,591-598,601-606,617-625,633-643,658-664,676-682,694-702,710-719,754-760,782-788,802-808,916-921,942-948,955-964,973-979,992-998,1006-1011,1016-1023,1030-1038,1046-1053,1059-1066,1088-1098,1119-1126,1129-1135,1156-1171,1173-1181,1202-1210,1255-1261,1268-1280,1295-1310,1312-1320,1375-1381,1406-1417,1450-1471,1478-1492,1498-1506,1569-1578,1603-1608,1611-1624,1648-1655,1663-1670,1680-1698,1702-1707,1713-1719,1737-1742,1747-1753,1762-1769,1771-1785,1790-1804,1811-1818,1830-1836,1838-1852,1874-1886,1893-1899,1902-1909,1942-1948,1952-1962,1980-1986,2001-2017,2020-2028,2042-2050,2052-2068,2074-2079,2083-2095,2107-2113,2147-2155,2177-2194,2203-2211,2236-2241,2251-2258,2267-2274,2285-2292,2314-2328,2330-2340,2358-2365,2390-2401,2408-2418,2432-2453,2463-2476,2486-2507,2528-2537,2540-2548,2552-2558,2568-2576,2596-2601,2610-2622,2629-2638,2653-2669,2718-2727,2749-2767,2777-2784,2789-2795,2806-2815,2817-2824,2835-2843,2847-2854,2860-2881	B: 1, E: 2, H: 2, I: 3, L: 7	511-523, 612-630, 1790-1803	31, 209
HP0292	hypothetical protein	4-54,61-68,72-82,86-93,100-108,115-130,147-154,187-194,196-207,224-229,236-251,275-287	E:14	96-109	32, 210

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
HP0295	flagellin B homolog (fla)	31-39,62-69,91-101,158-172,175-180,186-193,201-208,210-223,243-250,273-286,293-299,319-325,343-354,356-365,368-384,414-435,471-491,512-518,550-556,567-581,584-589,633-639,680-692,697-708,716-721,747-754,779-786,810-816	A: 1, B: 2, C: 3	366-503	33, 211
HP0349	CTP synthetase (pyrG)	5-20,22-48,57-65,96-101,111-122,130-145,154-164,170-181,193-199,201-216,224-241,244-262,281-323,342-351,359-367,369-396,406-416,424-433,450-456,485-491,493-499,501-515,517-535	M:2	289-305	34, 212
HP0351	flagellar basal-body M-ring protein (fliF)	4-17,22-44,53-60,66-83,87-94,101-106,110-116,131-137,148-183,189-207,209-215,233-242,251-262,264-272,290-296,308-327,359-373,375-380,397-405,415-420,426-433,444-475,478-484,529-536,548-558	G: 9, I: 1	106-126	35, 213
HP0380	glutamate dehydrogenase (gdhA)	4-38,42-50,58-64,72-81,92-118,140-146,157-165,172-192,198-204,208-216,227-234,238-258,271-278,288-293,311-322,327-346,357-370,375-383,395-409,411-417,425-432,436-445	H: 6, I: 1, L: 4	109-129, 370-380	36, 214
HP0392	histidine kinase (cheA)	23-30,36-49,52-64,86-94,97-104,121-129,257-272,279-286,288-294,307-327,334-340,369-375,377-386,406-412,418-423,430-438,441-447,459-465,469-476,482-488,510-546,550-580,584-622,638-645,653-659,675-683,692-705,723-731,752-761,788-795	B: 1, F: 2	54-72	37, 215
HP0401	3-phosphoshikimate 1-carboxyvinyltransferase (aroA)	11-33,36-46,88-104,116-126,134-170,189-195,199-217,225-250,255-261,266-273,280-291,296-313,334-341,343-349,354-360,362-369,373-380,387-401,406-420	E: 1, M: 12	259-273	38, 216
HP0406	hypothetical protein	9-14,28-44,57-64,72-79,86-93,104-111,116-126,142-150,159-164	M: 2	61-86	39, 217
HP0409	GMP synthase (guaA)	10-17,26-33,43-61,69-95,101-107,109-125,129-135,137-144,147-153,158-169,177-187,209-219,221-232,235-247,261-268,271-282,296-302,306-347,355-362,364-379,386-399,409-418,424-442,451-460,467-479,490-498	B: 1, F: 1	60-74	40, 218
HP0413	transposase-like protein, PS3IS	8-14,20-31,65-84,94-99,154-179,193-207,238-253	E: 9, F: 1, G: 1	96-118	41, 219
HP0459	virB4 homolog (virB4)	4-24,30-44,47-62,84-93,108-116,124-133,136-141,201-209,217-223,228-235,238-245,247-270,275-	M: 6	167-189	42, 220

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
		285,290-314,328-338,342-349,353-365,375-383,386-392,394-402,417-427,443-459,465-481,492-514,516-524,550-566,602-617,630-639,666-676,687-693,719-730,747-753,783-790,799-816,824-831,837-842			
HP0480	GTP-binding protein, fusA-homolog (yihK)	6-15,18-28,58-66,84-101,106-129,136-151,154-165,182-203,205-211,214-220,222-228,233-240,251-260,270-277,284-291,306-315,322-328,363-369,378-388,392-405,443-452,495-501,512-523,574-583	H: 1	362-375	43, 221
HP0485	catalase-like protein	5-25,27-34,47-59,64-70,76-86,145-158,166-183,189-202,217-231,235-242,260-270,278-309	A: 1, B: 2, C: 3, K: 2	1-102	44, 222
HP0508	hypothetical protein	4-19,24-76,78-83,90-99,102-109,114-122,137-147,154-174,177-188,203-212,217-223,227-239	A: 1	226-325	45, 223
HP0519	conserved hypothetical protein	7-37,71-90,94-109,117-128,141-153,179-192,199-206,225-231,237-243,258-264	B: 2, H: 1	40-51	46, 224
HP0525	virB11 homolog	13-19,25-30,46-59,75-91,101-107,114-124,129-135,137-145,160-167,171-179,187-194,209-215,217-222,229-239,243-249,257-265,269-275,299-308,310-327	D: 5	282-300	47, 225
HP0527	cag pathogenicity island protein (cag7-cagY)	86-100,216-230,342-369,382-388,424-430,438-445,452-458,488-494,501-518,554-560,568-574,584-592,603-609,611-629,639-645,652-661,669-699,708-714,726-738,747-753,763-775,785-791,794-807,815-824,826-845,854-860,863-868,870-883,892-898,901-906,909-921,930-937,946-959,968-974,977-990,998-1007,1009-1027,1037-1043,1046-1051,1053-1066,1075-1081,1084-1089,1092-1103,1113-1119,1122-1135,1143-1152,1154-1172,1182-1188,1191-1196,1200-1210,1220-1226,1229-1235,1237-1249,1259-1265,1268-1281,1289-1298,1305-1318,1328-1334,1337-1343,1345-1357,1367-1373,1390-1396,1405-1411,1418-1423,1426-1435,1445-1455,1474-1483,1493-1500,1505-1512,1517-1524,1538-1544,1568-1578,1595-1601,1674-1682,1687-1720,1728-1736,1738-1744,1754-1761,1764-1774,1798-1824,1836-1842,1886-1893,1895-1903	A: 316, B: 88, C: 61, F: 12, G: 1, H: 1, I: 7, J: 274, K: 93, L: 14, M: 12	366-781, 782-1518, 1731-1747	48, 226
HP0540	cag pathogenicity	4-17,20-39,46-55,60-66,102-110,114-122,125-	A: 2, B: 6,	169-381	49, 227

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
	island protein (cag19)	131,161-167,172-178,185-190,195-202,218-232,236-252,264-291,293-302,309-315,324-339	C: 2, I: 1		
HP0541	cag pathogenicity island protein (cag20)	5-10,13-40,42-53,69-75,83-89,120-135,150-161,174-190,203-225,229-247,257-287,318-348	B: 2, G: 1	30-200	50, 228
HP0542	cag pathogenicity island protein (cag21-cagG)	7-19,43-53,64-72,124-139	B: 2, L: 18, M: 2	52-84, 120-131	51, 229
HP0544	cag pathogenicity island protein (cag23-cagE)	12-19,39-48,58-100,117-123,154-162,164-187,189-195,202-216,218-235,241-246,262-278,315-328,333-347,354-366,372-379,391-405,422-429,431-442,444-450,458-466,478-485,494-501,504-510,520-535,573-580,589-598,615-625,666-676,686-698,722-729,737-746,756-767,787-796,805-816,824-829,833-848,856-864,866-876,879-886,898-904,918-924,927-934,941-960,967-978	H: 1	561-575	52, 230
HP0545	cag pathogenicity island protein (cag24)	11-29,49-55,70-77,84-100,102-112,148-155,160-177,181-204	A: 1, B: 3, I: 2, K: 1	1-104	53, 231
HP547	cag pathogenicity island protein (cag26-cagA)	27-44,64-71,122-133,151-156,164-178,214-220,226-232,235-244,253-262,282-288,294-310,317-325,350-356,362-368,376-383,438-443,449-454,459-464,492-498,500-511,529-535,538-546,567-573,597-603,660-665,674-679,724-734,763-769,773-784,791-801,807-815,821-826,840-848,863-868,897-902,908-928,932-953,956-975,980-987,990-996,1012-1018,1042-1063,1095-1116,1149-1157,1160-1167	A: 72, B: 65, C: 175, D: 74, F: 51, G: 7, H: 10, I: 108, J: 9, K: 23, L: 33, M: 129	110-357, 358-501, 502-1161	54,232
HP0563	hypothetical protein	4-21,64-71,73-84,128-138,144-162,203-217,240-263,288-298,300-308,310-317,325-351,369-380,391-411	L: 134	330-345	55, 233
HP0604	uroporphyrinogen decarboxylase (hemE)	5-11,25-31,39-48,51-79,89-98,100-122,135-148,166-201,203-227,230-250,254-260,266-272,274-282,299-305,328-337	A: 2, B: 1, F: 1, K: 2	31-45	56, 234
HP0607	acriflavine resistance protein (acrB)	12-23,29-48,51-60,66-72,75-81,83-93,103-115,133-148,168-174,195-204,222-229,231-240,242-251,270-280,286-305,322-344,349-360,364-370,378-400,421-441,448-484,486-493,495-501,504-534,547-561,567-	F: 2, G: 1, I: 1, L: 2	915-940	57, 235

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
		590,597-607,621-635,643-649,658-685,688-694,702-711,717-731,737-742,759-765,767-772,776-786,803-809,815-825,854-908,910-919,923-930,942-948,961-975,994-1014			
HP0630	modulator of drug activity (mda66)	4-9,32-47,51-61,75-96,139-191	A: 1, F: 1, H: 2, I: 1	1-124	58, 236
HP0635	hypothetical protein	4-13,17-38,43-49,55-76,88-95,110-121,128-146,151-157,162-214,222-240,243-249,251-273,275-281,292-298,300-309,312-320,322-331,355-369,376-408,446-460,471-482,485-509	F: 2, H: 1	191-203	59, 237
HP0655	protective surface antigen D15	4-21,72-82,89-103,106-115,118-124,140-146,174-184,191-200,204-213,218-224,261-266,282-293,299-309,311-340,342-358,362-372,381-389,391-402,413-421,438-447,457-464,470-478,501-507,545-560,578-624,631-641,658-670,680-689,717-738,753-759,795-805,816-822,830-838,842-848,869-881,892-898	G: 1, H: 2	33-51, 818-835	60, 238
HP0659	hypothetical protein	4-21,79-85,156-177,183-188,206-214,243-249,261-269,287-292,315-322,334-345,360-366,374-390,402-411	A: 4, B: 1, K: 2	37-97, 260-399	61, 239
HP0683	UDP-N-acetylglucosamine pyrophosphorylase (glmU)	4-9,19-54,58-78,97-104,111-120,126-134,137-145,163-173,178-188,193-203,211-224,246-286,288-324,337-346,355-362,374-390,392-398,409-417	G:8	240-249	62, 240
HP0687	iron(II) transport protein (feoB)	5-12,14-31,35-41,43-61,82-92,97-105,134-145,155-166,184-203,215-223,225-251,272-279,281-306,310-345,358-418,435-473,482-490,525-532,538-547,549-563,578-604,613-639	F: 1, L: 3	144-154	63, 241
HP0696	N-methylhydantoinase	53-59,64-72,74-100,133-152,154-172,176-181,207-214,225-238,275-297,304-310,331-340,362-367,384-395,403-410,437-443,448-456,482-490,579-597,602-610,625-630,633-651,699-707,709-715,734-743,750-762	A: 5, B: 6, C: 13, E: 2, F: 1, G: 1, L: 1	544-685	64, 242
HP0701	DNA gyrase, sub A (gyrA)	12-18,22-40,45-83,89-97,103-109,147-153,159-173,195-204,210-219,243-253,259-265,273-282,303-309,315-325,332-340,346-358,362-367,377-390,393-402,418-426,447-455,467-480,505-512,514-525,548-561,566-576,584-596,619-626,638-645,649-659,661-	G: 2, H: 2, I: 3, L: 1	202-218, 282-299, 339-350, 617-628	65, 243

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
		680,699-708,714-720,753-759,766-772,775-781,801-808			
HP0706	outer membrane protein (omp15)	5-33,52-62,87-101,111-135,137-143,145-152,190-202,209-221,233-245,253-270	J: 1, K: 1, L: 37	151-215	66, 244
HP0714	RNA polymerase sigma-54 factor (rpoN)	19-29,32-39,42-48,75-94,124-135,137-145,152-160,176-182,193-203,215-236,266-273,275-291,297-306,311-319,322-342,348-360,369-378,394-401	F : 7	48-64	67, 245
HP0717	DNA polymerase III gamma and tau subunits (dnaX)	4-11,13-33,36-43,53-63,65-80,112-129,134-141,143-155,157-168,178-188,191-199,201-207,215-229,242-255,263-270,283-315,320-329,333-338,340-349,412-426,465-478,485-490,498-512,540-554	A: 2, B: 3, M: 2	390-516	68,246
HP0723	L-asparaginase II (ansB)	4-18,23-32,41-47,54-70,88-99,104-111,118-138,143-148,150-162,168-175,181-188,203-211,214-220,227-245,251-268,275-281,287-296,323-333	B: 1, F: 1, H: 6, K: 2	1-90	69, 247
HP0727	transcriptional regulator, putative	8-34,38-49,72-83,85-91,94-104,112-125,134-142,148-168,181-189,191-198,202-214,222-233,242-254,256-262,273-278,287-294,314-325	B: 2, G: 2, I: 2	141-159	70, 248
HP0752	flagellar hook-associated protein 2 (fliD)	4-24,30-36,47-75,82-105,124-134,151-157,192-202,208-214,219-226,234-247,285-290,318-324,332-340,343-349,380-386,453-462,472-478,484-501,531-540,550-557,604-612,620-625,642-648,652-671	A:7, B:4, C:2, G:1, H:1, I:3, J:1, K:2	64-84, 93-180, 181-446	71, 249
HP0760	conserved hypothetical protein	12-18,24-32,68-75,77-83,96-101,109-116,129-136,152-164,175-184,190-199,206-215,224-233,241-250,258-264,273-292,302-312,319-331,334-346,348-368,387-395,408-416,420-429,437-452	F: 3, G: 1	364-374	72, 250
HP0836	hypothetical protein	11-28,36-52,60-67,74-79,108-116	B: 1, L: 4	61-76	73, 251
HP0850	type I restriction enzyme M protein (hsdM)	20-27,38-49,69-74,84-107,138-145,161-168,179-195,210-226,228-252,267-281,283-296,305-311,333-340,342-356,361-372,380-399,401-414,458-466,475-481,492-507,515-520	H: 2	146-160	74, 252
HP0853	ABC transporter, ATP-binding protein (yheS)	43-61,68-74,76-90,120-128,130-149,156-161,164-182,206-234,242-252,269-274,291-304,332-345,349-355,360-371,374-388,434-440,447-453,459-465,469-496,504-522	M: 15	261-285	75, 253
HP0863	hypothetical protein	4-17,24-30,37-49,87-98,118-124,126-136,144-171,176-188,206-214,216-228,233-240,246-252,262-271,277-297,307-330,333-342,346-352,355-361,368-	E: 1, M: 11	401-427	76, 254

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
		386,391-400,413-420,474-480			
HP0874	hypothetical protein	15-26,31-46,51-72,80-93,96-109,131-137,150-158,179-185,189-209,211-219,221-234,241-247,255-262,265-271,283-288	F: 2	173-190	77, 255
HP0875	catalase	28-37,39-45,51-58,77-84,89-97,132-148,171-180,199-205,212-218,220-226,257-265,273-300,307-327,334-340,344-365,385-390,402-408,426-436,450-468,476-485	K: 6	425-497	78, 256
HP0876	iron-regulated outer membrane protein (frpB)	4-25,70-76,80-88,90-100,120-128,162-169,183-203,261-277,279-289,291-297,302-308,321-327,339-353,358-377,392-401,404-410,414-422,443-450,456-461,470-488,490-497,510-535,570-611,618-630,639-647,649-660,668-690,702-716,718-724,737-747,750-764	B: 1, E: 1, G: 1, I: 1	497-509	79, 257
HP0887	vacuolating cytotoxin	12-48,50-64,99-108,216-223,235-241,244-254,262-274,287-293,310-316,320-326,361-366,377-383,390-395,408-414,418-425,438-444,462-469,494-505,524-530,536-547,551-566,592-598,601-613,678-685,687-695,709-717,727-737,751-757,760-765,772-778,782-788,801-807,822-830,859-868,870-878,884-890,898-903,909-919,953-969,973-980,990-1000,1002-1019,1041-1047,1059-1065,1090-1095,1116-1127,1130-1139,1143-1149,1151-1168,1178-1183,1188-1195,1197-1209,1213-1220,1226-1234,1236-1247,1255-1274,1276-1282	A: 1, B: 5, C: 2, D: 3, E: 5, G: 2, H: 3, I: 2, K: 9, L: 29, M: 7	76-100, 270-284, 309-438, 493-505, 786-942, 947-967	80, 258
HP0891	conserved hypothetical protein	4-9,24-34,46-95,97-109,119-130	F: 2	138-156	81, 259
HP0910	adenine specific DNA methyltransferase (HINDIIM)	9-26,28-35,43-53,55-68,83-92,99-105,110-135,139-149,157-162,164-170,173-183,193-208,210-230,239-245,253-259,263-271,293-305,310-320,322-331,336-343,351-364,367-376	E: 33, H: 1	92-107, 154-173	82, 260
HP0913	outer membrane protein (omp21)	19-39,52-62,108-117,145-152,160-168,194-203,229-240,252-268,280-287,308-316,333-339,383-390,403-412,414-424,438-445,464-472,479-484,489-505,510-526	C: 1, I: 1	247-260	83, 261
HP0922	toxin-like outer membrane protein	5-17,25-52,60-77,105-113,118-125,162-167,228-234,272-279,328-334,341-357,381-395,400-406,512-	A: 1, B: 3, D: 1, F: 4,	394-549	84, 262

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
		518,557-569,586-592,645-651,690-695,701-709,720-726,733-743,751-758,781-786,879-886,929-934,939-944,952-960,965-975,994-1001,1039-1045,1102-1109,1164-1181,1198-1206,1223-1229,1253-1259,1283-1292,1312-1317,1339-1349,1360-1370,1389-1398,1400-1412,1452-1465,1470-1484,1490-1497,1519-1525,1554-1564,1578-1591,1623-1636,1638-1646,1669-1679,1685-1697,1704-1711,1713-1720,1730-1736,1738-1749,1756-1764,1778-1786,1796-1803,1817-1826,1849-1866,1975-1993,2017-2032,2044-2053,2070-2086,2091-2109,2116-2127,2156-2167,2182-2188,2197-2202,2244-2252,2281-2287,2290-2307,2350-2361,2383-2404,2425-2433,2445-2455,2495-2505	G: 2		
HP0925	recombinational DNA repair protein (recR)	9-24,31-53,57-67,69-79,84-114,133-141,144-172,178-186	E: 1, G: 1	13-46	85, 263
HP0953	hypothetical protein	4-25,27-35,43-52,59-70,79-91,115-130,136-152,154-163,170-179	J: 3	1-58	86, 264
HP0973	hypothetical protein	4-30,49-55,71-80,96-105,111-126,139-146,149-162,239-245,279-285,290-296,300-307,331-337,343-350	B: 3, K: 2	250-351	87, 265
HP0977	conserved hypothetical secreted protein	9-27,34-41,43-51,92-111,114-120,123-131,139-150,156-171,176-186,188-204,229-241,252-258,266-279,288-297,319-334,338-348,373-379,389-398,431-439,479-484	A: 2	214-398	88, 266
HP1019	serine protease (htrA)	4-15,18-27,47-52,68-83,91-97,104-110,115-121,139-147,157-164,198-206,227-236,241-254,264-273,278-289,311-320,353-361,372-383,405-420,426-434	A: 3, H: 1, I: 1	232-386	89, 267
HP1024	co-chaperone-curved DNA binding protein A (CbpA)	4-10,24-34,91-97,129-141,156-163,184-190,205-219,229-235,256-273,278-285	E: 1, G: 1, L: 24	93-116	90, 268
HP1052	UDP-3-0-acyl N-acetylglcosamine deacetylase (envA)	7-29,35-54,71-83,85-91,104-111,122-134,138-144,146-154,158-174,177-183,186-201,207-215,223-235,240-247,262-273,275-283,287-292	E: 1, F: 5, G: 14	48-66	91, 269

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
HP1090	cell division protein (ftsK)	7-27,31-47,49-70,75-102,110-149,157-171,217-223,235-251,294-302,358-364,367-375,387-393,395-412,423-430,441-451,456-470,472-486,488-495,499-509,515-529,536-549,556-570,574-603,607-615,625-633,642-658,670-676,683-702,708-716,720-726,747-756,763-784,803-812,815-826	D: 2, F: 1, G: 1, H: 1	475-490	92, 270
HP1098	conserved hypothetical secreted protein	7-22,30-38,53-59,64-75,83-95,97-112,120-131,133-142,145-151,154-166,172-180,189-203,227-238,277-287	A: 4, B: 1, F: 1, I: 2, K: 1	9-156, 174-287	93, 271
HP1116	hypothetical protein	13-23,25-32,111-117,150-164,185-193,207-212,216-224,230-236,263-272,304-311,342-348,374-385,391-407,444-458,480-487,489-499,523-542,544-558,572-579,620-640,686-696,703-710,742-755,765-772,817-822,830-837,865-872,931-937	I: 1, K: 2, L: 31	66-86	94, 272
HP1117	conserved hypothetical secreted protein	4-27,49-56,62-70,86-92,121-127,151-163,170-182,195-202,212-226,237-243	A: 1, F: 4	234-254	95; 273
HP1119	flagellar hook-associated protein 1 (HAP1) (flgK)	4-10,13-24,39-51,62-78,92-104,107-117,134-141,156-161,166-181,210-216,222-229,256-266,273-280,297-304,313-330,336-349,371-376,433-439,443-448,488-493,506-515,527-534,560-572,575-583,587-593	A: 7, B: 1, D: 1, F: 3, J: 1	252-483	96, 274
HP1126	colicin tolerance-like protein (tolB)	4-15,21-38,45-56,81-95,102-108,118-130,133-147,152-162,166-171,199-204,211-218,230-240,253-261,274-283,288-294,312-317,325-336,344-357,391-414	A: 3, B: 2, J: 1	24-146	97, 275
HP1152	signal recognition particle protein (ffh)	26-31,38-56,65-82,90-101,112-119,123-153,175-188,197-216,234-242,249-265,273-286,290-305,327-335,338-346,361-372,394-404	D : 1, F : 4, G : 10	290-306	98, 276
HP1153	valyl-tRNA synthetase (valS)	17-26,43-48,50-73,81-93,95-107,139-146,158-168,171-176,190-196,202-212,216-223,243-266,274-282,308-313,324-330,344-378,380-387,403-422,427-443,448-455,457-465,491-515,517-528,553-567,589-599,610-617,642-648,670-697,709-717,726-743,745-759,769-803,807-823,840-849	F: 4, G: 3, L: 3	820-851	99, 277
HP1186	carbonic anhydrase	4-18,39-48,53-63,66-90,102-117,125-134,137-145,156-162,169-197	D: 5, H: 1	26-40, 56-80	100, 278

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
HP1198	DNA-directed RNA polymerase, beta subunit (rpoB)	21-33,36-42,49-60,68-76,91-105,123-130,141-161,169-178,185-190,192-199,205-214,223-233,239-247,260-269,284-293,300-314,324-352,357-364,373-382,389-403,420-432,438-446,466-471,477-484,503-509,549-556,558-576,600-623,625-635,654-661,663-669,671-687,702-716,735-741,744-750,757-766,776-786,807-815,824-832,854-860,863-897,909-915,920-946,952-959,982-997,1024-1038,1049-1055,1071-1085,1104-1113,1121-1132,1138-1150,1187-1196,1212-1221,1227-1236,1257-1262,1264-1278,1282-1294,1307-1318,1353-1370,1382-1388,1396-1409,1434-1440,1446-1454,1465-1478,1485-1513,1516-1529,1540-1545,1563-1568,1575-1593,1607-1616,1628-1645,1648-1661,1676-1682,1689-1697,1713-1719,1739-1749,1753-1758,1763-1774,1797-1803,1807-1846,1855-1874,1877-1891,1893-1907,1912-1925,1931-1943,1955-1965,1976-1990,2032-2043,2045-2051,2099-2105,2131-2138,2161-2179,2188-2199,2205-2216,2219-2227,2235-2245,2247-2267,2277-2288,2294-2304,2314-2326,2346-2358,2365-2377,2383-2402,2407-2423,2437-2450,2454-2473,2489-2497,2525-2531,2557-2570,2580-2587,2589-2599,2621-2641,2647-2653,2661-2677,2685-2690,2697-2717,2722-2733,2739-2777,2786-2793,2801-2808,2811-2822,2825-2835,2838-2845,2859-2871,2877-2883	A: 26, B: 14, C: 25, D: 3, F: 1, G: 3, I: 3, J: 31, K: 2	213-344, 954-1080, 2524-2733	101, 279
HP1205	translation elongation factor EF-Tu (tufB)	10-16,18-23,28-41,63-69,77-91,101-109,118-136,146-153,155-162,168-179,192-207,217-226,229-235,239-254,279-286,294-307,313-319,334-341,344-353,363-377,390-396	A : 4, B : 1	178-328	102, 280
HP1229	aspartokinase (lysC)	18-42,68-84,89-95,100-105,107-115,125-135,154-177,189-195,205-228,236-243,252-259,279-300,309-316,323-331,340-351,353-364,377-402	I: 1, K: 1, L: 3	85-97	103, 281
HP1243	outer membrane protein (omp28)	4-18,26-32,66-76,100-126,151-159,178-186,188-194,200-210,241-248,253-259,262-279,284-291,307-313,315-322,327-337,376-386,399-407,432-441,467-	B: 3, F: 1, G: 1, H: 1	21-200, 468-480	104, 282

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
		473,487-497,499-505,543-549,560-568,585-593,598-604,608-614,630-642,647-653,690-703,717-730			
HP1254	biotin synthesis protein (bioC)	17-49,52-58,62-73,78-97,100-117,122-172,185-190,193-217,225-236	H: 2, I: 2	33-42	105, 283
HP1265	hypothetical protein	7-39,50-58,73-89,96-107,109-120,126-142,152-170,178-202,205-211,224-244,249-259,261-270,300-310,312-325	F: 2, G: 6, I: 1	158-169	106, 284
HP1282	anthranilate synthase component I (trpE)	4-31,40-64,71-82,85-92,102-124,126-139,147-152,159-173,176-188,195-207,210-216,234-241,249-256,258-276,279-293,296-302,310-315,349-356,363-378,380-403,411-426,435-441,448-459,463-476,488-494	E: 20, G: 1, I: 1	201-221	107, 285
HP1329	cation efflux system protein (czcA)	5-13,15-74,87-104,107-120,123-129,136-145,150-191,193-206,227-248,250-264,278-302,304-323,332-378,384-407,409-419,425-457,462-471,474-497,511-545,555-564,571-578,585-598,640-647,669-675,682-691,693-705,729-743,752-761,772-780,786-804,808-818,822-846,858-880,884-900,910-939,941-947,962-971,973-988,998-1003,1007-1027	B: 2, F: 1, J: 1, L: 2	236-259	108, 286
HP1339	biopolymer transport protein (exbB)	4-19,27-68,81-111,121-160	F: 5, I: 4	60-79	109, 287
HP1341	siderophore-mediated iron transport protein	4-37,40-46,52-57,199-205,222-229,236-244,250-267,269-282	A: 20, B: 23, C: 30, E: 31, F: 5, G: 3, H: 6, I: 1, J: 2, K: 5	27-197	110, 288
HP1342	outer membrane protein (omp29)	4-16, 24-30, 32-38, 63-75, 86-92, 98-111, 113-126, 160-165, 170-180, 198-204, 227-233, 239-245, 253-273, 308-314, 352-365, 382-387, 395-403, 423-429, 472-482, 484-493, 501-507, 518-526, 536-541, 543-550, 556-562, 586-600, 626-633, 649-661, 680-688	A: 1, B: 3, C: 1, D: 1, E: 1, F: 2, H: 7	546-559	111, 289
HP1345	phosphoglycerate kinase	16-33,48-59,63-71,77-92,94-109,117-124,139-151,169-181,184-227,233-249,251-261,263-275,282-294,297-321,326-332,341-355,383-399	D: 20, I: 6	258-272	112, 290
HP1350	protease	11-26,31-39,43-52,55-62,64-70,80-94,123-133,135-141,172-181,185-206,209-218,224-230,238-244,251-	A: 3, B: 1, C: 1, G: 1,	77-226, 350-429	113, 291

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
		262,264-271,290-301,306-324,333-340,350-357,367-375,390-397,434-441,443-448	K: 2, M: 12		
HP1374	ATP-dependent protease ATPase subunit (clpX)	4-13,22-27,31-45,50-59,72-96,99-114,131-141,143-150,159-176,180-186,189-198,208-214,234-253,271-287,294-299,310-366,382-390,398-416,424-443	G: 9, M: 2	283-305	114, 292
HP1393	DNA repair protein (recN)	9-26,30-53,62-72,86-95,112-122,136-145,153-160,209-221,227-237,241-268,281-288,291-298,308-314,321-328,336-346,351-379,388-397,409-416,423-433,443-481,511-519	E: 1, F: 2, G: 7, I: 1	213-232	115, 293
HP1448	ribonuclease P, protein component (rnpA)	12-18,25-31,38-50,59-67,71-82,96-126	G: 6	76-88	116, 294
HP1453	conserved hypothetical protein	4-25,39-44,64-71,74-88,100-113,128-138,151-162,164-177,185-190,204-213,233-239,246-254,281-286,293-306,309-318,333-347,349-359,385-398,404-423,458-465,477-484,490-499,501-533,554-566,582-590,596-616,624-629,631-639,654-680,694-720,735-743	B: 1, D: 4, F: 2, J: 1, K: 11, L: 3	2-100	117, 295
HP1454	hypothetical protein	4-16,36-41,52-75,98-107,109-117,122-128,133-139,141-155,159-165,169-182,187-193,195-201,211-224,230-236,247-269,278-290	B: 1, M: 8	75-92	118, 296
HP1460	DNA polymerase III alpha-subunit (dnaE)	7-21,25-33,37-43,87-94,103-120,131-147,168-174,197-203,207-212,227-237,247-257,263-271,279-287,298-306,320-325,332-340,363-374,379-384,390-401,403-414,428-433,448-457,462-475,483-490,513-519,525-535,543-554,559-566,571-620,625-631,636-642,659-670,688-706,708-723,770-779,787-793,796-807,820-840,848-854,863-874,895-905,912-919,934-942,968-975,983-1000,1012-1019,1026-1036,1050-1060,1064-1070,1081-1091,1094-1108,1112-1118,1140-1152,1164-1169,1172-1180,1187-1192	F: 3, G: 2, I: 3	732-748	119, 297
HP1497	peptidyl-tRNA hydrolase (pth)	23-40,42-59,66-73,78-97,111-128,130-141,157-166,178-183	E: 6, F: 1, H: 2	53-71	120, 298
HP1527	hypothetical protein	4-27,38-44,47-57,59-85,99-106,114-121,154-166,181-186,193-198,238-244,253-262,272-278,287-299,314-320,338-350,358-368,382-388,407-416,433-446,456-461,463-473	B: 3, C: 1, I: 7	86-195	121, 299

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
HP1564	outer membrane protein	5-24,38-59,64-80,87-99,105-126,134-142,149-163,165-179,181-202,205-220,227-233,243-250,257-263	A: 2, B: 1, C: 3, F: 1, H: 1	87-245	122, 300
HP1565	penicillin-binding protein 2 (pbp2)	5-32,47-53,66-79,81-97,115-151,155-174,183-188,196-210,215-226,230-238,253-258,263-270,276-282,295-301,304-325,334-344,360-390,397-412,425-432,434-462,478-494,508-526,539-564,571-579	A: 1, F: 2, H: 1, L: 5	347-371, 375-386	123, 301
HP1574	riboflavin synthase alpha subunit (ribC)	4-15,36-44,49-56,60-66,68-82,84-103,109-115,118-141,147-154,160-168,176-185	H: 1, M: 5	26-39	124, 302
ARF0044	Hypothetical protein	7-13,23-33	H: 1, I: 2	13-21	125, 303
ARF0048	Hypothetical protein	none	F: 1, G: 1, I: 4, L: 8	2-10	126, 304
ARF0143	Hypothetical protein	4-9,12-18,35-42,49-62	F: 1	6-18	127, 305
ARF0184	Hypothetical protein	19-25	A: 1, I: 6	1-13	128, 306
ARF0219	Hypothetical protein	15-21,27-45	E: 7	12-25	129, 307
ARF0308	Hypothetical protein	14-20	E: 41	1-14	130, 308
ARF0349	Hypothetical protein	4-18	G:11	13-26	131, 309
ARF0387	Hypothetical protein	8-21	G: 12, H: 2, K: 1	2-20	132, 310
ARF0402	Hypothetical protein	4-14	F: 2, G: 10, H: 1, M: 2	4-16	133, 311
ARF0501	Hypothetical protein	none	M: 2	3-12	134, 312
ARF0509	Hypothetical protein	6-14,6-25,35-57	G: 5, H: 1, M: 3	2-14	135, 313
ARF0522	Hypothetical protein	6-25,35-57	F: 1, I: 3, K: 2	17-31	136, 314
ARF0578	Hypothetical protein	14-25,32-46	E: 12, G: 1	5-19	137, 315
ARF0629	Hypothetical protein	18-31	G: 1, I: 7	5-16	138, 316
ARF0665	Hypothetical protein	19-24	L: 2, M: 5	4-26	139, 317
ARF0693	Hypothetical protein	13-21,29-34,47-58,61-73	G: 1, I: 6	36-47	140, 318
ARF0752	Hypothetical protein	4-15	D:3	5-24	141, 319

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
ARF0788	Hypothetical protein	none	B: 1, H: 1	6-18	142, 320
ARF0819	Hypothetical protein	13-20	F: 14	4-13	143, 321
ARF0839	Hypothetical protein	none	A: 2, C: 1, I: 1, K: 3	15-23	144, 322
ARF0868	Hypothetical protein	4-9	F: 2, G: 1	7-21	145, 323
ARF0948	Hypothetical protein	none	F: 1	1-10	146, 324
ARF0969	Hypothetical protein	none	B: 1, G: 1, M: 2	4-14	147, 325
ARF1100	Hypothetical protein	4-17,35-41,46-89,93-98	A: 1, B: 1, H: 1, I: 2, M: 5	70-88	148, 326
ARF1164	Hypothetical protein	none	G: 1, H: 3, J: 1, M: 2	1-13	149, 327
ARF1470	Hypothetical protein	4-16,26-32	G: 1, I: 1, M: 2	25-38	150, 328
ARF1553	Hypothetical protein	8-15,23-28	B: 2, F: 6, G: 2, H: 1, I: 1, K: 1	4-17	151, 329
CRF0017	Hypothetical protein	4-12	H: 1, I: 1, M: 5	1-15	152, 330
CRF0025	Hypothetical protein	4-29,31-42,52-58	E: 1, G: 1, L: 3, M: 1	6-16	153, 331
CRF0090	Hypothetical protein	4-9,24-32	F: 13, G: 1, H: 1, L: 1	9-19	154, 332
CRF0127	Hypothetical protein	4-12,18-27	L: 3, M: 10	5-18	155, 333
CRF0169	Hypothetical protein	4-11,37-56,58-92	D: 3	18-29	156, 334
CRF0190	Hypothetical protein	8-28	M: 14	20-35	157, 335
CRF0251	Hypothetical protein	none	D: 16, E: 2, G: 3	4-15	158, 336
CRF0258	Hypothetical protein	4-23,27-39,55-63	A: 1, B: 1, C: 1, F: 1, L: 5	35-58	159, 337
CRF0354	Hypothetical protein	6-26,28-54	F: 8, H: 1	28-47	160, 338
CRF0388	Hypothetical protein	4-10,38-52,58-82	H: 1, L: 3	30-49	161, 339

H. pylori antigenic protein	Putative function (by homology)	predicted immunogenic aa**	No. of selected clones per ORF and screen	Location of identified immunogenic region (aa)	Seq. ID (DNA, Prot.)
CRF0409	Hypothetical protein	4-22,29-35,44-50,53-68,70-80	G: 2, H: 1, M: 10	20-33	162, 340
CRF0421	Hypothetical protein	22-28,30-36	F: 4	18-33	163, 341
CRF0480	Hypothetical protein	4-11,13-21,25-30	E: 1, L: 8	20-30	164, 342
CRF0552	Hypothetical protein	10-22	G: 1, M: 5	10-23	165, 343
CRF0563	Hypothetical protein	4-11	G: 1, L: 1, M: 6	9-20	166, 344
CRF0578	Hypothetical protein	14-25,32-46	G: 1, L: 7, M: 12	6-19	167, 345
CRF0626	Hypothetical protein	5-30	L: 43	14-33	168, 346
CRF0870	Hypothetical protein	4-15,28-35,46-55,59-65,76-84	H: 6, I: 1, L: 8	9-24	169, 347
CRF0894	Hypothetical protein	27-33	L: 5	5-19	170, 348
CRF0922	Hypothetical protein	5-13	E: 11, F: 3, G: 1, H: 7, I: 1, L: 4	8-18	171, 349
CRF1012	Hypothetical protein	9-22,24-34	L: 3	21-40	172, 350
CRF1100	Hypothetical protein	4-17,35-41,46-89,93-98	E: 1, H: 5, I: 2, L: 4	71-89	173, 351
CRF1301	Hypothetical protein	4-12,14-24	H: 9, I: 2	2-17	174, 352
CRF1354	Hypothetical protein	9-17	I: 2, M: 16	5-16	175, 353
CRF1422	Hypothetical protein	7-41,48-58,63-75,80-89	G: 2, H: 1, L: 62	43-53	176, 354
CRF1489	Hypothetical protein	4-22,25-30	E: 1, F: 1, H: 5, L: 10	4-14	177, 355
CRF1549	Hypothetical protein	4-55	G: 1, M: 7	18-33	178, 356

Table 2: Gene distribution in *H. pylori* strains.

H. pylori antigenic protein	Putative function (by homology)	Gene distribution (presence in 28 strains)	Amino acid substitutions (in cancer patient isolate)*	Seq. ID (DNA, Prot.)
HP0009	outer membrane protein (omp1)	n.d.	n.d.	1, 179
HP0010	chaperone and heat shock protein (groEL)	n.d.	n.d.	2, 180
HP0043	mannose-6-phosphate isomerase (pmi)	28/28	11/247	3, 181
HP0063	hypothetical protein	n.d.	n.d.	4, 182
HP0067	urease accessory protein (ureH)	13/28	9/230	5, 183
HP0072	urease beta subunit (urea amidohydrolase) (ureB)	n.d.	n.d.	6, 184
HP0086	Conserved hypothetical protein	28/28	1/221	7, 185
HP0087	hypothetical protein	28/28	15/241	8, 186
HP0088	RNA polymerase sigma-70 factor (rpoD)	28/28	4/226	9, 187
HP0089	pfs protein (pfs)	28/28	5/199	10, 188
HP0115	flagellin B (flaB)	28/28	2/249	11, 189
HP0175	cell binding factor 2	n.d.	n.d.	12, 190
HP0121	phosphoenolpyruvate synthase (ppsA)	28/28	0/240	13, 191
HP0123	threonyl-tRNA synthetase (thrS)	28/28	7/238	14, 192
HP0130	hypothetical protein	28/28	8/241	15, 193
HP0150	hypothetical protein	28/28	5/111	16, 194
HP0183	serine hydroxymethyltransferase (glyA)	28/28	2/227	17, 195
HP0192	fumarate reductase, flavoprotein subunit (frdA)	28/28	3/219	18, 196
HP0197	S-adenosylmethionine synthetase 2 (metX)	28/28	1/243	19, 197
HP0201	fatty acid/phospholipid synthesis protein (plsX)	28/28	0/176	20, 198
HP0202	beta-ketoacyl-acyl carrier protein synthase III	28/28	7/232	21, 199
HP0210	chaperone and heat shock protein C62.5 (htpG)	n.d.	n.d.	22, 200
HP0211	conserved hypothetical secreted protein	28/28	3/201	23, 201
HP0228	conserved hypothetical integral membrane protein	28/28	3/248	24, 202
HP0229	outer membrane protein (omp6)	n.d.	n.d.	25, 203

H. pylori antigenic protein	Putative function (by homology)	Gene distribution (presence in 28 strains)	Amino acid substitutions (in cancer patient isolate)*	Seq. ID (DNA, Prot.)
HP0235	conserved hypothetical secreted protein	n.d.	n.d.	26, 204
HP0239	glutamyl-tRNA reductase (hemA)	7/28	4/257'	27, 205
HP0258	conserved hypothetical integral membrane protein	28/28	14/254	28, 206
HP0266	dihydroorotase (pyrC)	15/28	14/253	29, 207
HP0279	lipopolysaccharide heptosyltransferase-1 (rfaC)	28/28	15/246	30, 208
HP0289	toxin-like outer membrane protein	28/28	12/241	31, 209
HP0292	hypothetical protein	28/28	9/245	32, 210
HP0295	flagellin B homolog (fla)	14/28	9/224'	33, 211
HP0349	CTP synthetase (pyrG)	28/28	2/249	34, 212
HP0351	flagellar basal-body M-ring protein (fliF)	28/28	2/249	35, 213
HP0380	glutamate dehydrogenase (gdhA)	28/28	9/253	36, 214
HP0392	histidine kinase (cheA)	27/28	4/259; 5 aa inserted, 4 aa deleted	37, 215
HP0401	3-phosphoshikimate 1-carboxyvinyltransferase (aroA)	28/28	14/248	38, 216
HP0406	hypothetical protein	28/28	2/146	39, 217
HP0409	GMP synthase (guaA)	28/28	9/252	40, 218
HP0413	transposase-like protein, PS3IS	10/28	0/268'	41, 219
HP0459	virB4 homolog (virB4)	9/28	6/248'	42, 220
HP0480	GTP-binding protein, fusA-homolog (yihK)	n.d.	n.d.	43, 221
HP0485	catalase-like protein	28/28	7/252	44, 222
HP0508	hypothetical protein	28/28	3/260	45, 223
HP0519	conserved hypothetical protein	28/28	6/224; 1 aa inserted, 1 aa deleted	46, 224
HP0525	virB11 homolog	24/28	0/257	47, 225
HP0527	cag pathogenicity island protein (cag7-cagY)	22/28	4/214	48, 226
HP0540	cag pathogenicity island protein (cag19)	25/28	5/251	49, 227
HP0541	cag pathogenicity island protein (cag20)	26/28	3/251	50, 228

H. pylori antigenic protein	Putative function (by homology)	Gene distribution (presence in 28 strains)	Amino acid substitutions (in cancer patient isolate)*	Seq. ID (DNA, Prot.)
HP0542	cag pathogenicity island protein (cag21-cagG)	23/28	0/115	51, 229
HP0544	cag pathogenicity island protein (cag23-cagE)	11/28	n.d.	52, 230
HP0545	cag pathogenicity island protein (cag24)	25/28	1/153	53, 231
HP547	cag pathogenicity island protein (cag26-cagA)	24/28	20/256; 1 aa inserted#	54,232
HP0563	hypothetical protein	28/28	9/192	55, 233
HP0604	uroporphyrinogen decarboxylase (hemE)	28/28	5/260	56, 234
HP0607	acriflavine resistance protein (acrB)	28/28	0/254	57, 235
HP0630	modulator of drug activity (mda66)	28/28	2/112#	58, 236
HP0635	hypothetical protein	24/28	13/135	59, 237
HP0655	protective surface antigen D15	28/28	n.d.	60, 238
HP0659	hypothetical protein	6/28	14/187	61, 239
HP0683	UDP-N-acetylglucosamine pyrophosphorylase (glmU)	28/28	8/193	62, 240
HP0687	iron(II) transport protein (feoB)	28/28	2/203	63, 241
HP0696	N-methylhydantoinase	28/28	2/206	64, 242
HP0701	DNA gyrase, sub A (gyrA)	28/28	5/224	65, 243
HP0706	outer membrane protein (omp15)	28/28	2/167	66, 244
HP0714	RNA polymerase sigma-54 factor (rpoN)	28/28	8/200	67, 245
HP0717	DNA polymerase III gamma and tau subunits (dnaX)	28/28	15/137; 2 aa inserted#	68,246
HP0723	L-asparaginase II (ansB)	28/28	12/220	69, 247
HP0727	transcriptional regulator, putative	28/28	4/207	70, 248
HP0752	flagellar hook-associated protein 2 (fliD)	28/28	2/191	71, 249
HP0760	conserved hypothetical protein	28/28	2/211	72, 250
HP0836	hypothetical protein	28/28	1/82	73, 251
HP0850	type I restriction enzyme M protein (hsdM)	28/28	10/181	74, 252
HP0853	ABC transporter, ATP-binding protein (yheS)	19/28	2/198#	75, 253

H. pylori antigenic protein	Putative function (by homology)	Gene distribution (presence in 28 strains)	Amino acid substitutions (in cancer patient isolate)*	Seq. ID (DNA, Prot.)
HP0863	hypothetical protein	27/28	2/161	76, 254
HP0874	hypothetical protein	28/28	3/243	77, 255
HP0875	catalase	n.d.	n.d.	78, 256
HP0876	iron-regulated outer membrane protein (frpB)	28/28	4/193	79, 257
HP0887	vacuolating cytotoxin	28/28	9/228'	80, 258
HP0891	conserved hypothetical protein	18/28	2/149'	81, 259
HP0910	adenine specific DNA methyltransferase (HINDIIM)	27/28	3/205	82, 260
HP0913	outer membrane protein (omp21)	28/28	12/172 ; 1 aa deleted	83, 261
HP0922	toxin-like outer membrane protein	28/28	27/198	84, 262
HP0925	recombinational DNA repair protein (recR)	28/28	1/159	85, 263
HP0953	hypothetical protein	28/28	2/164	86, 264
HP0973	hypothetical protein	19/28	6/248; 1 aa deleted	87, 265
HP0977	conserved hypothetical secreted protein	28/28	9/238	88, 266
HP1019	serine protease (htrA)	n.d.	n.d.	89, 267
HP1024	co-chaperone-curved DNA binding protein A (CbpA)	25/28	5/167	90, 268
HP1052	UDP-3-0-acyl N-acetylglcosamine deacetylase (envA)	28/28	5/186	91, 269
HP1090	cell division protein (ftsK)	28/28	2/223	92, 270
HP1098	conserved hypothetical secreted protein	n.d.	n.d.	93, 271
HP1116	hypothetical protein	28/28	192/283	94, 272
HP1117	conserved hypothetical secreted protein	n.d.	n.d.	95, 273
HP1119	flagellar hook-associated protein 1 (HAP1) (flgK)	28/28	7/213	96, 274
HP1126	colicin tolerance-like protein (tolB)	28/28	4/241	97, 275
HP1152	signal recognition particle protein (ffh)	n.d.	n.d.	98, 276
HP1153	valyl-tRNA synthetase (valS)	28/28	14/243	99, 277
HP1186	carbonic anhydrase			100, 278
HP1198	DNA-directed RNA polymerase,	28/28	7/232	101, 279

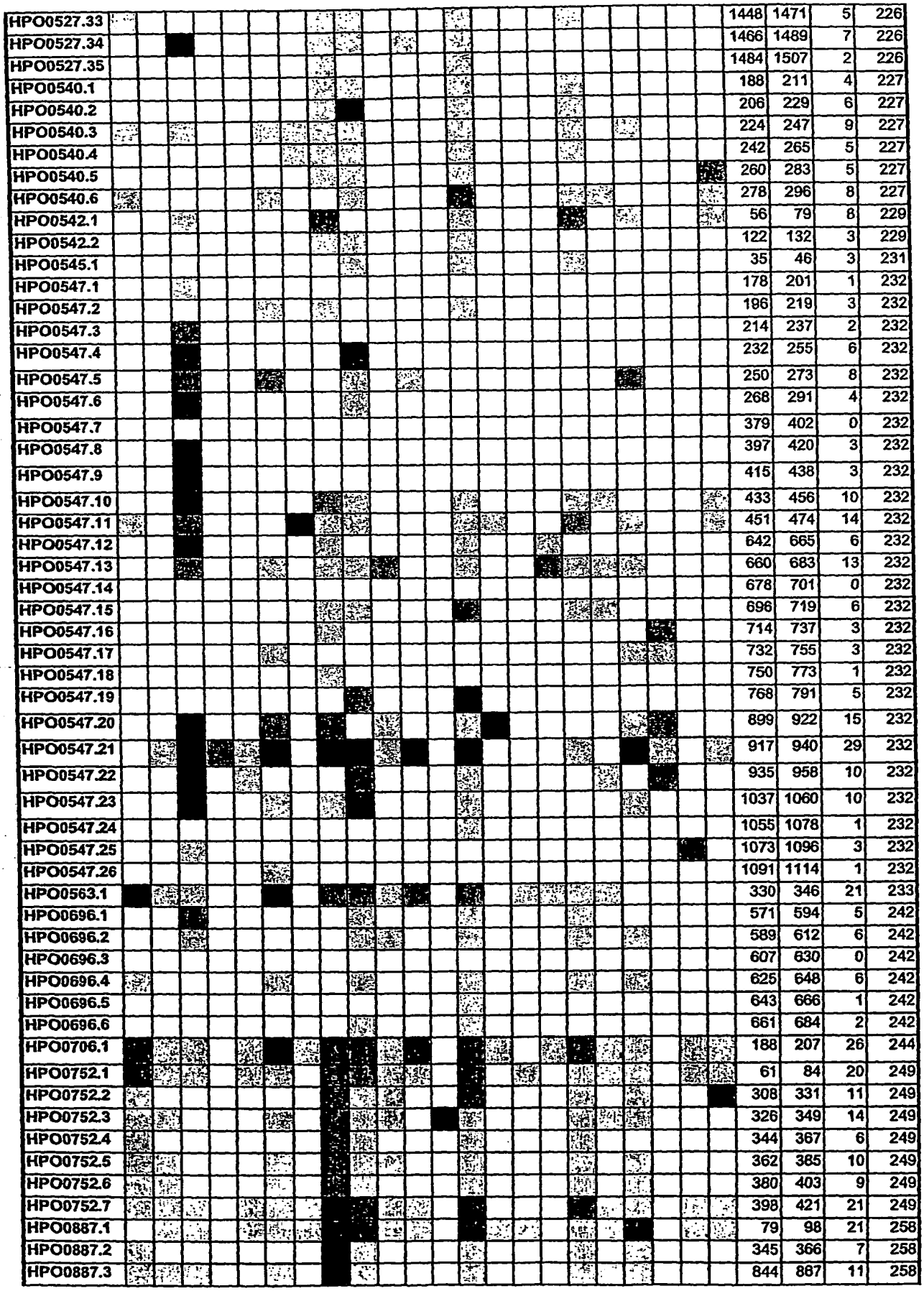
H. pylori antigenic protein	Putative function (by homology)	Gene distribution (presence in 28 strains)	Amino acid substitutions (in cancer patient isolate)*	Seq. ID (DNA, Prot.)
	beta subunit (rpoB)			
HP1205	translation elongation factor EF-Tu (tufB)	n.d.	n.d.	102, 280
HP1229	aspartokinase (lysC)	2728	4/245#	103, 281
HP1243	outer membrane protein (omp28)	n.d.	n.d.	104, 282
HP1254	biotin synthesis protein (bioC)	28/28	9/169	105, 283
HP1265	hypothetical protein	28/28	19/216	106, 284
HP1282	anthranilate synthase component I (trpE)	28/28	12/193	107, 285
HP1329	cation efflux system protein (czcA)	28/28	3/196	108, 286
HP1339	biopolymer transport protein (exbB)	27/28	1/109#	109, 287
HP1341	siderophore-mediated iron transport protein	28/28	12/179#	110, 288
HP1342	outer membrane protein (omp29)	n.d.	n.d.	111, 289
HP1345	phosphoglycerate kinase	28/28	3/220	112, 290
HP1350	protease	n.d.	n.d.	113, 291
HP1374	ATP-dependent protease ATPase subunit (clpX)	28/28	0/211	114, 292
HP1393	DNA repair protein (recN)	28/28	4/209	115, 293
HP1448	ribonuclease P, protein component (rnpA)	19/28	5/124#	116, 294
HP1453	conserved hypothetical protein	28/28	8/200	117, 295
HP1454	hypothetical protein	n.d.	n.d.	118, 296
HP1460	DNA polymerase III alpha-subunit (dnaE)	28/28	2/225	119, 297
HP1497	peptidyl-tRNA hydrolase (pth)	28/28	4/155	120, 298
HP1527	hypothetical protein	28/28	14/202	121, 299
HP1564	outer membrane protein	n.d.	n.d.	122, 300
HP1565	penicillin-binding protein 2 (pbp2)	28/28	3/178	123, 301
HP1574	riboflavin synthase alpha subunit (ribC)	23/28	4/153#	124, 302
ARF0044	Hypothetical protein	n.d.	n.d.	125, 303
ARF0048	Hypothetical protein	n.d.	n.d.	126, 304
ARF0143	Hypothetical protein	n.d.	n.d.	127, 305
ARF0184	Hypothetical protein	n.d.	n.d.	128, 306

H. pylori antigenic protein	Putative function (by homology)	Gene distribution (presence in 28 strains)	Amino acid substitutions (in cancer patient isolate)*	Seq. ID (DNA, Prot.)
ARF0219	Hypothetical protein	n.d.	n.d.	129, 307
ARF0308	Hypothetical protein	n.d.	n.d.	130, 308
ARF0349	Hypothetical protein	n.d.	n.d.	131, 309
ARF0387	Hypothetical protein	n.d.	n.d.	132, 310
ARF0402	Hypothetical protein	n.d.	n.d.	133, 311
ARF0501	Hypothetical protein	n.d.	n.d.	134, 312
ARF0509	Hypothetical protein	n.d.	n.d.	135, 313
ARF0522	Hypothetical protein	n.d.	n.d.	136, 314
ARF0578	Hypothetical protein	n.d.	n.d.	137, 315
ARF0629	Hypothetical protein	n.d.	n.d.	138, 316
ARF0665	Hypothetical protein	n.d.	n.d.	139, 317
ARF0693	Hypothetical protein	n.d.	n.d.	140, 318
ARF0752	Hypothetical protein	n.d.	n.d.	141, 319
ARF0788	Hypothetical protein	n.d.	n.d.	142, 320
ARF0819	Hypothetical protein	n.d.	n.d.	143, 321
ARF0839	Hypothetical protein	n.d.	n.d.	144, 322
ARF0868	Hypothetical protein	n.d.	n.d.	145, 323
ARF0948	Hypothetical protein	n.d.	n.d.	146, 324
ARF0969	Hypothetical protein	n.d.	n.d.	147, 325
ARF1100	Hypothetical protein	n.d.	n.d.	148, 326
ARF1164	Hypothetical protein	n.d.	n.d.	149, 327
ARF1470	Hypothetical protein	n.d.	n.d.	150, 328
ARF1553	Hypothetical protein	n.d.	n.d.	151, 329
CRF0017	Hypothetical protein	n.d.	n.d.	152, 330
CRF0025	Hypothetical protein	n.d.	n.d.	153, 331
CRF0090	Hypothetical protein	n.d.	n.d.	154, 332
CRF0127	Hypothetical protein	n.d.	n.d.	155, 333
CRF0169	Hypothetical protein	n.d.	n.d.	156, 334
CRF0190	Hypothetical protein	n.d.	n.d.	157, 335
CRF0251	Hypothetical protein	n.d.	n.d.	158, 336
CRF0258	Hypothetical protein	n.d.	n.d.	159, 337
CRF0354	Hypothetical protein	n.d.	n.d.	160, 338
CRF0388	Hypothetical protein	n.d.	n.d.	161, 339
CRF0409	Hypothetical protein	n.d.	n.d.	162, 340
CRF0421	Hypothetical protein	n.d.	n.d.	163, 341
CRF0480	Hypothetical protein	n.d.	n.d.	164, 342
CRF0552	Hypothetical protein	n.d.	n.d.	165, 343
CRF0563	Hypothetical protein	n.d.	n.d.	166, 344
CRF0578	Hypothetical protein	n.d.	n.d.	167, 345

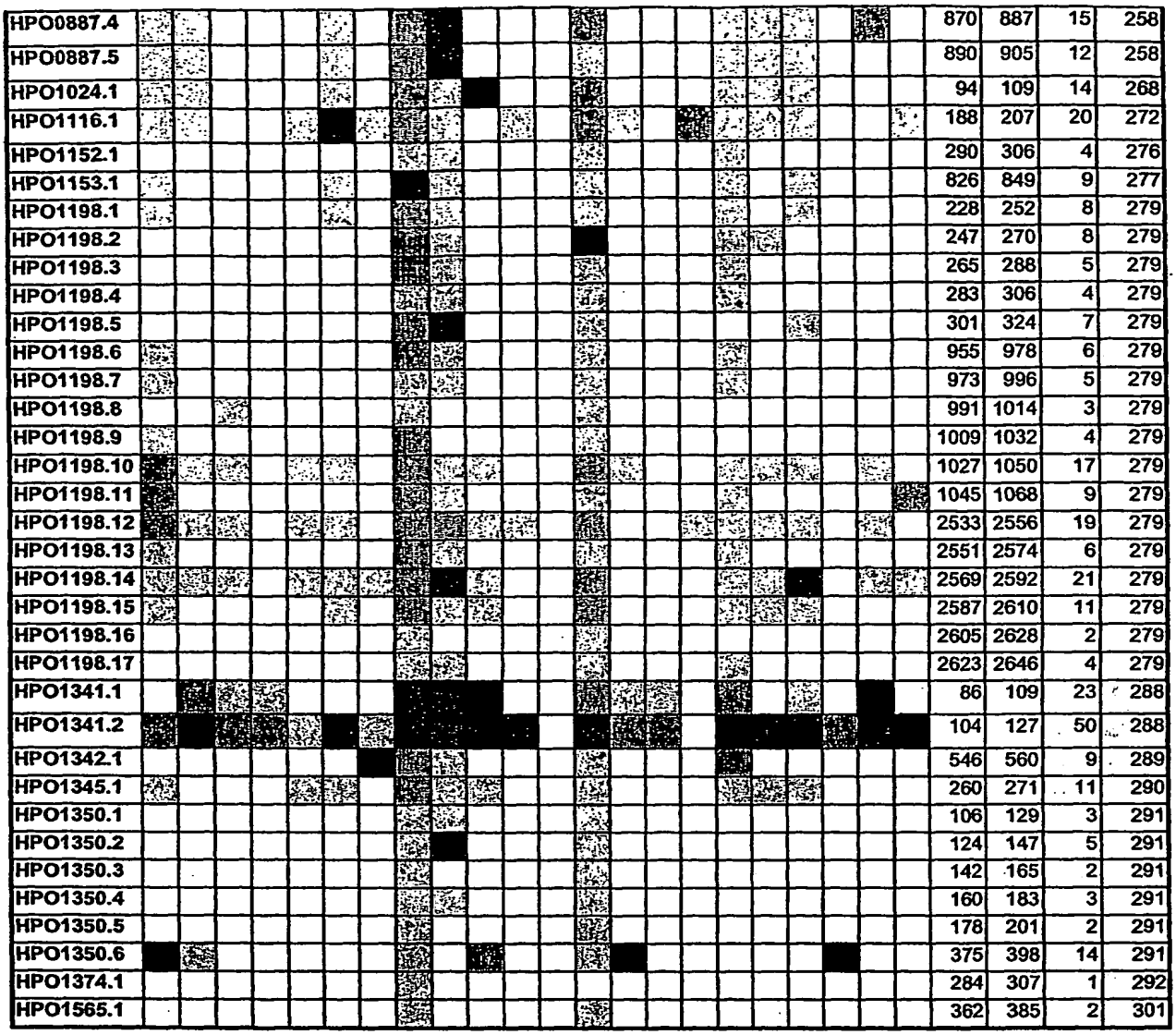
H. pylori antigenic protein	Putative function (by homology)	Gene distribution (presence in 28 strains)	Amino acid substitutions (in cancer patient isolate)*	Seq. ID (DNA, Prot.)
CRF0626	Hypothetical protein	n.d.	n.d.	168, 346
CRF0870	Hypothetical protein	n.d.	n.d.	169, 347
CRF0894	Hypothetical protein	n.d.	n.d.	170, 348
CRF0922	Hypothetical protein	n.d.	n.d.	171, 349
CRF1012	Hypothetical protein	n.d.	n.d.	172, 350
CRF1100	Hypothetical protein	n.d.	n.d.	173, 351
CRF1301	Hypothetical protein	n.d.	n.d.	174, 352
CRF1354	Hypothetical protein	n.d.	n.d.	175, 353
CRF1422	Hypothetical protein	n.d.	n.d.	176, 354
CRF1489	Hypothetical protein	n.d.	n.d.	177, 355
CRF1549	Hypothetical protein	n.d.	n.d.	178, 356

Table 3.

	P1	P2	P3	P4	P5	P6	P7	P8	P9	P10	P11	P12	P13	P14	P15	P16	P17	P18	N1	N2	N3	N4	from	to	S	SeqID
HPO0009.1																							262	280	16	179
HPO0087.1																							131	146	18	186
HPO0089.1																							207	224	6	188
HPO0115.1																							27	50	4	189
HPO0115.2																							203	217	2	189
HPO0115.3																							313	325	8	189
HPO0123.1																							110	129	12	192
HPO0175.1																							156	179	3	190
HPO0175.2																							174	197	15	190
HPO0175.3																							192	215	6	190
HPO0175.4																							210	233	7	190
HPO0175.5																							228	251	13	190
HPO0175.6																							246	267	12	190
HPO0192.1																							377	400	32	196
HPO0229.1																							34	43	3	203
HPO0229.2																							234	257	9	203
HPO0229.3																							350	367	9	203
HPO0266.1																							304	327	8	207
HPO0485.1																							25	48	20	222
HPO0485.2																							43	66	1	222
HPO0485.3																							61	82	10	222
HPO0527.1																							398	421	6	226
HPO0527.2																							416	439	6	226
HPO0527.3																							434	457	6	226
HPO0527.4																							452	475	6	226
HPO0527.5																							470	493	24	226
HPO0527.6																							488	511	5	226
HPO0527.7																							506	529	21	226
HPO0527.8																							524	547	4	226
HPO0527.9																							621	644	13	226
HPO0527.10																							639	664	7	226
HPO0527.11																							707	730	8	226
HPO0527.12																							725	748	16	226
HPO0527.13																							743	766	13	226
HPO0527.14																							761	784	10	226
HPO0527.15																							779	802	9	226
HPO0527.16																							797	820	20	226
HPO0527.17																							984	1007	9	226
HPO0527.18																							1002	1025	14	226
HPO0527.19																							1020	1043	24	226
HPO0527.20																							1038	1061	21	226
HPO0527.21																							1056	1079	26	226
HPO0527.22																							1074	1097	7	226
HPO0527.23																							1092	1115	25	226
HPO0527.24																							1286	1309	2	226
HPO0527.25																							1304	1327	6	226
HPO0527.26																							1322	1345	7	226
HPO0527.27																							1340	1363	5	226
HPO0527.28																							1358	1381	7	226
HPO0527.29																							1376	1399	4	226
HPO0527.30																							1394	1417	4	226
HPO0527.31																							1412	1435	5	226
HPO0527.32																							1430	1453	5	226



HPO0527.33	1448	1471	5	226
HPO0527.34	1466	1489	7	226
HPO0527.35	1484	1507	2	226
HPO0540.1	188	211	4	227
HPO0540.2	206	229	6	227
HPO0540.3	224	247	9	227
HPO0540.4	242	265	5	227
HPO0540.5	260	283	5	227
HPO0540.6	278	296	8	227
HPO0542.1	56	79	8	229
HPO0542.2	122	132	3	229
HPO0545.1	35	46	3	231
HPO0547.1	178	201	1	232
HPO0547.2	196	219	3	232
HPO0547.3	214	237	2	232
HPO0547.4	232	255	6	232
HPO0547.5	250	273	8	232
HPO0547.6	268	291	4	232
HPO0547.7	379	402	0	232
HPO0547.8	397	420	3	232
HPO0547.9	415	438	3	232
HPO0547.10	433	456	10	232
HPO0547.11	451	474	14	232
HPO0547.12	642	665	6	232
HPO0547.13	660	683	13	232
HPO0547.14	678	701	0	232
HPO0547.15	696	719	6	232
HPO0547.16	714	737	3	232
HPO0547.17	732	755	3	232
HPO0547.18	750	773	1	232
HPO0547.19	768	791	5	232
HPO0547.20	899	922	15	232
HPO0547.21	917	940	29	232
HPO0547.22	935	958	10	232
HPO0547.23	1037	1060	10	232
HPO0547.24	1055	1078	1	232
HPO0547.25	1073	1096	3	232
HPO0547.26	1091	1114	1	232
HPO0563.1	330	346	21	233
HPO0696.1	571	594	5	242
HPO0696.2	589	612	6	242
HPO0696.3	607	630	0	242
HPO0696.4	625	648	6	242
HPO0696.5	643	666	1	242
HPO0696.6	661	684	2	242
HPO0706.1	188	207	26	244
HPO0752.1	61	84	20	249
HPO0752.2	308	331	11	249
HPO0752.3	326	349	14	249
HPO0752.4	344	367	6	249
HPO0752.5	362	385	10	249
HPO0752.6	380	403	9	249
HPO0752.7	398	421	21	249
HPO0887.1	79	98	21	258
HPO0887.2	345	366	7	258
HPO0887.3	844	887	11	258



HPO0887.4	870	887	15	258
HPO0887.5	890	905	12	258
HPO1024.1	94	109	14	268
HPO1116.1	188	207	20	272
HPO1152.1	290	306	4	276
HPO1153.1	826	849	9	277
HPO1198.1	228	252	8	279
HPO1198.2	247	270	8	279
HPO1198.3	265	288	5	279
HPO1198.4	283	306	4	279
HPO1198.5	301	324	7	279
HPO1198.6	955	978	6	279
HPO1198.7	973	996	5	279
HPO1198.8	991	1014	3	279
HPO1198.9	1009	1032	4	279
HPO1198.10	1027	1050	17	279
HPO1198.11	1045	1068	9	279
HPO1198.12	2533	2556	19	279
HPO1198.13	2551	2574	6	279
HPO1198.14	2569	2592	21	279
HPO1198.15	2587	2610	11	279
HPO1198.16	2605	2628	2	279
HPO1198.17	2623	2646	4	279
HPO1341.1	86	109	23	288
HPO1341.2	104	127	50	288
HPO1342.1	546	560	9	289
HPO1345.1	260	271	11	290
HPO1350.1	106	129	3	291
HPO1350.2	124	147	5	291
HPO1350.3	142	165	2	291
HPO1350.4	160	183	3	291
HPO1350.5	178	201	2	291
HPO1350.6	375	398	14	291
HPO1374.1	284	307	1	292
HPO1565.1	362	385	2	301

Claims:

1. An isolated nucleic acid molecule encoding a hyperimmune serum reactive antigen or a fragment thereof comprising a nucleic acid sequence which is selected from the group consisting of:
   a) a nucleic acid molecule having at least 70% sequence identity to a nucleic acid molecule selected from **Seq ID No** 3-4, 16, 19-21, 28-29, 33-38, 41-42, 44, 48-52, 55, 57-58, 61, 63, 65, 67-68, 72, 74-75, 81, 84, 91, 94, 96-97, 101, 105-108, 112, 115-117, 119, 123-178,
   b) a nucleic acid molecule which is complementary to the nucleic acid molecule of a),
   c) a nucleic acid molecule comprising at least 15 sequential bases of the nucleic acid molecule of a) or b)
   d) a nucleic acid molecule which anneals under stringent hybridisation conditions to the nucleic acid molecule of a), b), or c)
   e) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid molecule defined in a), b), c) or d).

2. The isolated nucleic acid molecule according to claim 1, wherein the sequence identity is at least 80%, preferably at least 95%, especially 100%.

3. An isolated nucleic acid molecule encoding a hyperimmune serum reactive antigen or a fragment thereof comprising a nucleic acid sequence selected from the group consisting of
   a) a nucleic acid molecule having at least 96% sequence identity to a nucleic acid molecule selected from **Seq ID No** 8-10, 13-15, 17-18, 24, 27, 32, 39-40, 45-47, 56, 59, 62, 69-70, 73, 77, 79, 82, 85-86, 88, 90, 103, 109-110, 114, 121.
   b) a nucleic acid molecule which is complementary to the nucleic acid molecule of a),
   c) a nucleic acid molecule comprising at least 15 sequential bases of the nucleic acid molecule of a) or b)
   d) a nucleic acid molecule which anneals under stringent hybridisation conditions to the nucleic acid molecule of a), b) or c),
   e) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid defined in a), b), c) or d).

4. An isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of
   a) a nucleic acid molecule selected from **Seq ID No** 5, 7, 30-31, 53, 60, 66, 76, 83, 87, 92, 99, 120,
   b) a nucleic acid molecule which is complementary to the nucleic acid of a),
   c) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid defined in a), b), c) or d).

5. The nucleic acid molecule according to any one of the claims 1, 2, 3 or 4, wherein the nucleic acid is DNA.

6. The nucleic acid molecule according to any one of the claims 1,2, 3, 4, or 5 wherein the nucleic acid is RNA.

7. An isolated nucleic acid molecule according to any one of claims 1 to 5, wherein the nucleic acid molecule is isolated from a genomic DNA, especially from a *H. pylori* genomic DNA.

8. A vector comprising a nucleic acid molecule according to any one of claims 1 to 7.

9. A vector according to claim 8, wherein the vector is adapted for recombinant expression of the hyperimmune serum reactive antigens or fragment thereof encoded by the nucleic acid molecule according to any one of claims 1 to 7.

10. A host cell comprising the vector according to claim 8 or 9.

11. A hyperimmune serum-reactive antigen comprising an amino acid sequence being encoded by a nucleic acid molecule according to any one of the claims 1, 2, 5, 6 or 7 and fragments thereof, wherein the amino acid sequence is selected from the group consisting of **Seq ID No** 181-182, 194, 197-199, 206-207, 211-216, 219-220, 222, 226-230, 233, 235-236, 239, 241, 243, 245-246, 250, 252-253, 259, 262, 269, 272, 274-275, 279, 283-286, 290, 293-295, 297, 301-356.

12. A hyperimmune serum-reactive antigen comprising an amino acid sequence being encoded by a nucleic acid molecule according to any one of the claims 3, 5, 6, or 7 and fragments thereof, wherein the amino acid sueqnece is selected from the group consisting of **Seq ID No** 186-188, 191-193, 195-196, 202, 205, 210, 217-218, 223-225, 234, 237, 240, 247-248, 251, 255, 257, 260, 263-264, 266, 268, 281, 287-288, 292, 299.

13. A hyperimmune serum-reactive antigen comprising an amino acid sequence being encoded by a nucleic acid molecule according to any one of the claims 4, 5, 6, or 7 and fragments thereof, wherein the amino acid sequence is selected from the group consisting of **Seq ID No** 183, 185, 208-209, 231, 238, 244, 254, 261, 265, 270, 277, 298.

14. Fragments of hyperimmune serum-reactive antigens selected from the group consisting of peptides comprising amino acid sequences of column "predicted immunogenic aa" and "location of identified immunogenic region" of Table 1, the serum reactive epitope of Table 3 especially peptides comprising amino acid 63-91, 95-101, 110-116, 134-148, 150-156, 158-164, 188-193, 197-209, 226-241, 247-254, 291-297, 312-319, 338-346, 351-358, 366-378, 404-410, 420-438, 448-454, 465-473, 482-488, 490-498, 503-510, 512-519, 531-543, 547-554, 568-575, 589-604, 610-631 and 239-308 of **Seq ID No** 179; 16-29, 35-47, 50-68, 70-79, 91-101, 143-149, 158-163, 185-191, 196-206, 215-224, 230-237, 244-251, 258-278, 290-311, 319-325, 338-351, 365-385, 396-429, 445-454, 458-466, 491-499, 501-521, 17-79 and 218-233 of **Seq ID No** 180; 4-10, 16-41, 46-66, 77-84, 91-97, 102-118, 125-144, 187-200, 202-214, 245-253, 255-261, 286-295, 300-330, 335-342, 350-361, 363-381, 385-392, 396-416, 435-450 and 460-470 of **Seq ID No** 181; 11-19, 27-48, 52-59, 77-82, 84-107, 118-125, 127-154, 178-183, 192-209, 215-221, 286-295, 302-313, 350-357, 402-415, 417-431, 453-463, 465-493 and 313-331 of **Seq ID No** 182; 19-26, 30-43, 47-55, 63-68, 72-80, 97-104, 107-119, 129-146, 160-175, 194-216, 231-251, 254-260 and 26-43 of **Seq ID No** 183; 7-13, 29-37, 65-81, 110-120, 123-131, 135-152, 230-249, 254-260, 284-290, 292-299, 317-326, 329-336, 403-444, 452-458, 466-477, 490-498, 510-519, 541-550, 557-566 and 533-567 of **Seq ID No** 184; 5-47, 71-77, 79-86, 89-95, 120-126, 137-144, 176-181, 184-196, 202-208, 211-232, 236-282, 301-313, 317-325, 341-347, 353-384, 394-400, 412-433, 436-443 and 59-75 of **Seq ID No** 185; 4-18, 22-38, 59-69, 106-112, 116-130, 138-149, 156-170, 175-197, 200-214, 216-223, 233-244, 255-261, 266-276, 279-286, 325-333, 342-348, 366-399, 402-420, 429-441, 1-104 and 130-147 of **Seq ID No** 186; 50-58, 69-95, 97-113, 131-136, 157-163, 170-175, 188-212, 220-226, 254-259, 265-277, 283-289, 297-308, 311-318, 347-358, 360-369, 378-401, 416-421, 440-450, 454-462, 470-476, 493-502, 506-514, 536-567, 585-590, 598-607, 613-618, 653-659 and 35-46 of **Seq ID No** 187; 16-29, 32-60, 65-87, 89-123, 128-134, 137-158, 162-173, 178-196, 210-216, 218-228 and 206-225 of **Seq ID No** 188; 10-20, 26-35, 51-64, 86-91, 94-100, 113-122, 154-160, 185-191, 193-201, 211-217, 225-230, 237-246, 251-257, 298-304, 306-312, 316-328, 340-348, 357-389, 391-397, 415-421, 449-456, 458-471, 488-495, 502-511, 24-55 and 236-341 of **Seq ID No** 189; 5-22, 41-51, 87-93, 114-122, 127-136, 150-156, 158-166, 223-233, 245-263, 291-296, 9-126 and 127-285 of **Seq ID No** 190; 30-43, 46-56, 61-70, 72-83, 85-93, 103-113, 119-125, 151-166, 179-191, 212-218, 225-231, 236-243, 262-267, 291-307, 331-344, 349-355, 366-372, 380-386, 414-422, 428-447, 459-464, 469-478, 507-519, 525-544, 563-569, 576-590, 620-626, 633-643, 654-659, 665-671, 684-707, 717-723, 725-733, 747-779, 782-801 and 347-361 of **Seq ID No** 191; 4-12, 14-26, 37-80, 107-115, 133-139, 144-150, 154-165, 173-180, 191-199, 205-211, 221-231, 237-244, 254-284, 307-340, 342-353, 360-368, 370-380, 479-493, 495-503,

509-522, 525-536, 539-547, 554-560, 565-573, 578-583, 7-23 and 465-479 of Seq ID No 192; 4-17, 47-55, 76-83, 85-100, 104-112, 117-123, 126-135, 142-148, 156-167, 174-182, 267-273 and 258-283 of Seq ID No 193; 8-32, 36-42, 65-88, 102-108, 112-140, 147-163, 170-179, 183-193 and 117-124 of Seq ID No 194; 12-18, 45-50, 62-77, 82-95, 99-113, 115-123, 125-147, 155-177, 187-209, 211-223, 244-253, 259-270, 278-297, 302-307, 311-318, 329-334, 350-356, 359-365, 390-400, 402-413 and 333-350 of Seq ID No 195; 4-13, 15-27, 30-46, 53-58, 68-74, 82-95, 115-126, 134-139, 148-153, 159-176, 182-199, 201-217, 220-225, 227-235, 237-248, 253-266, 300-315, 322-336, 390-396, 412-426, 438-445, 448-459, 477-484, 502-508, 515-527, 529-537, 553-568, 643-651, 658-667, 690-703 and 376-400 of Seq ID No 196; 4-10, 24-32, 38-55, 59-67, 70-77, 80-87, 89-97, 123-129, 134-151, 166-172, 178-189, 191-216, 218-235, 245-259, 271-315, 326-339, 341-360 and 73-94 of Seq ID No 197; 13-25, 31-38, 43-57, 79-85, 92-99, 106-112, 117-128, 130-139, 146-158, 160-175, 194-204, 211-222, 225-232, 234-242, 263-270, 278-292, 299-320, 322-333 and 240-256 of Seq ID No 198; 4-17, 55-63, 66-101, 109-131, 135-143, 145-151, 155-161, 164-170, 177-185, 192-198, 213-218, 223-238, 246-256, 258-268, 273-283, 309-314, 322-328 and 195-221 of Seq ID No 199; 13-24, 31-39, 41-50, 63-69, 90-96, 104-109, 116-141, 148-153, 161-167, 173-178, 190-209, 253-258, 265-272, 279-289, 295-312, 317-343, 355-366, 376-389, 400-407, 430-451, 453-464, 466-472, 487-493, 499-505, 523-538, 554-559, 568-579, 584-601 and 344-363 of Seq ID No 200; 5-22, 30-36, 53-59, 61-70, 82-92, 99-106, 120-131, 135-148, 154-167, 169-183, 187-199, 204-212, 231-247 and 111-249 of Seq ID No 201; 17-36, 40-66, 71-144, 148-171, 173-191, 199-214, 220-252, 265-272, 278-288, 298-333, 342-385 and 287-307 of Seq ID No 202; 4-16, 22-28, 30-36, 42-48, 95-116, 154-162, 164-174, 239-252, 258-263, 273-285, 306-313, 323-333, 341-357, 363-369, 372-379, 395-401, 430-436, 438-453, 464-480, 33-44, 233-258 and 349-369 of Seq ID No 203; 4-21, 30-37, 46-53, 59-68, 80-92, 98-104, 118-143, 150-160, 165-185, 187-200, 204-211, 224-236, 241-246, 252-258, 271-280, 288-294, 311-320, 335-341 and 191-350 of Seq ID No 204; 4-16, 37-59, 64-70, 79-87, 93-102, 107-127, 143-165, 172-188, 197-204, 207-218, 221-227, 242-248, 258-277, 289-296, 298-316, 332-338, 344-365, 367-373, 375-382, 400-408, 415-425, 438-446 and 235-250 of Seq ID No 205; 4-37, 39-66, 84-98, 101-127, 140-149, 157-163, 166-172, 175-182, 184-193, 203-208, 215-232, 234-247, 250-299, 303-345 and 183-204 of Seq ID No 206; 10-20, 41-61, 73-87, 112-141, 176-192, 194-201, 205-222, 230-237, 257-264, 276-282, 284-310, 312-318, 330-337, 349-357 and 304-328 of Seq ID No 207; 4-31, 42-103, 105-113, 121-153, 160-181, 188-196, 210-226, 231-264, 272-287, 297-304, 328-336 and 304-318 of Seq ID No 208; 21-43, 46-52, 54-70, 72-79, 94-107, 133-141, 160-166, 217-253, 311-317, 359-365, 374-381, 390-395, 434-440, 488-494, 497-502, 511-522, 554-563, 565-574, 577-585, 591-598, 601-606, 617-625, 633-643, 658-664, 676-682, 694-702, 710-719, 754-760, 782-788, 802-808, 916-921, 942-948, 955-964, 973-979, 992-998, 1006-1011, 1016-1023, 1030-1038, 1046-1053, 1059-1066, 1088-1098, 1119-1126, 1129-1135, 1156-1171, 1173-1181, 1202-1210, 1255-1261, 1268-1280, 1295-1310, 1312-1320, 1375-1381, 1406-1417, 1450-1471, 1478-1492, 1498-1506, 1569-1578, 1603-1608, 1611-1624, 1648-1655, 1663-1670, 1680-1698, 1702-1707, 1713-1719, 1737-1742, 1747-1753, 1762-1769, 1771-1785, 1790-1804, 1811-1818, 1830-1836, 1838-1852, 1874-1886, 1893-1899, 1902-1909, 1942-1948, 1952-1962, 1980-1986, 2001-2017, 2020-2028, 2042-2050, 2052-2068, 2074-2079, 2083-2095, 2107-2113, 2147-2155, 2177-2194, 2203-2211, 2236-2241, 2251-2258, 2267-2274, 2285-2292, 2314-2328, 2330-2340, 2358-2365, 2390-2401, 2408-2418, 2432-2453, 2463-2476, 2486-2507, 2528-2537, 2540-2548, 2552-2558, 2568-2576, 2596-2601, 2610-2622, 2629-2638, 2653-2669, 2718-2727, 2749-2767, 2777-2784, 2789-2795, 2806-2815, 2817-2824, 2835-2843, 2847-2854, 2860-2881, 511-523, 612-630 and 1790-1803 of Seq ID No 209; 4-54, 61-68, 72-82, 86-93, 100-108, 115-130, 147-154, 187-194, 196-207, 224-229, 236-251, 275-287 and 96-109 of Seq ID No 210; 31-39, 62-69, 91-101, 158-172, 175-180, 186-193, 201-208, 210-223, 243-250, 273-286, 293-299, 319-325, 343-354, 356-365, 368-384, 414-435, 471-491, 512-518, 550-556, 567-581, 584-589, 633-639, 680-692, 697-708, 716-721, 747-754, 779-786, 810-816 and 366-503 of Seq ID No 211; 5-20, 22-48, 57-65, 96-101, 111-122, 130-145, 154-164, 170-181, 193-199, 201-216, 224-241, 244-262, 281-323, 342-351, 359-367, 369-396, 406-416, 424-433, 450-456, 485-491, 493-499, 501-515, 517-535 and 289-305 of Seq ID No 212; 4-17, 22-44, 53-60, 66-83, 87-94, 101-106, 110-116, 131-137, 148-183, 189-207, 209-215, 233-242, 251-262, 264-272, 290-296, 308-327, 359-373, 375-380, 397-405, 415-420, 426-433, 444-475, 478-484, 529-536, 548-558 and 106-126 of Seq ID No 213; 4-38, 42-50, 58-64, 72-81, 92-118, 140-146, 157-165, 172-192, 198-204, 208-216, 227-234, 238-258, 271-278, 288-293, 311-322, 327-346, 357-370, 375-383, 395-409, 411-417, 425-432, 436-445, 109-129 and 370-380 of Seq ID No 214; 23-30, 36-49, 52-

64, 86-94, 97-104, 121-129, 257-272, 279-286, 288-294, 307-327, 334-340, 369-375, 377-386, 406-412, 418-423, 430-438, 441-447, 459-465, 469-476, 482-488, 510-546, 550-580, 584-622, 638-645, 653-659, 675-683, 692-705, 723-731, 752-761, 788-795 and 54-72 of Seq ID No 215; 11-33, 36-46, 88-104, 116-126, 134-170, 189-195, 199-217, 225-250, 255-261, 266-273, 280-291, 296-313, 334-341, 343-349, 354-360, 362-369, 373-380, 387-401, 406-420 and 259-273 of Seq ID No 216; 9-14, 28-44, 57-64, 72-79, 86-93, 104-111, 116-126, 142-150, 159-164 and 61-86 of Seq ID No 217; 10-17, 26-33, 43-61, 69-95, 101-107, 109-125, 129-135, 137-144, 147-153, 158-169, 177-187, 209-219, 221-232, 235-247, 261-268, 271-282, 296-302, 306-347, 355-362, 364-379, 386-399, 409-418, 424-442, 451-460, 467-479, 490-498 and 60-74 of Seq ID No 218; 8-14, 20-31, 65-84, 94-99, 154-179, 193-207, 238-253 and 96-118 of Seq ID No 219; 4-24, 30-44, 47-62, 84-93, 108-116, 124-133, 136-141, 201-209, 217-223, 228-235, 238-245, 247-270, 275-285, 290-314, 328-338, 342-349, 353-365, 375-383, 386-392, 394-402, 417-427, 443-459, 465-481, 492-514, 516-524, 550-566, 602-617, 630-639, 666-676, 687-693, 719-730, 747-753, 783-790, 799-816, 824-831, 837-842 and 167-189 of Seq ID No 220; 6-15, 18-28, 58-66, 84-101, 106-129, 136-151, 154-165, 182-203, 205-211, 214-220, 222-228, 233-240, 251-260, 270-277, 284-291, 306-315, 322-328, 363-369, 378-388, 392-405, 443-452, 495-501, 512-523, 574-583 and 362-375 of Seq ID No 221; 5-25, 27-34, 47-59, 64-70, 76-86, 145-158, 166-183, 189-202, 217-231, 235-242, 260-270, 278-309 and 1-102 of Seq ID No 222; 4-19, 24-76, 78-83, 90-99, 102-109, 114-122, 137-147, 154-174, 177-188, 203-212, 217-223, 227-239 and 226-325 of Seq ID No 223; 7-37, 71-90, 94-109, 117-128, 141-153, 179-192, 199-206, 225-231, 237-243, 258-264 and 40-51 of Seq ID No224; 13-19, 25-30, 46-59, 75-91, 101-107, 114-124, 129-135, 137-145, 160-167, 171-179, 187-194, 209-215, 217-222, 229-239, 243-249, 257-265, 269-275, 299-308, 310-327 and 282-300 of Seq ID No 225; 86-100, 216-230, 342-369, 382-388, 424-430, 438-445, 452-458, 488-494, 501-518, 554-560, 568-574, 584-592, 603-609, 611-629, 639-645, 652-661, 669-699, 708-714, 726-738, 747-753, 763-775, 785-791, 794-807, 815-824, 826-845, 854-860, 863-868, 870-883, 892-898, 901-906, 909-921, 930-937, 946-959, 968-974, 977-990, 998-1007, 1009-1027, 1037-1043, 1046-1051, 1053-1066, 1075-1081, 1084-1089, 1092-1103, 1113-1119, 1122-1135, 1143-1152, 1154-1172, 1182-1188, 1191-1196, 1200-1210, 1220-1226, 1229-1235, 1237-1249, 1259-1265, 1268-1281, 1289-1298, 1305-1318, 1328-1334, 1337-1343, 1345-1357, 1367-1373, 1390-1396, 1405-1411, 1418-1423, 1426-1435, 1445-1455, 1474-1483, 1493-1500, 1505-1512, 1517-1524, 1538-1544, 1568-1578, 1595-1601, 1674-1682, 1687-1720, 1728-1736, 1738-1744, 1754-1761, 1764-1774, 1798-1824, 1836-1842, 1886-1893, 1895-1903, 366-781, 782-1518 and 1731-1747 of Seq ID No 226; 4-17, 20-39, 46-55, 60-66, 102-110, 114-122, 125-131, 161-167, 172-178, 185-190, 195-202, 218-232, 236-252, 264-291, 293-302, 309-315, 324-339 and 169-381 of Seq ID No 227; 5-10, 13-40, 42-53, 69-75, 83-89, 120-135, 150-161, 174-190, 203-225, 229-247, 257-287, 318-348 and 30-200 of Seq ID No 228; 7-19, 43-53, 64-72, 124-139, 52-84 and 120-131 of Seq ID No 229; 12-19, 39-48, 58-100, 117-123, 154-162, 164-187, 189-195, 202-216, 218-235, 241-246, 262-278, 315-328, 333-347, 354-366, 372-379, 391-405, 422-429, 431-442, 444-450, 458-466, 478-485, 494-501, 504-510, 520-535, 573-580, 589-598, 615-625, 666-676, 686-698, 722-729, 737-746, 756-767, 787-796, 805-816, 824-829, 833-848, 856-864, 866-876, 879-886, 898-904, 918-924, 927-934, 941-960, 967-978 and 561-575 of Seq ID No 230; 11-29, 49-55, 70-77, 84-100, 102-112, 148-155, 160-177, 181-204 and 1-104 of Seq ID No 231; 27-44, 64-71, 122-133, 151-156, 164-178, 214-220, 226-232, 235-244, 253-262, 282-288, 294-310, 317-325, 350-356, 362-368, 376-383, 438-443, 449-454, 459-464, 492-498, 500-511, 529-535, 538-546, 567-573, 597-603, 660-665, 674-679, 724-734, 763-769, 773-784, 791-801, 807-815, 821-826, 840-848, 863-868, 897-902, 908-928, 932-953, 956-975, 980-987, 990-996, 1012-1018, 1042-1063, 1095-1116, 1149-1157, 1160-1167, 110-357, 358-501 and 502-1161 of Seq ID No 232; 4-21, 64-71, 73-84, 128-138, 144-162, 203-217, 240-263, 288-298, 300-308, 310-317, 325-351, 369-380, 391-411 and 330-345 of Seq ID No 233; 5-11, 25-31, 39-48, 51-79, 89-98, 100-122, 135-148, 166-201, 203-227, 230-250, 254-260, 266-272, 274-282, 299-305, 328-337 and 31-45 of Seq ID No 234; 12-23, 29-48, 51-60, 66-72, 75-81, 83-93, 103-115, 133-148, 168-174, 195-204, 222-229, 231-240, 242-251, 270-280, 286-305, 322-344, 349-360, 364-370, 378-400, 421-441, 448-484, 486-493, 495-501, 504-534, 547-561, 567-590, 597-607, 621-635, 643-649, 658-685, 688-694, 702-711, 717-731, 737-742, 759-765, 767-772, 776-786, 803-809, 815-825, 854-908, 910-919, 923-930, 942-948, 961-975, 994-1014 and 915-940 of Seq ID No 235; 4-9, 32-47, 51-61, 75-96, 139-191 and 1-124 of Seq ID No 236; 4-13, 17-38, 43-49, 55-76, 88-95, 110-121, 128-146, 151-157, 162-214, 222-240, 243-249, 251-273, 275-281, 292-298, 300-309, 312-320, 322-331, 355-369, 376-408, 446-460, 471-482, 485-509

and 191-203 of Seq ID No 237; 4-21, 72-82, 89-103, 106-115, 118-124, 140-146, 174-184, 191-200, 204-213, 218-224, 261-266, 282-293, 299-309, 311-340, 342-358, 362-372, 381-389, 391-402, 413-421, 438-447, 457-464, 470-478, 501-507, 545-560, 578-624, 631-641, 658-670, 680-689, 717-738, 753-759, 795-805, 816-822, 830-838, 842-848, 869-881, 892-898, 33-51 and 818-835 of Seq ID No 238; 4-21, 79-85, 156-177, 183-188, 206-214, 243-249, 261-269, 287-292, 315-322, 334-345, 360-366, 374-390, 402-411, 37-97 and 260-399 of Seq ID No 239; 4-9, 19-54, 58-78, 97-104, 111-120, 126-134, 137-145, 163-173, 178-188, 193-203, 211-224, 246-286, 288-324, 337-346, 355-362, 374-390, 392-398, 409-417 and 240-249 of Seq ID No 240; 5-12, 14-31, 35-41, 43-61, 82-92, 97-105, 134-145, 155-166, 184-203, 215-223, 225-251, 272-279, 281-306, 310-345, 358-418, 435-473, 482-490, 525-532, 538-547, 549-563, 578-604, 613-639 and 144-154 of Seq ID No 241; 53-59, 64-72, 74-100, 133-152, 154-172, 176-181, 207-214, 225-238, 275-297, 304-310, 331-340, 362-367, 384-395, 403-410, 437-443, 448-456, 482-490, 579-597, 602-610, 625-630, 633-651, 699-707, 709-715, 734-743, 750-762 and 544-685 of Seq ID No 242; 12-18, 22-40, 45-83, 89-97, 103-109, 147-153, 159-173, 195-204, 210-219, 243-253, 259-265, 273-282, 303-309, 315-325, 332-340, 346-358, 362-367, 377-390, 393-402, 418-426, 447-455, 467-480, 505-512, 514-525, 548-561, 566-576, 584-596, 619-626, 638-645, 649-659, 661-680, 699-708, 714-720, 753-759, 766-772, 775-781, 801-808, 202-218, 282-299, 339-350 and 617-628 of Seq ID No 243; 5-33, 52-62, 87-101, 111-135, 137-143, 145-152, 190-202, 209-221, 233-245, 253-270 and 151-215 of Seq ID No 244; 19-29, 32-39, 42-48, 75-94, 124-135, 137-145, 152-160, 176-182, 193-203, 215-236, 266-273, 275-291, 297-306, 311-319, 322-342, 348-360, 369-378, 394-401 and 48-64 of Seq ID No 245; 4-11, 13-33, 36-43, 53-63, 65-80; 112-129, 134-141, 143-155, 157-168, 178-188, 191-199, 201-207, 215-229, 242-255, 263-270, 283-315, 320-329, 333-338, 340-349, 412-426, 465-478, 485-490, 498-512, 540-554 and 390-516 of Seq ID No 246; 4-18, 23-32, 41-47, 54-70, 88-99, 104-111, 118-138, 143-148, 150-162, 168-175, 181-188, 203-211, 214-220, 227-245, 251-268, 275-281, 287-296, 323-333 and 1-90 of Seq ID No 247; 8-34, 38-49, 72-83, 85-91, 94-104, 112-125, 134-142, 148-168, 181-189, 191-198, 202-214, 222-233, 242-254, 256-262, 273-278, 287-294, 314-325 and 141-159 of Seq ID No 248; 4-24, 30-36, 47-75, 82-105, 124-134, 151-157, 192-202, 208-214, 219-226, 234-247, 285-290, 318-324, 332-340, 343-349, 380-386, 453-462, 472-478, 484-501, 531-540, 550-557, 604-612, 620-625, 642-648, 652-671, 64-84, 93-180 and 181-446 of Seq ID No 249; 12-18, 24-32, 68-75, 77-83, 96-101, 109-116, 129-136, 152-164, 175-184, 190-199, 206-215, 224-233, 241-250, 258-264, 273-292, 302-312, 319-331, 334-346, 348-368, 387-395, 408-416, 420-429, 437-452 and 364-374 of Seq ID No 250; 11-28, 36-52, 60-67, 74-79, 108-116 and 61-76 of Seq ID No 251; 20-27, 38-49, 69-74, 84-107, 138-145, 161-168, 179-195, 210-226, 228-252, 267-281, 283-296, 305-311, 333-340, 342-356, 361-372, 380-399, 401-414, 458-466, 475-481, 492-507, 515-520 and 146-160 of Seq ID No 252; 43-61, 68-74, 76-90, 120-128, 130-149, 156-161, 164-182, 206-234, 242-252, 269-274, 291-304, 332-345, 349-355, 360-371, 374-388, 434-440, 447-453, 459-465, 469-496, 504-522 and 261-285 of Seq ID No 253; 4-17, 24-30, 37-49, 87-98, 118-124, 126-136, 144-171, 176-188, 206-214, 216-228, 233-240, 246-252, 262-271, 277-297, 307-330, 333-342, 346-352, 355-361, 368-386, 391-400, 413-420, 474-480 and 401-427 of Seq ID No 254; 15-26, 31-46, 51-72, 80-93, 96-109, 131-137, 150-158, 179-185, 189-209, 211-219, 221-234, 241-247, 255-262, 265-271, 283-288 and 173-190 of Seq ID No 255; 28-37, 39-45, 51-58, 77-84, 89-97, 132-148, 171-180, 199-205, 212-218, 220-226, 257-265, 273-300, 307-327, 334-340, 344-365, 385-390, 402-408, 426-436, 450-468, 476-485 and 425-497 of Seq ID No 256; 4-25, 70-76, 80-88, 90-100, 120-128, 162-169, 183-203, 261-277, 279-289, 291-297, 302-308, 321-327, 339-353, 358-377, 392-401, 404-410, 414-422, 443-450, 456-461, 470-488, 490-497, 510-535, 570-611, 618-630, 639-647, 649-660, 668-690, 702-716, 718-724, 737-747, 750-764 and 497-509 of Seq ID No 257; 12-48, 50-64, 99-108, 216-223, 235-241, 244-254, 262-274, 287-293, 310-316, 320-326, 361-366, 377-383, 390-395, 408-414, 418-425, 438-444, 462-469, 494-505, 524-530, 536-547, 551-566, 592-598, 601-613, 678-685, 687-695, 709-717, 727-737, 751-757, 760-765, 772-778, 782-788, 801-807, 822-830, 859-868, 870-878, 884-890, 898-903, 909-919, 953-969, 973-980, 990-1000, 1002-1019, 1041-1047, 1059-1065, 1090-1095, 1116-1127, 1130-1139, 1143-1149, 1151-1168, 1178-1183, 1188-1195, 1197-1209, 1213-1220, 1226-1234, 1236-1247, 1255-1274, 1276-1282, 76-100, 270-284, 309-438, 493-505, 786-942 and 947-967 of Seq ID No 258; 4-9, 24-34, 46-95, 97-109, 119-130 and 138-156 of Seq ID No 259; 9-26, 28-35, 43-53, 55-68, 83-92, 99-105, 110-135, 139-149, 157-162, 164-170, 173-183, 193-208, 210-230, 239-245, 253-259, 263-271, 293-305, 310-320, 322-331, 336-343, 351-364, 367-376, 92-107 and 154-173 of Seq ID No 260; 19-39, 52-62, 108-117, 145-152, 160-168, 194-203, 229-240, 252-

268, 280-287, 308-316, 333-339, 383-390, 403-412, 414-424, 438-445, 464-472, 479-484, 489-505, 510-526 and 247-260 of Seq ID No 261; 5-17, 25-52, 60-77, 105-113, 118-125, 162-167, 228-234, 272-279, 328-334, 341-357, 381-395, 400-406, 512-518, 557-569, 586-592, 645-651, 690-695, 701-709, 720-726, 733-743, 751-758, 781-786, 879-886, 929-934, 939-944, 952-960, 965-975, 994-1001, 1039-1045, 1102-1109, 1164-1181, 1198-1206, 1223-1229, 1253-1259, 1283-1292, 1312-1317, 1339-1349, 1360-1370, 1389-1398, 1400-1412, 1452-1465, 1470-1484, 1490-1497, 1519-1525, 1554-1564, 1578-1591, 1623-1636, 1638-1646, 1669-1679, 1685-1697, 1704-1711, 1713-1720, 1730-1736, 1738-1749, 1756-1764, 1778-1786, 1796-1803, 1817-1826, 1849-1866, 1975-1993, 2017-2032, 2044-2053, 2070-2086, 2091-2109, 2116-2127, 2156-2167, 2182-2188, 2197-2202, 2244-2252, 2281-2287, 2290-2307, 2350-2361, 2383-2404, 2425-2433, 2445-2455, 2495-2505 and 394-549 of Seq ID No 262; 9-24, 31-53, 57-67, 69-79, 84-114, 133-141, 144-172, 178-186 and 13-46 of Seq ID No 263; 4-25, 27-35, 43-52, 59-70, 79-91, 115-130, 136-152, 154-163, 170-179 and 1-58 of Seq ID No 264; 4-30, 49-55, 71-80, 96-105, 111-126, 139-146, 149-162, 239-245, 279-285, 290-296, 300-307, 331-337, 343-350 and 250-351 of Seq ID No 265; 9-27, 34-41, 43-51, 92-111, 114-120, 123-131, 139-150, 156-171, 176-186, 188-204, 229-241, 252-258, 266-279, 288-297, 319-334, 338-348, 373-379, 389-398, 431-439, 479-484 and 214-398 of Seq ID No 266; 4-15, 18-27, 47-52, 68-83, 91-97, 104-110, 115-121, 139-147, 157-164, 198-206, 227-236, 241-254, 264-273, 278-289, 311-320, 353-361, 372-383, 405-420, 426-434 and 232-386 of Seq ID No 267; 4-10, 24-34, 91-97, 129-141, 156-163, 184-190, 205-219, 229-235, 256-273, 278-285 and 93-116 of Seq ID No 268; 7-29, 35-54, 71-83, 85-91, 104-111, 122-134, 138-144, 146-154, 158-174, 177-183, 186-201, 207-215, 223-235, 240-247, 262-273, 275-283, 287-292 and 48-66 of Seq ID No 269; 7-27, 31-47, 49-70, 75-102, 110-149, 157-171, 217-223, 235-251, 294-302, 358-364, 367-375, 387-393, 395-412, 423-430, 441-451, 456-470, 472-486, 488-495, 499-509, 515-529, 536-549, 556-570, 574-603, 607-615, 625-633, 642-658, 670-676, 683-702, 708-716, 720-726, 747-756, 763-784, 803-812, 815-826 and 475-490 of Seq ID No 270; 7-22, 30-38, 53-59, 64-75, 83-95, 97-112, 120-131, 133-142, 145-151, 154-166, 172-180, 189-203, 227-238, 277-287, 9-156 and 174-287 of Seq ID No 271; 13-23, 25-32, 111-117, 150-164, 185-193, 207-212, 216-224, 230-236, 263-272, 304-311, 342-348, 374-385, 391-407, 444-458, 480-487, 489-499, 523-542, 544-558, 572-579, 620-640, 686-696, 703-710, 742-755, 765-772, 817-822, 830-837, 865-872, 931-937 and 66-86 of Seq ID No 272; 4-27, 49-56, 62-70, 86-92, 121-127, 151-163, 170-182, 195-202, 212-226, 237-243 and 234-254 of Seq ID No 273; 4-10, 13-24, 39-51, 62-78, 92-104, 107-117, 134-141, 156-161, 166-181, 210-216, 222-229, 256-266, 273-280, 297-304, 313-330, 336-349, 371-376, 433-439, 443-448, 488-493, 506-515, 527-534, 560-572, 575-583, 587-593 and 252-483 of Seq ID No 274; 4-15, 21-38, 45-56, 81-95, 102-108, 118-130, 133-147, 152-162, 166-171, 199-204, 211-218, 230-240, 253-261, 274-283, 288-294, 312-317, 325-336, 344-357, 391-414 and 24-146 of Seq ID No 275; 26-31, 38-56, 65-82, 90-101, 112-119, 123-153, 175-188, 197-216, 234-242, 249-265, 273-286, 290-305, 327-335, 338-346, 361-372, 394-404 and 290-306 of Seq ID No 276; 17-26, 43-48, 50-73, 81-93, 95-107, 139-146, 158-168, 171-176, 190-196, 202-212, 216-223, 243-266, 274-282, 308-313, 324-330, 344-378, 380-387, 403-422, 427-443, 448-455, 457-465, 491-515, 517-528, 553-567, 589-599, 610-617, 642-648, 670-697, 709-717, 726-743, 745-759, 769-803, 807-823, 840-849 and 820-851 of Seq ID No 277; 4-18, 39-48, 53-63, 66-90, 102-117, 125-134, 137-145, 156-162, 169-197, 26-40 and 56-80 of Seq ID No 278; 21-33, 36-42, 49-60, 68-76, 91-105, 123-130, 141-161, 169-178, 185-190, 192-199, 205-214, 223-233, 239-247, 260-269, 284-293, 300-314, 324-352, 357-364, 373-382, 389-403, 420-432, 438-446, 466-471, 477-484, 503-509, 549-556, 558-576, 600-623, 625-635, 654-661, 663-669, 671-687, 702-716, 735-741, 744-750, 757-766, 776-786, 807-815, 824-832, 854-860, 863-897, 909-915, 920-946, 952-959, 982-997, 1024-1038, 1049-1055, 1071-1085, 1104-1113, 1121-1132, 1138-1150, 1187-1196, 1212-1221, 1227-1236, 1257-1262, 1264-1278, 1282-1294, 1307-1318, 1353-1370, 1382-1388, 1396-1409, 1434-1440, 1446-1454, 1465-1478, 1485-1513, 1516-1529, 1540-1545, 1563-1568, 1575-1593, 1607-1616, 1628-1645, 1648-1661, 1676-1682, 1689-1697, 1713-1719, 1739-1749, 1753-1758, 1763-1774, 1797-1803, 1807-1846, 1855-1874, 1877-1891, 1893-1907, 1912-1925, 1931-1943, 1955-1965, 1976-1990, 2032-2043, 2045-2051, 2099-2105, 2131-2138, 2161-2179, 2188-2199, 2205-2216, 2219-2227, 2235-2245, 2247-2267, 2277-2288, 2294-2304, 2314-2326, 2346-2358, 2365-2377, 2383-2402, 2407-2423, 2437-2450, 2454-2473, 2489-2497, 2525-2531, 2557-2570, 2580-2587, 2589-2599, 2621-2641, 2647-2653, 2661-2677, 2685-2690, 2697-2717, 2722-2733, 2739-2777, 2786-2793, 2801-2808, 2811-2822, 2825-2835, 2838-2845, 2859-2871, 2877-2883, 213-344, 954-1080 and 2524-2733 of Seq ID No 279; 10-16, 18-23, 28-41, 63-69, 77-91, 101-109, 118-

136, 146-153, 155-162, 168-179, 192-207, 217-226, 229-235, 239-254, 279-286, 294-307, 313-319, 334-341, 344-353, 363-377, 390-396 and 178-328 of Seq ID No 280; 18-42, 68-84, 89-95, 100-105, 107-115, 125-135, 154-177, 189-195, 205-228, 236-243, 252-259, 279-300, 309-316, 323-331, 340-351, 353-364, 377-402 and 85-97 of Seq ID No 281; 4-18, 26-32, 66-76, 100-126, 151-159, 178-186, 188-194, 200-210, 241-248, 253-259, 262-279, 284-291, 307-313, 315-322, 327-337, 376-386, 399-407, 432-441, 467-473, 487-497, 499-505, 543-549, 560-568, 585-593, 598-604, 608-614, 630-642, 647-653, 690-703, 717-730, 21-200 and 468-480 of Seq ID No 282; 17-49, 52-58, 62-73, 78-97, 100-117, 122-172, 185-190, 193-217, 225-236 and 33-42 of Seq ID No 283; 7-39, 50-58, 73-89, 96-107, 109-120, 126-142, 152-170, 178-202, 205-211, 224-244, 249-259, 261-270, 300-310, 312-325 and 158-169 of Seq ID No 284; 4-31, 40-64, 71-82, 85-92, 102-124, 126-139, 147-152, 159-173, 176-188, 195-207, 210-216, 234-241, 249-256, 258-276, 279-293, 296-302, 310-315, 349-356, 363-378, 380-403, 411-426, 435-441, 448-459, 463-476, 488-494 and 201-221 of Seq ID No 285; 5-13, 15-74, 87-104, 107-120, 123-129, 136-145, 150-191, 193-206, 227-248, 250-264, 278-302, 304-323, 332-378, 384-407, 409-419, 425-457, 462-471, 474-497, 511-545, 555-564, 571-578, 585-598, 640-647, 669-675, 682-691, 693-705, 729-743, 752-761, 772-780, 786-804, 808-818, 822-846, 858-880, 884-900, 910-939, 941-947, 962-971, 973-988, 998-1003, 1007-1027 and 236-259 of Seq ID No 286; 4-19, 27-68, 81-111, 121-160 and 60-79 of Seq ID No 287; 4-37, 40-46, 52-57, 199-205, 222-229, 236-244, 250-267, 269-282 and 27-197 of Seq ID No 288; 4-16, 24-30, 32-38, 63-75, 86-92, 98-111, 113-126, 160-165, 170-180, 198-204, 227-233, 239-245, 253-273, 308-314, 352-365, 382-387, 395-403, 423-429, 472-482, 484-493, 501-507, 518-526, 536-541, 543-550, 556-562, 586-600, 626-633, 649-661, 680-688 and 546-559 of Seq ID No 289; 16-33, 48-59, 63-71, 77-92, 94-109, 117-124, 139-151, 169-181, 184-227, 233-249, 251-261, 263-275, 282-294, 297-321, 326-332, 341-355, 383-399 and 258-272 of Seq ID No 290; 11-26, 31-39, 43-52, 55-62, 64-70, 80-94, 123-133, 135-141, 172-181, 185-206, 209-218, 224-230, 238-244, 251-262, 264-271, 290-301, 306-324, 333-340, 350-357, 367-375, 390-397, 434-441, 443-448, 77-226 and 350-429 of Seq ID No 291; 4-13, 22-27, 31-45, 50-59, 72-96, 99-114, 131-141, 143-150, 159-176, 180-186, 189-198, 208-214, 234-253, 271-287, 294-299, 310-366, 382-390, 398-416, 424-443 and 283-305 of Seq ID No 292; 9-26, 30-53, 62-72, 86-95, 112-122, 136-145, 153-160, 209-221, 227-237, 241-268, 281-288, 291-298, 308-314, 321-328, 336-346, 351-379, 388-397, 409-416, 423-433, 443-481, 511-519 and 213-232 of Seq ID No 293; 12-18, 25-31, 38-50, 59-67, 71-82, 96-126 and 76-88 of Seq ID No 294; 4-25, 39-44, 64-71, 74-88, 100-113, 128-138, 151-162, 164-177, 185-190, 204-213, 233-239, 246-254, 281-286, 293-306, 309-318, 333-347, 349-359, 385-398, 404-423, 458-465, 477-484, 490-499, 501-533, 554-566, 582-590, 596-616, 624-629, 631-639, 654-680, 694-720, 735-743 and 2-100 of Seq ID No 295; 4-16, 36-41, 52-75, 98-107, 109-117, 122-128, 133-139, 141-155, 159-165, 169-182, 187-193, 195-201, 211-224, 230-236, 247-269, 278-290 and 75-92 of Seq ID No 296; 7-21, 25-33, 37-43, 87-94, 103-120, 131-147, 168-174, 197-203, 207-212, 227-237, 247-257, 263-271, 279-287, 298-306, 320-325, 332-340, 363-374, 379-384, 390-401, 403-414, 428-433, 448-457, 462-475, 483-490, 513-519, 525-535, 543-554, 559-566, 571-620, 625-631, 636-642, 659-670, 688-706, 708-723, 770-779, 787-793, 796-807, 820-840, 848-854, 863-874, 895-905, 912-919, 934-942, 968-975, 983-1000, 1012-1019, 1026-1036, 1050-1060, 1064-1070, 1081-1091, 1094-1108, 1112-1118, 1140-1152, 1164-1169, 1172-1180, 1187-1192 and 732-748 of Seq ID No 297; 23-40, 42-59, 66-73, 78-97, 111-128, 130-141, 157-166, 178-183 and 53-71 of Seq ID No 298; 4-27, 38-44, 47-57, 59-85, 99-106, 114-121, 154-166, 181-186, 193-198, 238-244, 253-262, 272-278, 287-299, 314-320, 338-350, 358-368, 382-388, 407-416, 433-446, 456-461, 463-473 and 86-195 of Seq ID No 299; 5-24, 38-59, 64-80, 87-99, 105-126, 134-142, 149-163, 165-179, 181-202, 205-220, 227-233, 243-250, 257-263 and 87-245 of Seq ID No 300; 5-32, 47-53, 66-79, 81-97, 115-151, 155-174, 183-188, 196-210, 215-226, 230-238, 253-258, 263-270, 276-282, 295-301, 304-325, 334-344, 360-390, 397-412, 425-432, 434-462, 478-494, 508-526, 539-564, 571-579, 347-371 and 375-386 of Seq ID No 301; 4-15, 36-44, 49-56, 60-66, 68-82, 84-103, 109-115, 118-141, 147-154, 160-168, 176-185 and 26-39 of Seq ID No 302; 7-13, 23-33 and 13-21 of Seq ID No 303; 2-10 of Seq ID No 304; 4-9, 12-18, 35-42, 49-62 and 6-18 of Seq ID No 305; 19-25 and 1-13 of Seq ID No 306; 15-21, 27-45 and 12-25 of Seq ID No 307; 14-20 and 1-14 of Seq ID No 308; 4-18 and 13-26 of Seq ID No 309; 8-21 and 2-20 of Seq ID No 310; 4-14 and 4-16 of Seq ID No 311; 3-12 of Seq ID No 312; 6-14, 6-25, 35-57 and 2-14 of Seq ID No 313; 6-25, 35-57 and 17-31 of Seq ID No 314; 14-25, 32-46 and 5-19 of Seq ID No 315; 18-31 and 5-16 of Seq ID No 316; 19-24 and 4-26 of Seq ID No 317; 13-21, 29-34, 47-58, 61-73 and 36-47 of Seq ID No 318; 4-15 and 5-24 of Seq

ID No 319; 6-18 of Seq ID No 320; 13-20 and 4-13 of Seq ID No 321; 15-23 of Seq ID No 322; 4-9 and 7-21 of Seq ID No 323; 1-10 of Seq ID No 324; 4-14 of Seq ID No 325; 4-17, 35-41, 46-89, 93-98 and 70-88 of Seq ID No 326; 1-13 of Seq ID No 327; 4-16, 26-32 and 25-38 of Seq ID No 328; 8-15, 23-28 and 4-17 of Seq ID No 329; 4-12 and 1-15 of Seq ID No 330; 4-29, 31-42, 52-58 and 6-16 of Seq ID No 331; 4-9, 24-32 and 9-19 of Seq ID No 332; 4-12, 18-27 and 5-18 of Seq ID No 333; 4-11, 37-56, 58-92 and 18-29 of Seq ID No 334; 8-28 and 20-35 of Seq ID No 335; 4-15 of Seq ID No 336; 4-23, 27-39, 55-63 and 35-58 of Seq ID No 337; 6-26, 28-54 and 28-47 of Seq ID No 338; 4-10, 38-52, 58-82 and 30-49 of Seq ID No 339; 4-22, 29-35, 44-50, 53-68, 70-80 and 20-33 of Seq ID No 340; 22-28, 30-36 and 18-33 of Seq ID No 341; 4-11, 13-21, 25-30 and 20-30 of Seq ID No 342; 10-22 and 10-23 of Seq ID No 343; 4-11 and 9-20 of Seq ID No 344; 14-25, 32-46 and 6-19 of Seq ID No 345; 5-30 and 14-33 of Seq ID No 346; 4-15, 28-35, 46-55, 59-65, 76-84 and 9-24 of Seq ID No 347; 27-33 and 5-19 of Seq ID No 348; 5-13 and 8-18 of Seq ID No 349; 9-22, 24-34 and 21-40 of Seq ID No 350; 4-17, 35-41, 46-89, 93-98 and 71-89 of Seq ID No 351; 4-12, 14-24 and 2-17 of Seq ID No 352; 9-17 and 5-16 of Seq ID No 353; 7-41, 48-58, 63-75, 80-89 and 43-53 of Seq ID No 354; 4-22, 25-30 and 4-14 of Seq ID No 355; 4-55 and 18-33 of Seq ID No 356; 262-280 of Seq ID No 179; 131-146 of Seq ID No 186; 207-224 of Seq ID No 188; 27-50, 203-217 and 313-325 of Seq ID No 189; 110-129 of Seq ID No 192; 156-179, 174-197, 192-215, 210-233, 228-251 and 246-267 of Seq ID No 190; 377-400 of Seq ID No 196; 34-43, 234-257 and 350-367 of Seq ID No 203; 304-327 of Seq ID No 207; 25-48, 43-66 and 61-82 of Seq ID No 222; 398-421, 416-439, 434-457, 452-475, 470-493, 488-511, 506-529, 524-547, 621-644, 639-664, 707-730, 725-748, 743-766, 761-784, 779-802, 797-820, 984-1007, 1002-1025, 1020-1043, 1038-1061, 1056-1079, 1074-1097, 1092-1115, 1286-1309, 1304-1327, 1322-1345, 1340-1363, 1358-1381, 1376-1399, 1394-1417, 1412-1435, 1430-1453, 1448-1471, 1466-1489 and 1484-1507 of Seq ID No 226; 188-211, 206-229, 224-247, 242-265, 260-283 and 278-296 of Seq ID No 227; 56-79 and 122-132 of Seq ID No 229; 35-46 of Seq ID No 231; 178-201, 196-219, 214-237, 232-255, 250-273, 268-291, 379-402, 397-420, 415-438, 433-456, 451-474, 642-665, 660-683, 678-701, 696-719, 714-737, 732-755, 750-773, 768-791, 899-922, 917-940, 935-958, 1037-1060, 1055-1078, 1073-1096 and 1091-1114 of Seq ID No 232; 330-346 of Seq ID No 233; 571-594, 589-612, 607-630, 625-648, 643-666 and 661-684 of Seq ID No 242; 188-207 of Seq ID No 244; 61-84, 308-331, 326-349, 344-367, 362-385, 380-403 and 398-421 of Seq ID No 249; 79-98, 345-366, 844-867, 870-887 and 890-905 of Seq ID No 258; 94-109 of Seq ID No 268; 188-207 of Seq ID No 272; 290-306 of Seq ID No 276; 826-849 of Seq ID No 277; 228-252, 247-270, 265-288, 283-306, 301-324, 955-978, 973-996, 991-1014, 1009-1032, 1027-1050, 1045-1068, 2533-2556, 2551-2574, 2569-2592, 2587-2610, 2605-2628 and 2623-2646 of Seq ID No 279; 86-109 and 104-127 of Seq ID No 288; 546-560 of Seq ID No 289; 260-271 of Seq ID No 290; 106-129, 124-147, 142-165, 160-183, 178-201 and 375-398 of Seq ID No 291; 284-307 of Seq ID No 292; 362-385 of Seq ID No 301.

15. A process for producing a *H. pylori* hyperimmune serum reactive antigen or a fragment thereof according to any one of the claims 11 to 14 comprising expressing the nucleic acid molecule according to any one of claims 1 to 7.

16. A process for producing a cell, which expresses a *H. pylori* hyperimmune serum reactive antigen or a fragment thereof according to any one of the claims 11 to 14 comprising transforming or transfecting a suitable host cell with the vector according to claim 8 or claim 9.

17. A pharmaceutical composition, especially a vaccine, comprising a hyperimmune serum-reactive antigen or a fragment thereof, as defined in any one of claims 11 to 14 or a nucleic acid molecule according to any one of claims 1 to 7.

18. A pharmaceutical composition, especially a vaccine, according to claim 17, characterized in that it further comprises an immunostimulatory substance, preferably selected from the group comprising polycationic polymers, especially polycationic peptides, immunostimulatory deoxynucleotides (ODNs), peptides containing at least two LysLeuLys motifs, neuroactive compounds, especially human growth hormone, alumn, Freund's complete or incomplete

adjuvants or combinations thereof.

19. Use of a nucleic acid molecule according to any one of claims 1 to 7 or a hyperimmune serum-reactive antigen or fragment thereof according to any one of claims 11 to 14 for the manufacture of a pharmaceutical preparation, especially for the manufacture of a vaccine against *H. pylori* infection.

20. An antibody, or at least an effective part thereof, which binds at least to a selective part of the hyperimmune serum-reactive antigen or a fragment thereof according to any one of claims 11 to 14.

21. An antibody according to claim 20, wherein the antibody is a monoclonal antibody.

22. An antibody according to claim 20 or 21, wherein said effective part comprises Fab fragments.

23. An antibody according to any one of claims 20 to 22, wherein the antibody is a chimeric antibody.

24. An antibody according to any one of claims 20 to 23, wherein the antibody is a humanized antibody.

25. A hybridoma cell line, which produces an antibody according to any one of claims 20 to 24.

26. A method for producing an antibody according to claim 20, characterized by the following steps:
- initiating an immune response in a non-human animal by administrating an hyperimmune serum-reactive antigen or a fragment thereof, as defined in any one of the claims 11 to 14, to said animal,
- removing an antibody containing body fluid from said animal, and
- producing the antibody by subjecting said antibody containing body fluid to further purification steps.

27. Method for producing an antibody according to claim 21, characterized by the following steps:
- initiating an immune response in a non-human animal by administrating an hyperimmune serum-reactive antigen or a fragment thereof, as defined in any one of the claims 12 to 15, to said animal,
- removing the spleen or spleen cells from said animal,
- producing hybridoma cells of said spleen or spleen cells,
- selecting and cloning hybridoma cells specific for said hyperimmune serum-reactive antigens or a fragment thereof,
- producing the antibody by cultivation of said cloned hybridoma cells and optionally further purification steps.

28. Use of the antibodies according to any one of claims 20 to 24 for the preparation of a medicament for treating or preventing *H. pylori* infections.

29. An antagonist which binds to the hyperimmune serum-reactive antigen or a fragment thereof according to any one of claims 11 to 14.

30. A method for identifying an antagonist capable of binding to the hyperimmune serum-reactive antigen or fragment thereof according to any one of claims 11 to 14 comprising:

a) contacting an isolated or immobilized hyperimmune serum-reactive antigen or a fragment thereof according to any one of claims 11 to 14 with a candidate antagonist under conditions to permit binding of said candidate antagonist to said hyperimmune serum-reactive antigen or

fragment, in the presence of a component capable of providing a detectable signal in response to the binding of the candidate antagonist to said hyperimmune serum reactive antigen or fragment thereof; and

b) detecting the presence or absence of a signal generated in response to the binding of the antagonist to the hyperimmune serum reactive antigen or the fragment thereof.

31. A method for identifying an antagonist capable of reducing or inhibiting the interaction activity of a hyperimmune serum-reactive antigen or a fragment thereof according to any one of claims 11 to 14 to its interaction partner comprising:

a) providing a hyperimmune serum reactive antigen or a hyperimmune fragment thereof according to any one of claims 11-14,
b) providing an interaction partner to said hyperimmune serum reactive antigen or a fragment thereof, especially an antibody according to any one of the claims 20 to 24,
c) allowing interaction of said hyperimmune serum reactive antigen or fragment thereof to said interaction partner to form a interaction complex,
d) providing a candidate antagonist,
e) allowing a competition reaction to occur between the candidate antagonist and the interaction complex,
f) determining whether the candidate antagonist inhibits or reduces the interaction activities of the hyperimmune serum reactive antigen or the fragment thereof with the interaction partner.

32. Use of any of the hyperimmune serum reactive antigen or fragment thereof according to any one of claims 11 to 14 for the isolation and/or purification and/or identification of an interaction partner of said hyperimmune serum reactive antigen or fragment thereof.

33. A process for *in vitro* diagnosing a disease related to expression of the hyperimmune serum-reactive antigen or a fragment thereof according to any one of claims 11 to 14 comprising determining the presence of a nucleic acid sequence encoding said hyperimmune serum reactive antigen and fragment according to any one of claims 1 to 7 or the presence of the hyperimmune serum reactive antigen or fragment thereof according to any one of claims 11-14.

34. A process for *in vitro* diagnosis of a bacterial infection, especially a *H. pylori* infection, comprising analysing for the presence of a nucleic acid sequence encoding said hyperimmune serum reactive antigen and fragment according to any one of claims 1 to 7 or the presence of the hyperimmune serum reactive antigen or fragment thereof according to any one of claims 11 to 14.

35. Use of the hyperimmune serum reactive antigen or fragment thereof according to any one of claims 11 to 14 for the generation of a peptide binding to said hyperimmune serum reactive antigen or fragment thereof, wherein the peptide is selected from the group comprising anticalines.

36. Use of the hyperimmune serum-reactive antigen or fragment thereof according to any one of claims 11 to 14 for the manufacture of a functional nucleic acid, wherein the functional nucleic acid is selected from the group comprising aptamers and spiegelmers.

37. Use of a nucleic acid molecule according to any one of claims 11 to 14 for the manufacture of a functional ribonucleic acid, wherein the functional ribonucleic acid is selected from the group comprising ribozymes, antisense nucleic acids and siRNA.

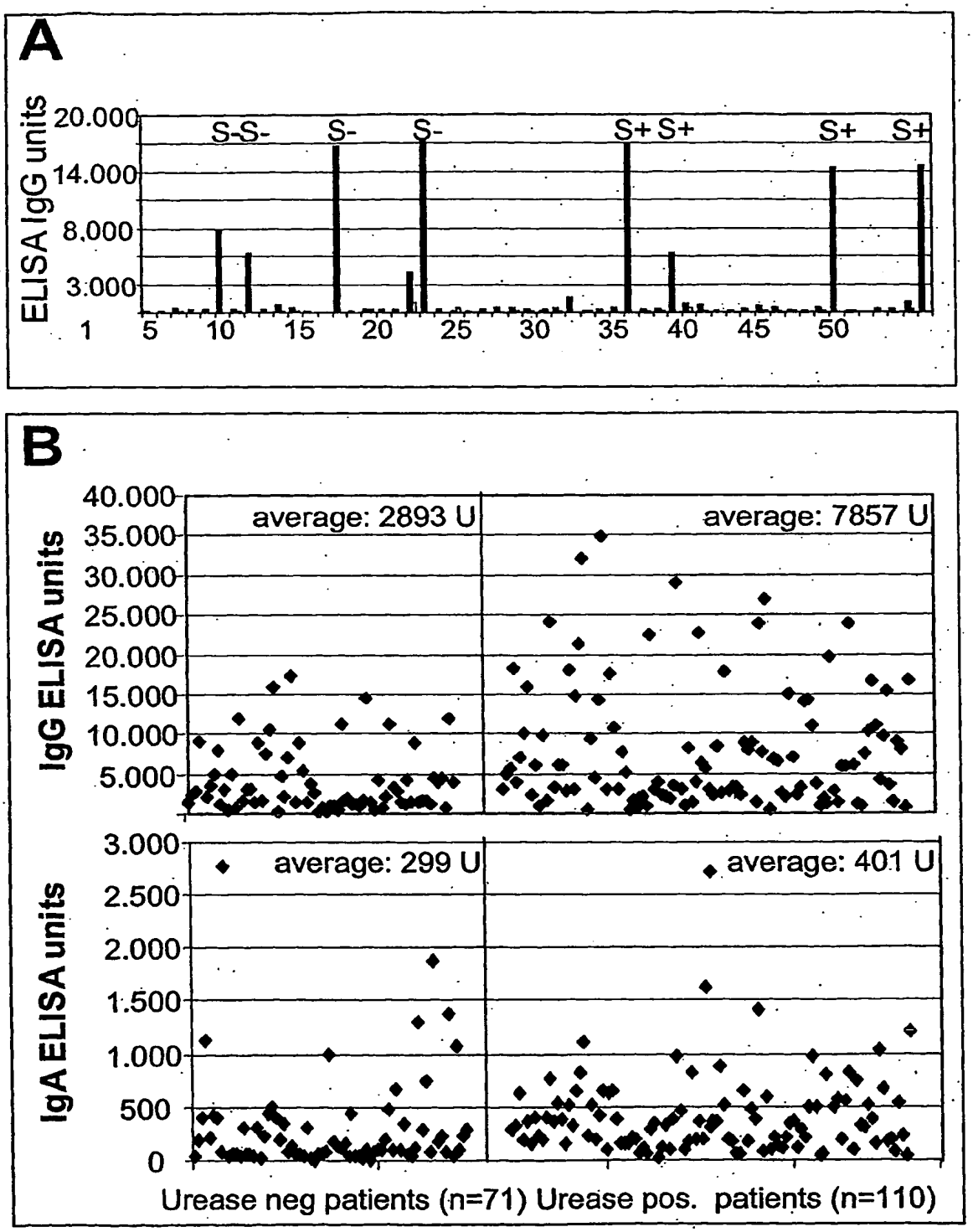


Fig. 1

Figure 1

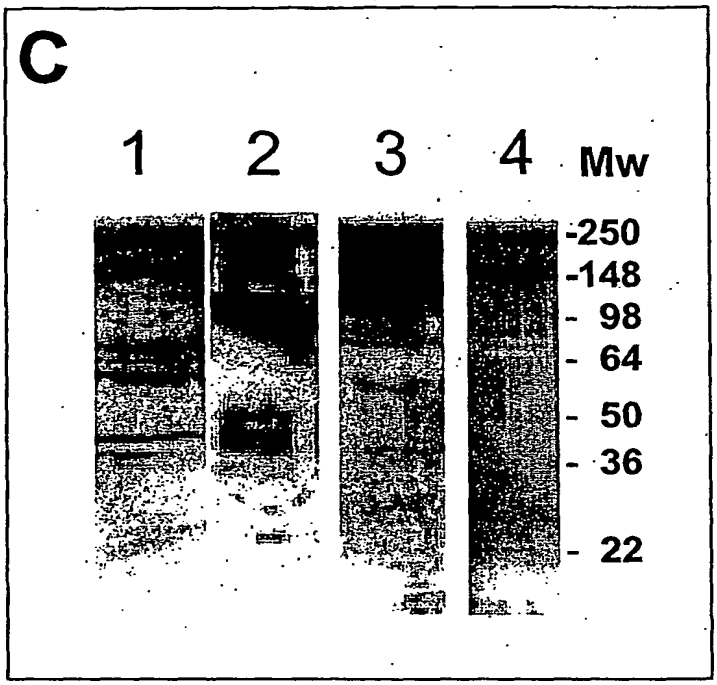
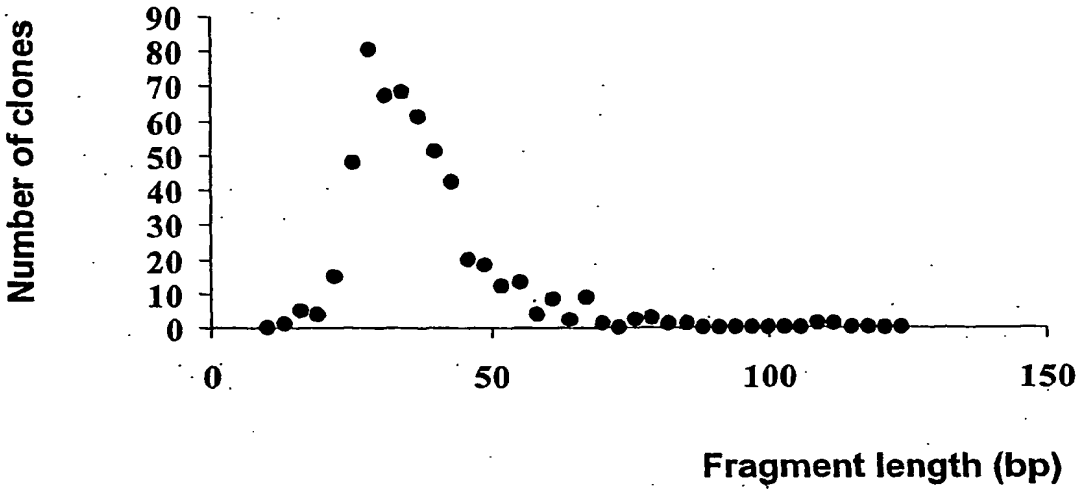
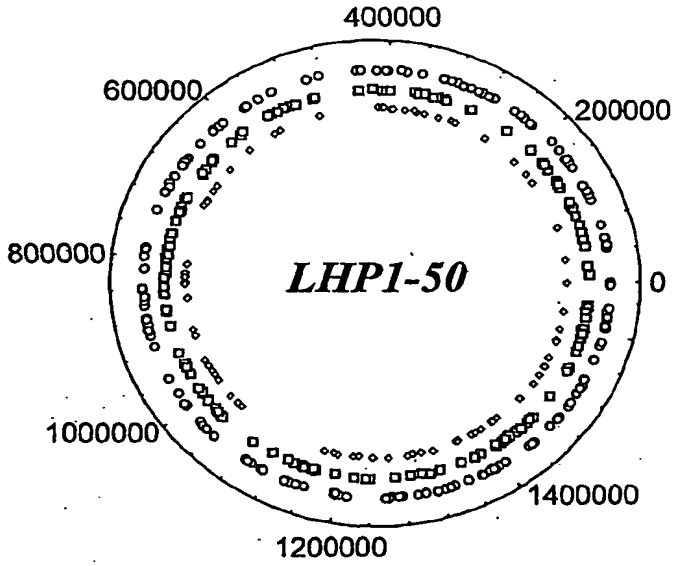


Fig. 1

A.



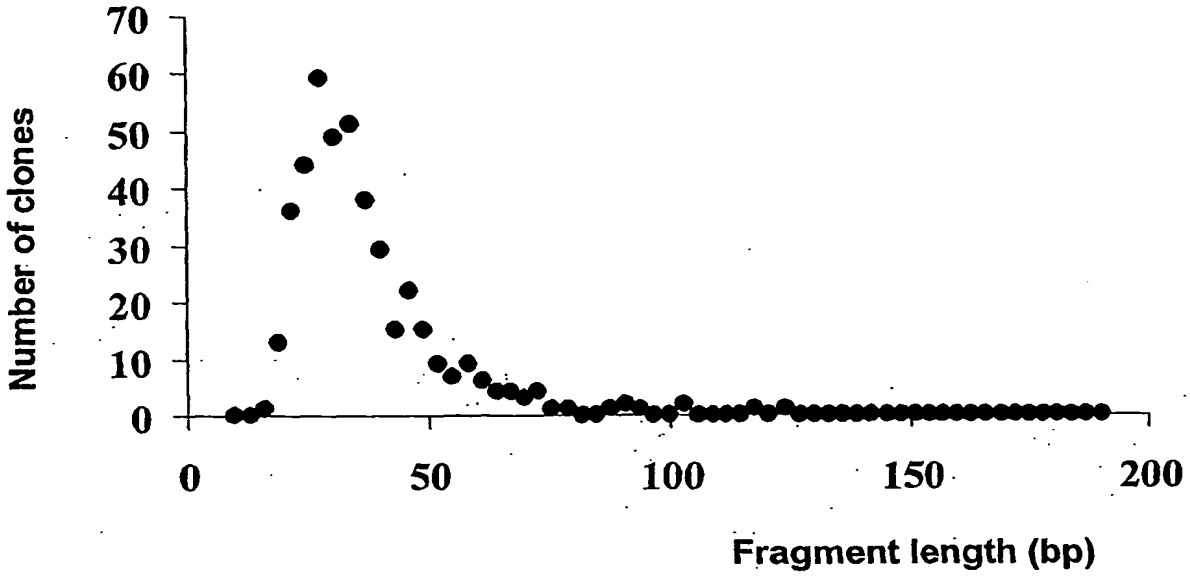
B.



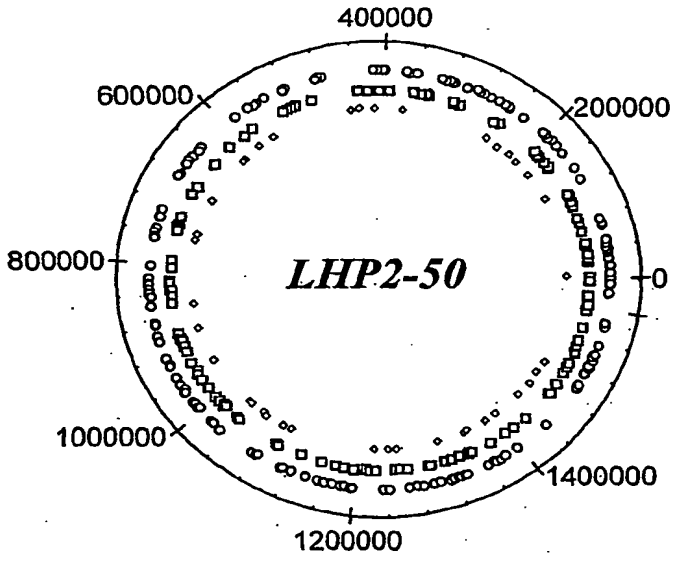
Total (trimmed)		562	(100,0 %)
ORF (+/+, +/-)	○	207	(36,8 %)
non-ORF (+/+, +/-)	□	185	(32,9 %)
chimeric	◇	88	(15,7 %)
non-blastable		82	(14,6 %)

Figure 2

A.



B.



Total (trimmed)		439	(100,0 %)
ORF (+/+, +/-)	○	162	(36,9 %)
non-ORF (+/+, +/-)	□	141	(32,1 %)
chimeric	◇	40	(9,1 %)
non-blastable		96	(21,9 %)

Figure 3

A

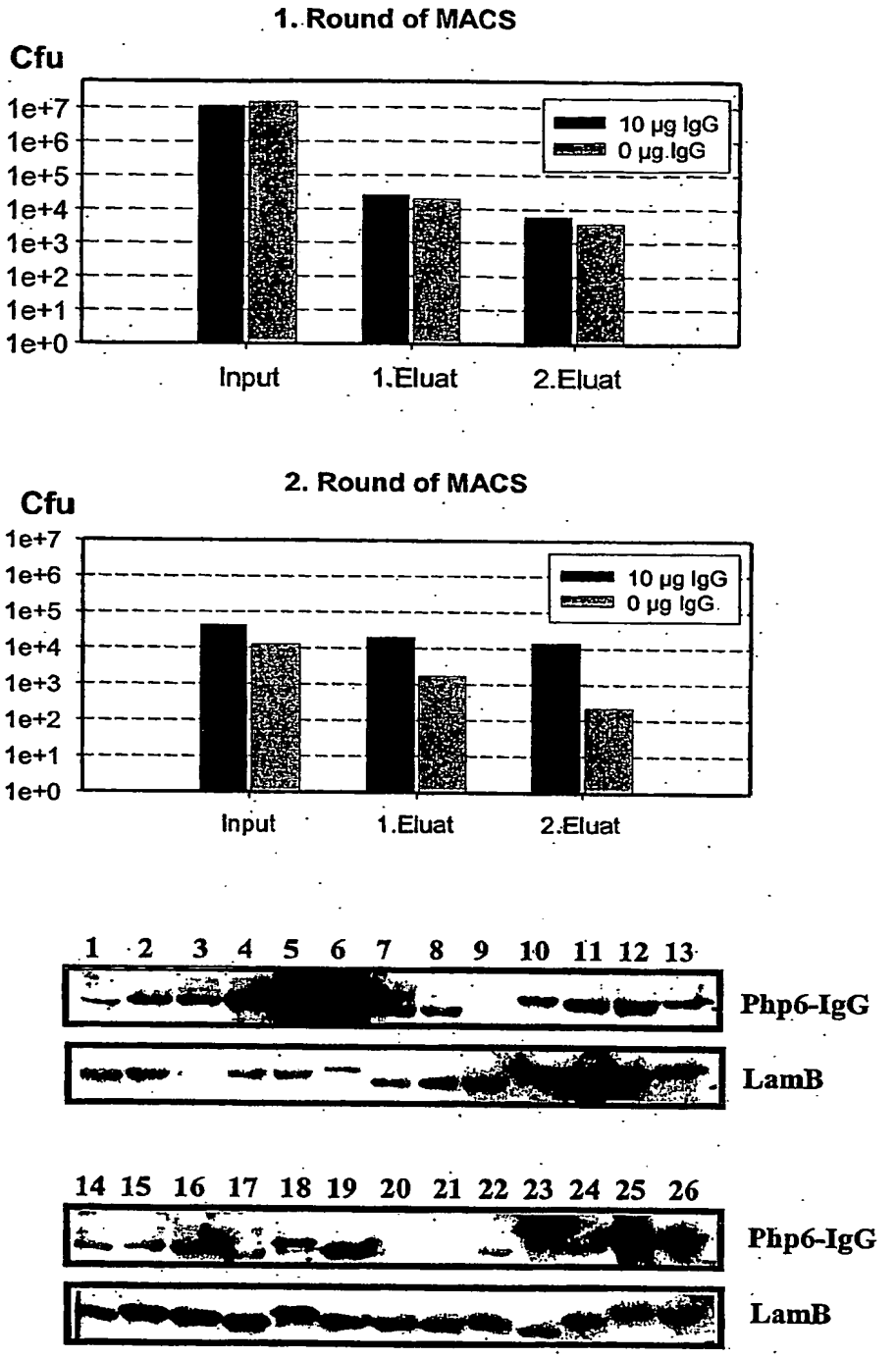

1. Round of MACS
Cfu
1e+7
1e+6
1e+5
1e+4
1e+3
1e+2
1e+1
1e+0
10 µg IgG
0 µg IgG
Input
1.Eluat
2.Eluat
2. Round of MACS
Cfu
1e+7
1e+6
1e+5
1e+4
1e+3
1e+2
1e+1
1e+0
10 µg IgG
0 µg IgG
Input
1.Eluat
2.Eluat
1 2 3 4 5 6 7 8 9 10 11 12 13
Php6-IgG
LamB
14 15 16 17 18 19 20 21 22 23 24 25 26
Php6-IgG
LamB

Figure 4

SEQUENCE LISTING

Seq ID 1

```
atggtgaaaa acaccggcga attgaaaaaa ctttcagaca cttatgagaa tttgagcaac     60
cttttaacca attttaacaa cctcaatcaa gcggtaacga acgcgagcag cccttcagaa    120
atcaatgcca cgatcgataa tttaaaagca aacacgcaag ggctgattgg cgaaaaaacc    180
aattccccgg cgtatcaagc ggtgtatttg gcgctcaatg cggcggtggg gctgtggaat    240
gtgatagcct ataatgtcca atgcggtcct ggtaagagtg gggatcaaag cgtaattttt    300
gatggccaac caggacatga ttcaagatcc attaattgca atttaaccgg ttataacaac    360
ggggttagcg gccctttatc cattgacaat tttaaaacgc ttaatcaagc ttatcaaact    420
atccaacaag ctttaaaaca agatagcgga tttcctgttt tggatagtaa aggaaaacaa    480
gtaactataa aaataacaac acaaactaat ggagctaata aaagtgaaac tactactact    540
actactacta ctaatgacgc tcaaaccctt ttgcaagaag ccagtaaaat gataagcgtc    600
ctcactacaa actgcccatg ggtaaatacc gctcataact caaacggggg tgcaccgtgg    660
aatttaaata cgacagggaa tgtgtgtcag gtttttgcca cggagtttag cgccgttact    720
agcatgatca aaaacgcgca agaaatcgta acgcaagctc aaagccttaa caacccgcaa    780
agcaatcaaa acgcgccgaa agatttcaat ccttacacct ctgctgatag ggctttcgct    840
caaaacatgc tcaatcacgc gcaagcgcaa gccaagatgc ttgaactagc cgatcaaatg    900
aaaaaagacc ttaacactat cccaaaacaa tttatcacaa actacttggc agcttgccgc    960
aatgggggtg ggacattacc tgatgcaggg gttacttcta acacttgggg ggccggttgc   1020
gcctatgtgg aagagacgat aaccgcccta aataacagcc ttgcgcattt tggcactcaa   1080
gccgatcaaa tcaagcaatc tgagttgttg gcgcgcacga tacttgattt tagaggcagc   1140
cttaaggatt taaacaacac ttataacagc atcaccacga ccgcttcaaa cacgcccaat   1200
tccccattcc ttaaaaattt gataagccaa tccactaacc ctaataaccc cgggggctta   1260
caggccgttt atcaagtcaa ccaaagcgct tattcgcaat tattaagcgc cacgcaagaa   1320
ttagggcata acccctttcag acgcgttggc ttaatcagct ctcaaaccaa caacggtgcg   1380
atgaatggga tcggcgtgca aataggggtat aaacaatttt ttggtgaaaa aagaagatgg   1440
gggttaaggt attatggttt ttttgattac aaccatgctt atatcaaatc cagctttttc   1500
aactccgcct ctgatgtgtt cacttatggg gtaggaacag atgtcctcta taactttatc   1560
aacgataaag ccaccaaaaa caataagatt tcttttgggg tgtttggggg gattgcgtta   1620
gctggcactt cgtggcttaa ttctcaatac gtgaatttag cgacattcaa taatttttac   1680
agcgctaaaa tgaatgtggc gaatttccaa ttcttattca acttgggctt gagaatgaat   1740
ctcgctaaaa acaaaaagaa agcgagcgat catgtagctc agcatggcgt ggaactaggc   1800
gtgaagatcc ctacgatcaa cacgaattac tattctttgc taggcactca actccaatac   1860
cgcaggcttt atagcgtgta tttgaattat gtgtttgctt ac                      1902
```

Seq ID 2

```
atggcaaaag aaatcaaatt ttcagatagc gcgagaaacc ttttatttga aggcgtgaga     60
caactccatg acgctgttaa agtaaccatg gggccaagag gcaggaacgt gttgatccaa    120
aaaagctatg gcgctccaag catcactaaa gatggcgtga gcgtggctaa agagattgaa    180
ttaagttgcc cggtagctaa catgggcgct caactcgtta aagaagtagc gagcaaaacc    240
gctgatgctg ccggcgatgg cacgaccaca gcgaccgtgc tggcttatag catttttaaa    300
gaaggtttga ggaacatcac ggctggggct aaccctattg aagtgaaacg aggcatggat    360
aaagccgctg aagccattat taatgagctt aaaaaagcga gcaaaaaagt gggcggtaaa    420
gaagaaatca cccaagtggc gaccatttct gcaaactccg atcacaatat cgggaaactc    480
atcgctgacg ctatggaaaa agtgggtaaa gacggcgtga tcaccgttga agaagctaag    540
ggcattgaag atgaactaga tgttgtagaa ggcatgcaat ttgatagagg ctacctctcc    600
ccttattttg taacaaacgc tgagaaaatg accgctcaat tggataacgc ttacatcctt    660
ttaacggata aaaaaatctc tagcatgaaa gacattctcc cgctactaga aaaaaccatg    720
aaagagggca aaccgctttt aatcatcgct gaagacattg agggcgaagc tttaacgact    780
ctagtggtga ataaattaag aggcgtgttg aatatcgcag cggttaaagc tccaggcttt    840
ggggacagaa gaaaagaaat gctcaaagac atcgctattt taaccggcgg tcaagttatt    900
agcgaagaat tgggcttgag tctagaaaac gctgaagtgg agtttttagg caaagccgga    960
aggattgtga ttgacaaaga caacaccacg atcgtagatg gcaaaggcca tagccatgat   1020
gtcaaagaca gagtcgcgca aatcaaaacc caaattgcaa gcacgacaag cgattatgac   1080
aaagaaaaat tgcaagaaag gttggctaaa ctctctggcg gtgtggctgt gattaaagtg   1140
ggcgctgcga gtgaagtgga aatgaaagag aaaaaagacc gggttgatga tgcgttgagc   1200
gcgactaaag cggctgttga agaaggtatt gtgattggcg gcggtgcggc tctcattcgc   1260
gcggctcaaa aagtgcattt gaatttgcac gatgatgaaa aagtgggcta tgaaatcatc   1320
atgcgcgcca ttaaagcccc attagctcaa atcgctatca atgccggtta tgatggcggt   1380
gtggtcgtga atgaagtaga aaaacacgaa gggcattttg gttttaacgc tagcaatggc   1440
aagtatgtgg atatgtttaa agaaggcatt attgacccct taaaagtaga aaggatcgct   1500
ttacaaaatg cggtttcggt ttcaagcctg cttttaacca cagaagccac cgtgcatgaa   1560
atcaaagaag aaaaagcggc cccagcaatg cctgatatgg gtggcatggg cggtatggga   1620
ggcatgggtg gcatgatg                                                 1638
```

Seq ID 3

```
atgaaaatta aaaatatctt actgagtggg gggagcggga aacgcctatg gcctttaagc     60
```

cgtagcctat accctaagca atttttaaag ctttttgacc ataaaagctt gtttgaattg 120
agttttaaaa gaaacgcttc cttagtagat gaaacgctca ttgtgtgcaa tgaaaagcat 180
tatttttag ccctagaaga gataaagaat gaaatcaaaa acaaaagcgt gggtttttta 240
ttagagagct tgagtaaaaa caccgctaac gccatcgctt tgagcgcttt aatgagcgat 300
aaagaagatt tgctcatcgt tacgccaagc gatcatttga ttaaagacct tcaagcgtat 360
gaaaacgcga taaaaaaagc gattgatcta gcccaaaaag gtttttagt cacttttggg 420
gtgagtattg acaagcccaa cacggagttt gggtatattg aaagccctaa tggtttagat 480
gtcaagcgat tcattgaaaa gccaagccta gacaaagcga tagagtttca aaaaagcggg 540
ggtttttatt tcaatagcgg catgtttgtt ttccaagcgg gcgtttttt agacgaacta 600
aaaaagcatg cccccactat tttaaagggg tgtgaaagag cgtttgaatc tttagaaaac 660
gcgtattttt ttgaaaaaaa gatcgctcgt ttgagcgaaa agagcatgca agatttagaa 720
gacatgagta ttgatatagc cttaatgcaa caaagccaca aaatcaaaat ggtagaattg 780
aacgccaaat ggagcgattt agggaatttt aacgctcttt ttgaagaagc ggctaacgag 840
cctaaagaaa atgtcagctt gaatcaaacg cctgtttttg ccaaagaaag cgaaaataat 900
ttagtgtttt ctcataaagt gagcgctctt ttaggcgttg agaatttagc ggttattgac 960
actaaagacg ctcttttaat cgctcataaa gacaaggcta aggatttaaa agctttagtg 1020
aacgaggtag aaacaaacaa ccaagaattg ttgcaaacgc acactaaagt ctatcgccct 1080
tgggggagtt atgaagtctt gcatgagagc ggttgttaca aggttaagat tttagaagtc 1140
aaaccaaacg caaggctttc tttacaaaag catttccaca ggagcgaaca ctgggtagtg 1200
attagcggga tggcgagcgt ggagttggat caccagttgt ttgaattgca agctaatgag 1260
tccacttata tccctaaaaa caccctacac cgcctggcta attacggcaa gatcccttta 1320
attatcatag aagttcaagt gggcgagtat gtcggtgaag acgatattgt gcgcattgat 1380
gatgatttta acagacaaaa tcaaaacgcc 1410

Seq ID 4

atggctgaat ggaaaacgga tacagaagaa gtcaaagagg ttgttaaaaa atgcagggaa 60
tttaaaagat ccttacaaga agaaaaatgc agtccattta tcaaagacct tgatagttac 120
gcgctaaaaa tcatagtgga gcgcagaaaa attgaacacc aattgcaaga agctatagaa 180
aaattaagaa gagccaaaaa aaagagaagt agcttttggg gatcctttgt agagggtgcg 240
agagatcttc ttgatatggt cagggagatt atcccacctg ctaaattggg tgctgaagct 300
tgtgataagg ttttaaatct tatggaagac aatatagaaa aatgggaaca caatgtaagg 360
ttattagaac gaatgcttga aatctacgcc actcaagcca aagcgagcgc ggaacttgta 420
gagggagctt ggaagagcgt taaaaagtcg ttggactttt ataccgataa gcaccaggaa 480
tttatcaaac gcttgaacta tgcgagtgaa gcgatagaca acgaatacaa tatcgcgccc 540
ccagaaattt tgaacgagag cgattttgaa agccctacga ttgtttataa ccctaaaaaa 600
agcgtttatg atgaacactt gaaagatttg agggaagatt ttagcttttc tttatacgct 660
gatttgaaaa acagaattaa cgcttcttct aagctagatc gcaccacaac ctctaaagag 720
caagaatttg aaaagaattt agaggatttg atgccaggct ttagaggtgg aactgacact 780
ttgtctggcg atgaattaga gcacatggca agctttagag ggcaagaatt tgaaaagaat 840
ttagaggatt tgatgccgag ttctttaggc gtgcattctt atgatgagag cttgaattta 900
gccaaaaaga attgcgttaa aaattgtaag aaagctttag gagattttac agaaaaaatc 960
aaagaatccc ccaacgattt gaacgctata aacgaagctt ttaatcattt ggaaacagag 1020
ttagaacgcg ctacagaaaa tttgagccaa aaaatagcgc ctattttaga gcggtatgaa 1080
aatgataagc ggcaaaaatt gggttatggc gagttttag aaaaagaaaa agagggcttt 1140
atggtagatg agcaaaaccc ttatccggaa gaagtccgct ttaatgagtt gcgtttagcg 1200
gaatttgaga gcgttttag cgccattgtg cctttagagg atttagataa acctgcatgc 1260
gctcatcatg ccctaaaggc tttagaagcc acgcttaaaa atagggattt gggctttgat 1320
gcgacagaat tggaacagat cgcaaaaggt ttcattccta aggggtattt gtggcatttt 1380
gacgcgaatg ttttagggaa tgtggcgttg gtgagagaag agttattatt aggcgtgaaa 1440
cacacgaaag gatacttact atggaaacaa ttcctgcaaa ctcagaac 1488

Seq ID 5

atgaacactt acgctcaaga atccaagctc aggttaaaaa ccaaaatagg ggctgatggg 60
cggtgcgtga ttgaagacaa ttttttcacg ccccccttta agctcatggc gccctttac 120
cctaaagacg atttagcgga aatcatgctt ttagcggtaa gccctggcat gatgaggggc 180
gatgcgcaag atgtgcaatt aaacatcggt ccaaattgca agttaaggat cacttcgcaa 240
tcctttgaaa aaatccataa cactgaagat gggtttgcca gcagagacat gcatattgtt 300
gtgggggaaa acgcttttt agattttgcg cctttcccgt taatcccctt tgaaaacgcg 360
cattttaagg gcaacaccac gatttctttg cgctctagct ctcaattgct ctatagtgaa 420
atcattgtcg cagggcgagt ggcgcgcaat gagttgttta aattcaaccg cttgcacacc 480
aaaatctcta ttttacaaga tgagaaaccc atctattatg acaacacgat tttagatccc 540
aaaaccaccg acttaaataa catgtgcatg tttgatggct atacgcatta tttgaatttg 600
gtgcttgtca attgccccat agagctctct ggtgtgcgag aatgcattga agaaagcgaa 660
ggggtggatg gggcagtgag tgaaaccgct agttctcatt tatgcgtgaa agctttagcg 720
aaaggctcag aacccttatt gcatttaaga gaaaaaatcg ctcgcttggt tacgcaaacc 780
accacgcaaa aggtt 795

Seq ID 6

atgaaaaaga ttagcagaaa agaatatgtt tctatgtatg gccctactac aggcgataaa 60
gtgagattgg gcgatacaga cttgatcgct gaagtagaac atgactacac catttatggc 120
gaagagctta aattcggtgg cggtaaaacc ctgagagaag gcatgagcca atccaacaac 180
cctagcaaag aagaattgga tctaatcatc actaacgctt taatcgtgga ttacaccggt 240
atttataaag cggatattgg tattaaagat ggcaaaatcg ctggcattgg taaaggcggt 300
aacaaagaca tgcaagatgg cgttaaaaac aatcttagcg taggtcctgc tactgaagcc 360
ttagccggtg aaggtttgat cgtaactgct ggtggtattg acacacacat ccacttcatt 420
tcaccccaac aaatccctac agcttttgca agcggtgtaa caaccatgat tggtggcgga 480
actggtcctg ctgatggcac taatgcgact actatcactc caggcagaag aaatttaaaa 540
tggatgctca gagcggctga agaatattct atgaacttag gtttcttggc taaaggtaac 600
gcttctaacg acgcgagctt agccgatcaa attgaagctg gtgcgattgg ctttaaaatc 660
cacgaagact ggggcaccac tccttctgca atcaatcatg cgttagatgt tgcagacaaa 720
tacgatgtgc aagtcgctat ccacacagac actttgaatg aagccggttg cgtggaagac 780
actatggcag ctattgccgg acgcactatg cacactttcc acactgaagg tgctggcggc 840
ggacacgctc ctgatattat taaagtagct ggtgaacaca acattcttcc cgcttccact 900
aaccccacta tccctttcac tgtgaataca gaagcagaac acatggacat gcttatggtg 960
tgccaccact tggataaaag cattaaagaa gatgttcagt tcgctgattc aaggatccgc 1020
cctcaaacca ttgcggctga agacactttg catgacatgg ggattttctc aatcaccagc 1080
tctgactctc aagctatggg tcgtgtgggt gaagttatca ctagaacttg gcaaacagct 1140
gacaaaaaca aaaaagaatt tggccgcttg aaagaagaaa aaggcgataa cgacaacttc 1200
aggatcaaac gctacttgtc taaatacacc attaacccag cgatcgctca tgggattagc 1260
gagtatgtag gttctgtaga agtgggcaaa gtggctgact tggtattgtg gagtcccgca 1320
ttctttggcg taaaacccaa catgatcatc aaaggcgggt tcattgcgtt gagtcaaatg 1380
ggtgacgcga acgcttctat ccctacccca caaccagttt attacagaga aatgttcgct 1440
catcatggta aagccaaata cgatgcaaac atcacttttg tgtctcaagc ggcttatgac 1500
aaaggcatta aagaagaatt agggcttgaa agacaagtgt tgccggtaaa aaattgcaga 1560
aacatcacta aaaaagacat gcaattcaac gacactaccg ctcacattga agtcaatcct 1620
gaaacttacc atgtgttcgt ggatggcaaa gaagtaactt ctaaaccagc caataaagtg 1680
agcttggcgc aactctttag cattttc 1707

Seq ID 7

atgaaaaaga ttagcagaaa agaatatgtt tctatgtatg gccctactac aggcgataaa 60
gtgagattgg gcgatacaga cttgatcgct gaagtagaac atgactacac catttatggc 120
gaagagctta aattcggtgg cggtaaaacc ctgagagaag gcatgagcca atccaacaac 180
cctagcaaag aagaattgga tctaatcatc actaacgctt taatcgtgga ttacaccggt 240
atttataaag cggatattgg tattaaagat ggcaaaatcg ctggcattgg taaaggcggt 300
aacaaagaca tgcaagatgg cgttaaaaac aatcttagcg taggtcctgc tactgaagcc 360
ttagccggtg aaggtttgat cgtaactgct ggtggtattg acacacacat ccacttcatt 420
tcaccccaac aaatccctac agcttttgca agcggtgtaa caaccatgat tggtggcgga 480
actggtcctg ctgatggcac taatgcgact actatcactc caggcagaag aaatttaaaa 540
tggatgctca gagcggctga agaatattct atgaacttag gtttcttggc taaaggtaac 600
gcttctaacg acgcgagctt agccgatcaa attgaagctg gtgcgattgg ctttaaaatc 660
cacgaagact ggggcaccac tccttctgca atcaatcatg cgttagatgt tgcagacaaa 720
tacgatgtgc aagtcgctat ccacacagac actttgaatg aagccggttg cgtggaagac 780
actatggcag ctattgccgg acgcactatg cacactttcc acactgaagg tgctggcggc 840
ggacacgctc ctgatattat taaagtagct ggtgaacaca acattcttcc cgcttccact 900
aaccccacta tccctttcac tgtgaataca gaagcagaac acatggacat gcttatggtg 960
tgccaccact tggataaaag cattaaagaa gatgttcagt tcgctgattc aaggatccgc 1020
cctcaaacca ttgcggctga agacactttg catgacatgg ggattttctc aatcaccagc 1080
tctgactctc aagctatggg tcgtgtgggt gaagttatca ctagaacttg gcaaacagct 1140
gacaaaaaca aaaaagaatt tggccgcttg aaagaagaaa aaggcgataa cgacaacttc 1200
aggatcaaac gctacttgtc taaatacacc attaacccag cgatcgctca tgggattagc 1260
gagtatgtag gttctgtaga agtgggcaaa gtggctgact tggtattgtg gagtcccgca 1320
ttctttggcg taaaacccaa catgatcatc aaaggcgggt tcattgcgtt gagtcaaatg 1380
ggtgacgcga acgcttctat ccctacccca caaccagttt attacagaga aatgttcgct 1440
catcatggta aagccaaata cgatgcaaac atcacttttg tgtctcaagc ggcttatgac 1500
aaaggcatta aagaagaatt agggcttgaa agacaagtgt tgccggtaaa aaattgcaga 1560
aacatcacta aaaaagacat gcaattcaac gacactaccg ctcacattga agtcaatcct 1620
gaaacttacc atgtgttcgt ggatggcaaa gaagtaactt ctaaaccagc caataaagtg 1680
agcttggcgc aactctttag cattttc 1707

Seq ID 8

atgcgttatt ttcttgtagt tttcttgttt ttgtttgtgg gttgcacaaa aaaggatttc 60
acgctcaaag atttatcctt gccccaagag gcttcaagct atcttgcaag ctctcaaaat 120
ggcagtaaca acaaccaaag cattgacccc caagcgttaa gagaaaatct gaaagagagc 180
tatctcaaag cgtggtattc cccatggcta gatatgaaag tcaaaagcaa taaaaaagaa 240
gtgttttgga tccttaagga gatgaataaa tccaccggtt atggcgaaga tctaaaaccc 300
aacgcaaaag ctttcaatga cgcactcatt aagagcatgg atattgagca ttaccctagc 360

gttaagatta gggctgttgt agcgcgagat agcgatgtga gggctgtgcc tactaacaaa 420
ccttattatc tttctcaaaa aggctatcct tttgataggt atcaaaattc gctgattttt 480
caaggcacgc cggttttaat cacgcatttt aatctagata aaacttatgc ccacattcaa 540
agcagttttg tttatggctg gatcaaagtt agcgatttag tctacatgca cgataaagac 600
atagagcttt taacccatct taaagattat gtcatgccta taaaagataa aatccccctt 660
tatacagact atggggattt ttacaccaac gccagagtgg gcgaattgtt cgctctcatc 720
ccccaaagtc aaaaaacacc tcaaaaaccc caaaaaaagg aattgaaagc ctatggtttt 780
ttgagagacg ctaagggtta tgcagcttta caaagcgtga tcttagaaga aaaggatttt 840
tttgttttcc ctaaggcttt taacagcgag aacatggcgt attttataga caccatgtta 900
gggcaaaaat acggctgggg cgggctattg ggtaataggg attgctcggc tttcaccaga 960
gatagttttg ctaattttgg tattttgctc cccagaaatt cctatgcgca aagccgttat 1020
gcgaacaatt atgtggattt aagctctatg aaagccaaag aaaaagaaga ctacatcctt 1080
aaaaacgcca cgccttttgg aacgctcatc tatttaaaag ggcatatcat gctttattta 1140
ggcgcacaca accatcaagc gatagtcgct cacagcattt ggtcggtgca aacccaaaag 1200
cattttaaaa ccttgagcca taaaatagga ggcgtggtga tcacttcgtt atggttagct 1260
gaagagcata atggggcgtt ttctaaaaag aaattattga ttgatagggt gcttggaatg 1320
agcgatttga aagattttgt caataaaact tcaagccctt taaatgcgaa t 1371

Seq ID 9
atgaaaaaga aagctaacga agaaaaagcc caaaaaagag ctaaaacaga agccaaagca 60
gaagccacac aagaaaataa aactaaagaa aacaataaag ccaaagaaag caaaattaaa 120
gaaagcaaaa tcaaagaagc taaagcgaaa gaacctattc ctgttaaaaa gcttagtttt 180
aatgaagcgt tagaagaatt gttcgctaat tccttaagcg attgcgtttc ttatgagtcc 240
atcattcaaa tcagcgcgaa agtccccact ctagcccaaa tcaaaaaaat caaagaattg 300
tgccaaaaat accaaaagaa attagtcagc tcttcagaat acgctaaaaa actcaatgcg 360
attgacaaga ttaaaaaaac cgaagaaaag caaaaagttt tagatgaaga attagaagat 420
ggctatgact ttttgaaaga aaaggatttt ttagagtgga gcagaagcga tagcccagtg 480
cgcatgtatt tgcgcgaaat gggggatata aaacttttaa gcaaagatga agagattgaa 540
ttgagcaagc aaatccgctt gggtgaagac attattttag acgcgatctg ctcggtgccg 600
tatttgattg attttatcta tgcgtataaa gacgctttaa tcaatcgtga aagaagggtt 660
aaagagcttt tcaggagctt tgatgatgac gatgaaaata gcgtgagcga ttctaaaaaa 720
gatgaagaca acgaagaaga tgaagaaaac gaagaaagga aaaaagtcgt ttctgaaaaa 780
gacaagaagc gtgtagaaaa ggttcaagaa agctttaaag ccctagacaa ggctaaaaaa 840
gaatggctta aagcccttga agcccccata gatgaaagag aagacgaatt ggtgcgttca 900
ttgaccctag cttacaaacg ccaaacactc aaagacagac tctatgattt agaacctacc 960
agcaaactga ttaatgaatt agtcaaaacg atggaaacca ctttaaaaag cggcgatggg 1020
tttgaaaaag agttgaaacg cttggaatac aaactgccct tattcaatga cactctatc 1080
gcaaaccata aaaaaatcct tgccaatatc actaacatga ctaaagaaga tattatcgct 1140
caagtgccag aagcgactat ggtgagcgtg tatatggatc ttaaaaagct ttttttgact 1200
aaagaagcga gcgaagaagg ctttgatcta gcccccaaca agctaaaaga aattttagag 1260
caaatcaaaa gagggaagtt gatttccgat cgcgctaaaa acaaaatggc taaatccaat 1320
ttaaggttgg tggtgagcat cgctaaacga ttcacgagca gaggcttacc attcttggat 1380
ttgattcaag agggcaatat tggcttgatg aaagcggtgg ataagtttga gcatgaaaag 1440
ggcttcaagt tttctaccta tgcgacctgg tggatcaaac aagctatcag cagagccata 1500
gccgatcagg cccgcactat ccgcatcccc attcacatga ttgatacgat taatcgcatc 1560
aataaagtca tgcgcaaaca cattcaagaa aacggcaaag agcctgattt agaagtggtg 1620
gctgaagaag tggggctttc gttagataaa gtgaagaatg tgattaaggt gactaaagag 1680
cctatcagtt tggaaacccc agtcggcaat gatgatgatg gcaagtttgg ggatttcgtg 1740
gaagataaga atatcgtcag ctccattgat cacatcatgc gagaagattt gaaagcacaa 1800
attgaaagcg ttttggatca gttgaatgag cgagaaaaag cggtgatccg catgcgtttt 1860
gggcttttag acgatgaaag cgatcgaact ttagaagaaa ttggcaagga attgaatgtt 1920
actagagaaa gggtgcgcca gattgaaagc tctgcgatta aaaaattgag aagcccgcag 1980
tacgggcgca ttttaagaaa ctatttgcgc att 2013

Seq ID 10
atggtgcaaa aaattggcat tttaggggcg atgagagaag aaataacccc tatactagaa 60
ttgtttggcg tggattttga agagatccct ttaggggga atgtcttcca taaaggcgtt 120
tatcacaaca aggaaatcat tgtcgcttat agcaagattg gcaaggtgca ttccacttta 180
accacaacga gcatgatttt agcgtttggc gttcaaaagg tgctttttag cggggtggct 240
ggaagcttag ttaaagattt aaaaatcaat gatttactag tggctattca attagtccag 300
catgatgtgg atttgagcgc gtttgatcac cctttagggt tcatcccaga aagcgcgatt 360
tttattgaaa cgagcgaaag tttgaacgct ttggctaaag aagtcgctaa tgaacagcat 420
atcgtgctca aagaaggcgt catcgcatca ggcgatcagt ttgtgcatag caaagaaagg 480
aaagagtttt tagttagcga gtttaaagcg agcgcggtgg aaatggaggg ggcgagcgtg 540
gcgtttgtgt gccaaaaatt tggcgtgcca tgctgtgtgt taaggagcat tagcgataac 600
gctgatgagg aagctaacat gagctttgat gcgtttttag aaaaaagcgc tcaaacttca 660
gcgaaattct taaaaagcat ggtggatgag ctt 693

Seq ID 11

```
atgagtttta ggataaatac caatatcgcc gctttaactt ctcatgcggt aggggttcaa     60
aacaacagag acctttcaag ctcgcttgaa aagttaagct cagggcttag gatcaataaa    120
gccgctgacg attctagtgg gatggcgatc gctgatagct taaggagtca aagcgcgaat    180
ttgggtcaag cgatccgcaa cgccaatgac gctattggta tggttcaaac cgcagataaa    240
gcgatggatg agcaaatcaa aatcttagac accattaaaa ccaaagccgt tcaagccgct    300
caagatgggc aaactttaga aagccgaaga gcgctccaga gcgatattca aaggttgtta    360
gaagaactgg acaatatcgc taacaccaca agctttaacg gccaacaaat gctttcagga    420
agtttttcta acaaagaatt tcaaattggc gcgtattcta acgccacggt taaagcgtct    480
attggctcaa cgagctcaga taagattggg catgtgcgca tggaaacttc ttcttttagc    540
ggtgcaggca tgctcgctag cgcggcggca caaaacttga ctgaagtggg attgaatttc    600
aaacaagtca atggcgtgaa tgattataag attgaaaccg tgcgcatttc tacgagtgct    660
ggcactggga ttggagcgtt aagcgaaatc atcaatcgtt tttctaacac tttaggcgtt    720
agggcttctt ataatgtcat ggctaccggc ggcactcccg tgcaatcagg aactgttagg    780
gagcttacca ttaatggcgt agaaattggg accgtgaatg atgtgcataa aaacgacgct    840
gatgggagat tgactaatgc aatcaactcc gtcaaagaca ggacgggtgt ggaagcgagc    900
ttggatattc aagggcgcat taatttacac tccattgacg ggcgcgcgat ttctgtgcat    960
gcagcgagcg cgagcggtca ggtttttggg ggagggaatt ttgcagggat ttctgggaca   1020
cagcatgcgg ttattgggcg cttaaccttg accagaaccg acgctagaga catcattgtg   1080
agcggtgtga atttcagcca tgtgggcttt cattccgctc aaggggtggc agaatacacc   1140
gtgaatttga gagcggttag gggcattttt gatgcgaatg tggcttcagc agccggagcg   1200
aacgctaatg gcgcgcaagc ggagaccaat tctcaaggta taggggctgg ggtaacaagc   1260
cttaaagggg cgatgattgt gatggatatg gcagattcag cgcgcacgca attggacaag   1320
atccgctcgg atatgggttc ggtgcaaatg gaattggtta caaccattaa taatatttct   1380
gtaacccaag tgaatgttaa agcggctgaa tctcaaatca gagatgtgga ttttgctgaa   1440
gagagcgcga acttttctaa atacaatatt ttggcgcaaa gcgggagttt tgctatggcg   1500
caagcgaatg cggtgcaaca aaatgtctta aggcttttac aa                      1542
```

Seq ID 12

```
atgaaaaaaa atatcttaaa tttagcgtta gtgggtgcgt tgagcacgtc gtttttgatg     60
gctaagccgg ctcataacgc aaataacgct acgcataaca cgaaaaaaac gactgattct    120
tcagcaggcg tgttagcgac agtggatggc agacctatca ctaaaagcga ttttgacatg    180
attaagcaac gaaatcctaa ttttgatttt gacaagctta aagagaaaga aaaagaagcc    240
ttgattgatc aagctattcg caccgccctt gtagaaaatg aagctaaaac cgagaaattg    300
gacagcactc cagaatttaa agcgatgatg gaagcggtta aaaaacaggc tttagtggaa    360
ttttgggcta aaaaacaggc tgaagaagtg aaaaaagtcc aaatcccaga aaaagaaatg    420
caagattttt acaacgctaa caaagatcag ctttttgtca agcaagaagc ccatgctagg    480
catattttag tgaaaaccga agatgaggct aaacggatta tttctgagat tgacaaacag    540
ccaaaggcta aaaaagaagc taaattcatt gagttagcca atcgggatac gattgatcct    600
aacagcaaga acgcgcaaaa tggcggtgat ttggggaaat tccaaaagaa ccaaatggct    660
ccggattttt ctaaagccgc tttcgcttta actcctgggg attacactaa aacccctgtt    720
aaaacagagt ttggttatca tattatctat ttgatttcta aagatagccc tgtaacttat    780
acttatgaac aggctaaacc taccattaag gggatgttac aagaaaagct tttccaagaa    840
cgcatgaatc aacgcattga ggaactaaga aagcacgcta aaattgttat caacaag       897
```

Seq ID 13

```
gtgcgatata tcaagttttt caaagagttg aacaataaaa atgtgaatct ggttgggggc     60
aagaacgcta gtattggtga aatgtttcaa gaattagtgc ctattggtat taaagtgcct    120
gatggctttg cgatcaccag cgaagcgtat tggtatcttt tagagcaagg aggggctaaa    180
caaaaaatca tagagctttt agaaaatgtt gatgccaccg aaattgatgt gttaaaaatc    240
cgctccaaac aaatcagaga gcttatttttt ggcacgcctt ttcctagcga tttgagagat    300
gagatttttc aagcttatga gattttaagc cagcaatacc acatgaaaga agccgatgtg    360
gctgtaagga gttccgctac tgcagaagat ttgccggacg cttcttttgc cgggcagcaa    420
gacacttatt taaacattaa gggtaaaacc gaattgatcc actatatcaa atcctgttta    480
gcgtcgcttt ttaccgatag agcgattagc tatagggcga gtcgtgggtt tgatcattta    540
aaagtcgcgc tcagcgtggg ggtgcaaaaa atggtgcgag cggataaagg cagcgcgggc    600
gtgatgtttt ctattgacac cgaaaccggt tttaaagacg cggtgtttat cacttcagcg    660
tgggggttag gcgaaaatgt ggtgggtggc acgataaacc ctgatgaatt ttatgtgttt    720
aagcccactt tagagcaaaa caaacgcccc attatcaaac gccaactcgg caataaaacg    780
caaaaaatgg tctatgcccc aaggggtagc gaacacccca ccagaaacat taaaaccacc    840
aaaaaagaat ggcaatcctt ttcattgagc gatgaagacg tgctgatttt agccaaatac    900
gccattgaaa ttgaaaaaca ctactctaaa gaagccaaac aataccgccc tatggatata    960
gaatgggcta aagatggcga gagcggggaa atctttatcg ttcaagcgcg cccagaaacc   1020
gttcaaagcc aaaaaagtaa agaagaaagt caagtctttg aaaaattcaa attcaaaaac   1080
cctaacgaaa agaaagagat tatcttacaa ggcagagcga ttgggagtaa aattggctca   1140
ggaaaagtgc gcatcatcaa tgatttggag cacatgaatt cttttaaaga gggcgaaatt   1200
ttagttacgg ataacaccga tccggactgg gagccttgca tgaaaaaagc gagcgcggtt   1260
atcactaatc gtggagggcg cacttgccat gccgctattg tggcgagaga aattggcgtg   1320
```

ccagctatcg ttggggtgag cggggcgact gatagccttt ataccggcat ggaaatcacg 1380
gtttcttgcg ctgagggcga agagggctat gtgtatgcgg gcatttatga gcatgaaatt 1440
gaaagggtgg agctttctaa catgcaagaa actcaaacaa aaatttacat caatattgga 1500
aaccctgaaa aagcctttgg cttttctcaa ctccctaatc acggcgtagg gctagccagg 1560
atggaaatga ttattttaaa tcaaatcaaa gcccaccctt tagctttagt ggatttgcac 1620
cacaaaaaaa gcgtgaaaga aaaaaatgaa attgaaaacc tcatggcagg ctatgctaac 1680
cctaaagatt tttttgtgaa aaaaatcgct gaaggcattg gcatgatcag tgcagcgttt 1740
taccctaaac ctgtcattgt gagaacgagc gatttcaaat ccaatgaata catgcgcatg 1800
cttggcggct ctagctatga gcctaatgaa gaaaacccca tgcttggcta taggggggct 1860
agtcggtatt attcagagag ctataatgaa gcgttttcgt gggagtgtga agccttagcg 1920
ttagtgaggg aagaaatggg attaaccaac atgaaagtga tgatcccttt tttgcgaacc 1980
attgaagagg gtaaaaaagt cctagaaatc ttaagaaaaa acaatttaga atccggtaaa 2040
aacgggcttg aaatttatat catgtgcgaa ttgccggtga atgtcatttt ggctgatgat 2100
ttcttgagct tgtttgatgg cttttctatt ggatcaaacg atttaaccca gctcacttta 2160
ggcgtggata gagacagcga attggtcagc catgtctttg atgaaaggaa tgaagcgatg 2220
ctaaagatgt ttaaaaaagc gattgaagct tgcaaaaggc acaacaaata ttgcgggatt 2280
tgcgggcaag ccccaagcga ttaccctgaa gtaacagagt ttttagtcaa agagggcatc 2340
acttccattt ctttaaaccc tgatagcgtg atccccactt ggaacgctgt agccaagtta 2400
gaaaaagaac taaaagaaca tggcttaact gaacat 2436

Seq ID 14

atgagtgcgg aactgattgc tgtttataaa gacgagcaaa taatagattt agagagcgcg 60
aaagtcttag ggctgagcga tgggattaaa gcgttaaacg ggacagagcc gatatatttt 120
gatgattcgc ctttggcttt agaggtgatt aggcattcat gcgcgcattt gcttgcgcaa 180
agcttgaaag ccctttatcc ggacgcgaaa ttttttgtag gccctgtggt agaagagggg 240
ttttattacg atttcaagac ttcttcaaaa atcagcgaag aggatttgcc taaaattgaa 300
gcgaaaatga aagagtttgc gaagttgaaa ctcgctatca ctaaagagac tttaaccaga 360
gagcaagctt tggagcgttt taagggcgat gaattaaagc atgcggtgat gagtaaaatc 420
ggtggcgatg cctttggcgt gtatcaacaa ggcgagtttg aagatttgtg taaggggccg 480
catctcccaa acacccgttt tttaaaccat tttaagctca ctaaactggc tggggcttat 540
ttgggcggcg atgaaaacaa tgaaatgctc attagaatct atggaatcgc ttttgccacc 600
aaagagggtt taaaagacta tcttttccaa atagaagaag cgaaaaaacg agatcacaga 660
aagctaggcg tggagctagg gctttttagc tttgatgatg agataggggc gggcttacct 720
ttatggctgc ctaaaggggc aaggcttagg aagcgcattg aagatttatt gagtcaagcg 780
ttacttttaa gaggctatga gccggttaaa ggtcctgaga ttttaaagag cgatgtgtgg 840
aaaatcagcg ggcattatga caactataaa gaaaacatgt atttcaccac gattgatgag 900
caagaatatg gcataaagcc tatgaactgc gtggggcata ttaaagtcta tcaaagcgct 960
ttgcacagct acagagattt gcccttaagg ttttatgaat acggcgtggt gcatcggcat 1020
gaaaaaagcg gcgtgttgca tgggctttta agggttaggg aatttaccca agatgatgca 1080
catatttttt gctcttttga acagatccaa agcgaagtga gcgcgatttt agattttacg 1140
cacaaaatca tgcaagcgtt tgattttagc tatgaaatgg aattatccac aaggccggct 1200
aaatccatag gcgatgataa agtttgggaa aaggccacta acgctttaaa agaagcctta 1260
aaagaacacc gcattgatta caagattgat gaagggggag gggctttcta tgggcctaag 1320
attgacatta aaatcactga cgctttaaag cgtaaatggc agtgtggcac gattcaagtg 1380
gatatgaatt tgcctgaacg cttcaagctc gctttcacta atgagtataa tcacgctgag 1440
cagccggtga tgatccacag agcgatttta ggctcgtttg aaaggtttat tgcgattttg 1500
agcgaacatt ttgggggggaa tttccctttc tttgtcgcgc ccactcaaat cgctctcatc 1560
cctattaatg aagagcatca tgtttttgct ttgaaattaa aagaggcgct aaaaaagcgc 1620
gatatttttg tagaagtgtt agataaaaac gacagcttga ataaaaaggt gcgattagcc 1680
gaaaagcaaa aaatccctat gattttagtg ttagggaatg aagaagtgga gaccgaaatt 1740
ttatccatta gagacagaga aaaacaagat caatataaaa tgcccttaaa ggagttttta 1800
aacatggttg aatctaagat gcaagaggtt agtttt 1836

Seq ID 15

gtgaaacgga ttttattttt tttagtagct acgacttttt tgttgagagc agaaacggat 60
tctgccacta ttaacactac agttgatccc aatgttatgt tttctgaaag ctccacaggg 120
aatgtgaaaa aagaccgcaa gagggtttta aagagcatgg ttaatttgga aaaagagcgc 180
gtgaagaatt ttaaccggta ttctgaaacc aagatgagta agggcgactt atccgctttt 240
ggagctttct ttaaggggag tttggaaagt tgtgtggatc aaaagatttg ttattatgag 300
cataaagatg gcaaggtttc ttttgtggtg aatgacaggg agaagtttta taaacatgtg 360
cttaaagact tagggacaga gctttcgctc cctttgttta actggcttta caaaggctcg 420
gattttgggg ctttgcatga gcagtttggg gatatgtatg atgggtatat caaatacttg 480
atcagtatgg ttagaataag ccaaaaagaa aaggctagaa aagtggatgc aatcgttctt 540
aagaaaatgg aagaacaagc tgagaaagac actaaggcag cgtttcaaaa gaggagcagt 600
ggggagcttg aaagccatac tgatagccct gaatttataa gctcttctaa gaggacacag 660
aacgcttcta attcggatct caattctatg accaatgcta acgcgctcaa agaaacagct 720
tcaaaagagc cagaggcttc ttcaaaaaaa gagaaaaagt ctaagaaaaa acgtcgcctt 780
tcaaagaaag aaaaacaaca acaagccttg caacaagagt ttgaaaaaca aattagcgac 840

tctagtaagt ctgaaaaa 858

Seq ID 16
atgaaagaaa aaaacttttg gcctttaggg atcatgagcg tgctcattct tgggcttggg 60
atcgtggtgt ttttggtggt gtttgcccta aaaaattcgc ctaaaaacga tttagtgtat 120
tttaagggcc ataacgaagt ggatttaaac tttaacgcta tgcttaaaac ctatgaaaac 180
tttaaatcca attatcgttt tttggtgggt ttaaagcccc ttattaaaag ccctaaaacc 240
cccatttttgc cctatttttc taaaggcacg catggggata aaaaactcca agaaaacctt 300
ttaaacaacg ctttgatttt ggaaaaatcc aacacgcttt atgcgcaatt gcaaccgctc 360
aaacccgctt tagattcgcc aaacattcaa gtgtatttag cgttttatcc cagtccatca 420
cagcccagat ggttaggaac gcttgattgt aaaaacgcat gcgagccttt aaaatttgat 480
ttgttagaga gcgacaaaat ggggcgttat aagatccttt ttaaatttgt ttttaaaaat 540
aaagaagaat tgattttaga acaactggct tttttcaagc aacgcatt 588

Seq ID 17
atggcgtatt ttttagaaca aacggatagt gaaatttttg agcttatctt tgaagaatac 60
aagcggcaaa atgagcattt agaaatgata gcgagcgaga attacacttt tgcaagcgtt 120
atggaggcta tggggagtgt tttaacgaat aaatacgctg aaggctaccc taacaagcgc 180
tattatggag gctgtgaagt ggtggataaa atagaaagcc tagccataga aagggctaaa 240
aagcttttta attgccagtt cgctaacgtg caagcgcatt caggctcaca agccaataac 300
gctgtctatc acgctctttt aaagccttat gacaagattt taggcatgga tttaagctgt 360
ggagggcatt taacgcatgg cgctaaagtg agtttaaccg gcaagcatta tcagagcttt 420
tcttatggcg tgaatttgga tggctatatt gattatgaag aggcgctaaa aatcgctcaa 480
agcgttaagc cagaaatcat cgtgtgcggg ttttcagcct atccaaggga gattgatttt 540
aagaaattta gagaaatcgc tgatgaagtg ggggcgttac tattaggcga tatagcccat 600
gtggcagggc ttgtggtaac cggtgagcat gcccatcctt tcccgcattg ccatgtggtt 660
tcaagcacca ctcataagac cttaagaggg cctagagggg ggattatttt aactaatgat 720
gaagagatag cggctaagat tgacaaagcg atttttccag gaactcaagg cgggcctttg 780
atgcatgtga ttgctgctaa agcggtgggt tttaaagaga atctaaaacc agaatttaaa 840
gcttatgcac aattagtgaa atctaacatg caagttttgg ctaaagcgtt aaaagaaaaa 900
aaccataagt tagtgagtgg tggcacttct aaccatttgc ttttaatgga ttttttagat 960
aagccttata gcgggaaaga cgctgatatt gcattaggga atgccggaat caccgtgaat 1020
aaaaacacca ttcctggtga aacgcgcagc ccttttgtaa cgagcgggat aaggattggc 1080
tcagcggcat tgagcgcaag gggcatggga gctaaggaat ttgaaatcat agggaataaa 1140
atatcagata ttttgaatga tattaataat gttagtttgc aattgcatgt gaaagaagaa 1200
ttgaaagcca tggtcaatca attccctgtg taccaccaac ctattttt 1248

Seq ID 18
atgaaaataa catattgtga tgcgctaatt attggaggcg gactagctgg gttaagggct 60
agtatcgcat gcaaacaaaa gggtttaaac accatcgttt taagcctagt gcctgtcagg 120
cgttcgcact ctgcagccgc tcaagggggc atgcaagcga gccttgcgaa cgctaaaaaa 180
agcgagggcg ataatgaaga tttacacttt ttagacacgg ttaaggggag cgattggggg 240
tgcgatcagc aagtggctag gatgtttgta accactgctc ctaaagccat tagggaattg 300
gccagttggg gggtgccttg gactaggatt aaaaagggcg ataggcctgc ggtcgtcaat 360
ggtgagcatg taactatcac tgaaagagac gacaggcatg gttatatctt aagccgtgat 420
tttggcggca ctaaaaaatg gcgcacatgc tttacggctg atgccacagg gcataccatg 480
ctttatgcgg tcgctaatga agccttacac cacaaagtgg atattcaaga cagaaaggac 540
atgctcgctt tcattcatca tgataataaa tgctatgggg cggtggtaag ggatttgatc 600
acaggcgaaa tttcagcgta tgtttctaaa ggcacgcttt tagctaccgg aggttatggg 660
cgcgtgtata aacacaccac taacgctgtg atttgcgatg gagccggggc tgcaagcgcc 720
ttagaaaccg gcgtggctaa attgggcaac atggaagcgg tgcaattcca ccctaccgct 780
ttagtgccaa gcgggatttt aatgaccgaa ggttgcaggg gcgatggcgg tgttttaaga 840
gacaagtttg gcagacgctt catgcccgct tatgagccgg agaaaaaaga gcttgcaagc 900
agagatgtgg tctcaaggcg gattttagag catatccaaa aaggctatgg agccaaatcg 960
ccttatgggg atcatgtgtg gctggatatt gctattttag ggcgtaacca tgtggaaaaa 1020
aacttaaggg atgtgcgcga tatagccatg acttttgcgg gcattgatcc ggctgatagc 1080
aaggaacaaa ccaaagacaa catgcaagga gtgcccgcaa atgagcctga atacgggcaa 1140
gcgatggcca agcaaaaagg ctggatcccc ataaaaccca tgcaacacta ttctatgggt 1200
ggggttagga caaaccctaa aggcgaaacc catttaaaag gcttgttttg cgcgggtgaa 1260
gcggcatgct gggatttgca tgggtttaac cgcttggggg gtaattctgt gagtgaagcg 1320
gtggtcgctg gcatgatcat tggggattat tttgcctcgc attgtttaga agcgcaaatt 1380
gaaatcaaca cgcaaaaagt tgaagctttc attaaagaaa gccaagacta tatgcatttt 1440
ttattgcata atgaaggcaa agaagatgtg tatgaaatta gagagcgcat gaaagaagtc 1500
atggatgaaa aagtgggcgt ttttagagaa ggcaaaaggc tagaagaagc ccttaaagaa 1560
ttgcaagagc tttatgcacg ctccaaaaac atttgcgtga aaaacaaggt tttacacaat 1620
aaccctgaat tagaagacgc ttaccgcacc aaaaaaatgc tcaaactcgc gctttgtatc 1680
actcaaggag cgttactgcg cactgaaagc agaggggctc acacaaggat tgactaccct 1740
aaaagagacg atgaaaaatg gcttaatcgg actctagcga gctggcctag cgctgagcaa 1800

gacatgccca cgattgaata cgaagaatta gatgtgatga aaatggaaat cagccctgat 1860
tttaggggct atggcaaaaa gggtaatttc atcccccacc ccaaaaaaga agagcgcgac 1920
gctgagattt tgaaaacgat tttagaacta gaaaagcttg gaaaagacag aatagaagtc 1980
caacatgcgc tcatgccttt tgaattgcaa gaaaaataca aggctaggaa tatgcgttta 2040
gaagatgagg aagtcagggc taggggggaa catttgtatt ctttcaatgt ccatgagtta 2100
ttggaccaac acaacgctaa cctaaaagga gaacaccatg ag 2142

Seq ID 19
atgaaagata gttttctttt cacttctgaa tcagtaaccg aggggcatcc tgacaaaatg 60
gctgatcaaa tcagcgatgc ggttttagat tacattattg agcgggatca aaaagccaaa 120
gtcgcatgcg agactttagt ttctaacggg ttttgcatga tcactggcga gttaaaaact 180
tctgtttatg cccctatgca agagattgca agagaagtgg ttaaaaagat tggttatacg 240
gacgctcttt atggctttga ttacaggagc gcggcggttt tgaatggcgt tggcgagcaa 300
agccctgata ttaatcaagg cgtggataga gaagatggcg agattggggc aggggatcaa 360
gggcttatgt ttggttatgc atgcaaagag actgaaacgc tcatgccctt acccattcat 420
ttagcgcacc agctcacttt cgctctggct caaaaaagaa aagacaacac tctgcctttt 480
ttaaggcctg atggcaagtc tcaagtgagc gtgcgttatg aaaacaacaa gcctgtaagc 540
attgatacga ttgtcatttc cacccaacat tccccagaag tttcacaaaa acatttaaaa 600
gaagctgtga ttgaagagat cgtgtataag gttttatcca aagaatattt gcatgacaat 660
atcaagtttt ttgtcaatcc tacaggaaaa ttcgttatcg gtgggccgca aggcgatgcg 720
ggcttgacgg gcagaaaaat catcgtggat acttatgggg ggagttgccc gcatggcggg 780
ggagcgttta gcgggaaaga ccctagcaaa gtggatagga gcgcggctta tgcggcccgc 840
tatgtggcta aaaatttggt agcgagtggg gtttgcgata aagcgaccgt gcagcttgct 900
tatgcgattg gggtgataga gccagtgtct atttatgtga acacgcataa cacgagcaag 960
tattcaagcg ctgagttgga aaaatgcgtg aaatcggttt tcaaactcac gccaaaaggc 1020
attattgaaa gcttggattt attaagaccc atttattcgc tcacttcagc ttatgggcat 1080
tttgggcgcg aattagagga attcacttgg gaaaaaacca acaaagctga ggagattaaa 1140
gcgttcttta agcgt 1155

Seq ID 20
atgatgaaaa ttgtaataga cttaatgggg gctgaccatg gggttttacc cgttattgag 60
ggagtctcaa gggctttaga aaataagagt tttagcacgg ttttagtggg ggataaagac 120
aaagcaaccc cttttatttc taaagagtta gccagcaaag tggaaatgat ccacacgcaa 180
gattacatca agatggaaga agccgccact gaggcgatca agcgtaagga atcttccatt 240
tacttgggca tggatatttt aaaaaatggg gctgacgctt tgatttcagc ggggcatagc 300
ggagcgacta tgggtttagc caccttgcgt ttagggcgta tcaaggggt tgaaaggcct 360
gctatttgca ctttgatgcc tagcgttggc aaacgcccta gcgtgctgtt agacgcagga 420
gcgaacaccg attgcaagcc tgaatatttg attgattttg ctcttatggg gtatgaatac 480
gctaaaagcg tgttgcatta tgatagccct aaggtgggtc ttttgagtaa tggcgaagaa 540
gatattaaag ggaacatgct cgttaaagaa acgcataaaa tgctgaaagc ttatgacttc 600
ttttatggca atgtggaggg gagcgatatc ttcaaagggg ttgtggatgt ggtagtttgc 660
gatggcttta tggggaatgt ggtcttaaag acaacagaag gggtcgctag cgcaataggc 720
tctattttta aagatgaaat taaaagctct tttaaatcta aaatgggggc tttgatgctt 780
aagaatgcgt ttgatatttt aaaacaaaaa accgattacg ctgaatatgg gggagcgccg 840
cttttgggcg tgaataaaag cgtgatcatc agccatggca agagcaacgc tagagcgatt 900
gaatgcgcga tttatcaggc tattagcgct gttgaaagtc aggtttgttt gaggattact 960
caagcgtttg agagcttgaa gcctagcgtt tctcaaagtg atcagcaaga cgct 1014

Seq ID 21
atggaatttt acgcctctct taaatccatt gcgatgcatg ttccaagcga gcgtgtgaaa 60
aatgcagagt tccagcaatt tttggatacc agcgatgagt ggatagaaaa aaggaccggt 120
atcaaagaac gccgtttcgc taacgatgaa gaaaaaagca gcgatttagg ggtaatagcg 180
gctaaacaag ccatagagag agcgcattta accccaaaag acattgattt ggtggttgta 240
gcgactttaa gccctgattt tttggccatg ccttcaaccg cttgcgtgtt gagcgcgaaa 300
ttaggcattg aaaacaagcc ggcgtttgat atttcagccg cttgcacggg ttttatctat 360
ttattatcgg tggctaaggc ttatgttgag agcgggatgt atgaaaatgt gctgattgtg 420
ggggcagaaa aaacgagcag cgtgttagat tttaaagaca gggggacttg tattttattt 480
ggcgatgggg ctggggcgtg cgtgataggc agaaccaagc gtttaaaaga aagcatttta 540
gatgtgcaaa tttcagcgaa cgggaatttt tctaattatc tctatacgcc aaggactcta 600
aaacccacgc cctttaacgc taaagaagaa gcttcagagc ctttttgtgc tatgaaaggc 660
aatgaagtgt ttaaactagc ggtaaaaacg cttttaaaag atgtggaaat gatcttagaa 720
aaaaacgctc tcaaacctga agacgtgcgt ttgtttatcc cgcatcaagc taattttagg 780
atcattcaag cggtgcggga gcatttggat tttaaagatg agcaagtggt tttaaccgtg 840
cataaatacg gcaacacttc agcagccagt atccctatgg ctatgggtga agcttatgaa 900
gaggggcgtt tgaaaaaggg cgatttaatg cttttagacg cttttggtgg aggattgact 960
tggggttcag cgttggtgta ttttggagga agt 993

Seq ID 22

atgtctaatc aagaatacac ctttcaaact gaaatcaacc agcttttgga tttgatgatc 60
cactctttgt attctaataa agagattttt ttaagagagt tggtttctaa cgcgagcgac 120
gctttggaca agctgaatta tttaatgctg accgatgaga aattaaaagg gctgaatacc 180
acgcctagca ttcatttgag ttttgatagc cagaaaaaga ccttaacgat taaagataat 240
ggtataggca tggataaaaa cgatctcatt gagcatctag gcacgatcgc taaatcaggc 300
acgaagaatt ttttaagcgc tttgagtggg gataagaaaa aagatagcgc tttaattggc 360
cagtttggcg tgggctttta ttcagcgttt atggtagcga gtaagatcgt cgttcaaacc 420
aaaaaggtaa atagcgatca ggcttatgca tgggtgagcg atggtaaggg caagtttgaa 480
atcagcgagt gcgttaaaga tgagcaaggc acagaaatca ccctcttttt aaaagatgaa 540
gattctcatt ttgcgagccg ttgggagatt gatagcgttg ttaaaaagta ttctgagcat 600
atccctttcc ctatttttt aacttacacc gatacgaaac atgagggcga aggggataat 660
caaaaagaaa ttaaagaaga aaaatgcgaa cagatcaatc aagcgagcgc tttatggaaa 720
atgaataaga gcgaattaaa agacaaagat tacaaagagt tttaccaatc gtttgcgcat 780
gataacagcg aacctttgag ctatatccat aataaagtgg aaggctcttt agaatacaca 840
acgctttttt acatccctag cacagcgccc tttgacatgt ttagggtgga ttataaaagc 900
ggggtcaaac tttatgttaa aagggtgttt atcactgatg atgacaaaga attgttgccc 960
tcttatttga ggtttgttaa aggcgtgatt gacagcgaag atttaccctt gaacgtgagc 1020
cgtgaaatct tacagcaaaa caagatttta gccaatatcc gttcggcttc agtgaaaaag 1080
attttaagcg agattgaacg cttgagcaaa gatgaaaaaa attaccataa attctatgag 1140
cctttcggga aagtgttaaa agaaggcttg tatggggatt ttgaaaacaa agaaaaactt 1200
ttagaattgt taagattcta ttctaaagac aaagaaaaat taatttcttt gaaagaatac 1260
aaagaaaatt taaaagaaaa tcaaaaaagc atttactacc ttttaggcga aaatttagat 1320
ttattaaagg cgtccccgct tttagaaaaa tacgctcaaa aaggctatga tgttttgtta 1380
ttgagcgatg aaattgatgc gtttgtgatg ccaggcgtga atgaatacga taaaacgccc 1440
tttaaagacg ctagccatag cgagagtctg aaagagcttg gtttggaaga aatccatgat 1500
gaggtaaaag atcagtttaa agatttaatg aaagcgtttg aagaaaatct taaagatgag 1560
attaaaggtg tagagctttc cagtcatctc acttcagcgg tggctttaat aggcgatgaa 1620
caaaatgcga tgatggctaa ttggatgcgt caaatgggtc aaagcgtgcc tgaaagcaag 1680
aaaacgctag aattaaaccc taaccacgcg attttgcaaa aactcttaaa atgtgaagat 1740
aaagagcagt tgagcgcttt tatctggttg ctttatgatg gggcgaaact tttagaaaaa 1800
ggggctttaa aagacgctaa aagttttaac gaacgcctaa atagcgtgct attgaaagcg 1860
ttg 1863

Seq ID 23
atgctaggaa acgttaaaaa aacccttttt ggggtcttgt gtttgggcac gttgtgtttg 60
agagggttaa tggcagagcc agacgctaaa gagcttgtta atttaggcat agagagcgcg 120
aagaagcaag atttcgctca agctaaaacg cattttgaaa aagcttgtga gttaaaaaat 180
ggctttggat gtgtttttt aggggcgttc tatgaagaag ggaaaggagt gggaaaagac 240
ttgaaaaaag ccatccaatt ttacactaaa ggttgtgaat taaatgatgg ttatgggtgt 300
aacctgctag gaaatttata ctataacgga caaggcgtgt caaaagacgc taaaaaagcc 360
tcacaatact actctaaagc ttgcgactta aaccatgctg aagggtgtat ggtattagga 420
agcttacacc attatggcgt aggcacgcct aaggatttaa gaaaggctct tgatttgtat 480
gaaaaagctt gcgatttaaa agacagccca gggtgtatta atgcaggata tatatatagt 540
gtaacaaaga attttaagga ggctatcgtt cgttattcta aagcatgcga attaaaagat 600
ggtaggggt gttataattt aggggttatg caatacaacg ctcaaggtac agcaaaggac 660
gaaaagcaag cggtagaaaa ctttaaaaaa ggctgcaaat caagcgttaa agaagcatgc 720
gacgctctca aggaattaaa aatagaactt 750

Seq ID 24
atgagaaaga aaggcatgtt tgaaaagata caaaaagaat ggctgagcaa cattcaaaag 60
gatttgttgt ctggttttgt ggtggggctt tctgtgatcc cagagacggc cggctttgcg 120
atcatggtgg gtttagatgt gggcgtggcg ttttatacga ccttttacat ggcttttgtt 180
ttgtctcttt ttggggctag aaaggcgatg attagcgcag cggccggctc agtggcgctc 240
attttagtgg gcgtggttaa aaactatggg cttgaatacg cgggcgtggc gactcttatg 300
gcaggggtgt tgcaaattct tttaggctat ttgaaaatag ggaatctttt gaggtttatc 360
ccccaatcag tgatgtatgg ctttgtgaac gcgctaggca ttttgctttt aatggagcaa 420
ttcaaattcc ttcaaaacca aaatttgggg gtgtttgtct tgctcgctat tgggatactc 480
atcatttatc tttttcctct aatcactaaa aaaatccccc ctaatctgat ttgtatcctt 540
atagtgagcg cgatcgcttt aatttttgat atgcatgcgc cgaatttggg gagcattgag 600
caaggggttt caggctttca tttcatcatt atccccaaaa atttggattt taaaataatg 660
atagagttgt tgccttacgc tctttcttta gcactagtgg gaacgataga aagcttattg 720
acggctaaaa ctttagatgt gattttaaaa gacggcgtga gcgataaaaa taaagaaact 780
aaagcgcaag gcttggggaa tatcatctca gggcttttgg ggggaatgac agggtgcgct 840
ttagtggggc agtctatcat taacgcaaaa tccggggcta aaacaaggct ttctactttt 900
tttgccggct tttctttaat ggtgctcata ttagtgttta atgaatatgt ggttaagatc 960
cccattgtgg cggttgtggc ggtaatggtg atgatttctt tcaccacttt taatttccaa 1020
tccattatta acattaaaaa aatcaagctc tatgacacgc tcaacatgct cttagtcgtg 1080
gcggtggttt tatacacgca taatttagcg ataggggttg tggtgggggt tttagtcaat 1140

gcgttatgga tcaaatctaa agggattgca 1170

Seq ID 25

atgaaaaaaa cgattttact ttctcttatg gtttcatcgc tcctcgctga aaatgacggc 60
gtttttatga gcgtgggcta tcaaatcggc gaagcggttc aacaagtgaa aaacaccggc 120
gaaatccaaa aagtctccaa cgcttacgaa aatttgaaca atcttttaac ccgctataac 180
gaactcaaac aaacggcctc taacaccaat tcaagtaccg ctcaagcgat tgataatcta 240
aaagagagcg ctagccgatt gaaaacgacc cccaatagcg ctaatcaagc cgtgtcttca 300
gcgctcagct ctgcggtagc catgtggcaa gtaatagtct ctaatttagc caataactcg 360
ctacccacta gtgaatacaa caaaatcaat gcgatttctc aatcgctcca aaacacccta 420
gaaaatаaaa acaatgatct taaaattgaa aatgactacg accatctttt aactcaagct 480
agcaccatta ttaataccct tcaaagccaa tgcccaggca tagacggagg caatggcaaa 540
ccatggggca ttaatgcaag cgggaacgca tgcaatattt ttggcaacac ctttaacgcc 600
atcactagca tgatagatag cgctaaaaaa gccgccgcag atgcccgaag aactgcccca 660
gaaagtccaa accaaccaag tgcgtttaac aacgctgatt tcaataaaaa ccttaatcaa 720
gtctcaagcg ttattaatga cacgatctct tacctcaaag gggacaattt agcaaccatc 780
tacaacaccc ttcaaaaaac gcccgattct aaagggtttc aaagtttggt gagccgatct 840
agctatagtt attccctcaa cgaaacccaa tattctgaat tccaaactac caccaaagag 900
tttggccata acccttttag aagcgtgggt ttaatcaact ctcaaagcaa taacggagcg 960
atgaatggcg tgggcgtgca attaggctat aagcaattct ttgggaaaaa taaatttttt 1020
gggatccgtt attatgcctt ttttgattac aaccatgcct atatcaaatc caacttttтc 1080
aactccgctt ccaatgtttt cacttatggc gcaggcagtg atcttttatt gaatttcatc 1140
aatggcggat ccgataaaaa ccgcaaagtc tcttttggca tttttggagg catcgctcta 1200
gcaggcacga catggcttaa ttcccaattt atgaatttaa aaaccaccaa tagcgcctac 1260
agcgctaaga tcaacaacac caatttccaa ttcttattca atactggttt aaggcttcaa 1320
gggattcacc atggcgttga attaggcgtg aaaatcccca ccatcaacac gaattactat 1380
tctttcatgg gcgctaaatt agcataccga agactttata gcgtgtattt caattatgtt 1440
ttggcctat 1449

Seq ID 26

atgggtgtca aatttttaaa aatattagtt tgtgggttat ttttttggag cttgaacgcc 60
catttatggg gaaaacaaga caatagtttt ttgggggttg ctgaaaaagc ctataaaagc 120
gggaattatt ctaaagccac atcttatttt aaaaaagcat gcaacgatgg ggtgagtgaa 180
ggttgcacgc aattaggaat catttatgaa aacgggcaag gcactagaat agattataaa 240
aaagccctag aatattataa aaccgcatgc caggctgatg atagggaagg gtgttttggt 300
ttaggggggc tttatgatga ggggttaggc acgactcaaa attatcaaga agccattgac 360
gcttatgcta aggcgtgcgt tttaaaacac cctgagagtt gctacaattt aggcattatt 420
tatgaccgaa aaatcaaagg caatgccgat caagcggtta cctactacca aaaaagctgt 480
aattttgata tggctaaggg gtgttatgtt ttgggcgtgg cttatgaaaa aggcttttta 540
gaagtcaaac aaagcaacca taaagccgtc atctattatt tgaaagcatg ccgattggat 600
gatgggcagg cttgtcgcgc gttagggagt ttgtttgaaa atggcgatgc agggcttgat 660
gaagattttg aagtggcgtt tgattacttg caaaaagctt gcgggttaaa caattctggt 720
ggttgcgcga gtttaggctc tatgtatatg ttaggcaggt atgtcaaaaa agatccccaa 780
aaggctttta atttttтcaa acaagcatgc gatatgggga gtgcggtgag ttgctctagg 840
atgggcttta tgtattccca aggggacgct gttccaaaag acttgaggaa agcccttgat 900
aattatgaaa ggggttgcga tatgggcgat gaagtgggtt gcttcgctct agcgggcatg 960
tattacaaca tgaaagacaa agaaaacgcc ataatgattt atgacaaggg ctgtaagcta 1020
ggcatgaaac aagcatgcga aaacctcact aaacttaggg ggtat 1065

Seq ID 27

atggagttag aaactcattt gtcaaaatat ttcaccctag cctttacgca taaaagcatg 60
agcttagaaa tgcgagaaaa actcgctatt aattcgaatg caacgcttaa agaattttta 120
caaaccatta aaaaccattg ccctaacatc aaagagtgca tggtgttatc cacatgcaat 180
cgctttgaaa tctatgcgag cctaaaacac ggcgctaata ctaatgaaca aaaaaacgca 240
ctattaaaga ttttggctca aaataaaaaa atgagcgtgt ctgatttaga aaaatgcgtt 300
ttaatgaaca ctgatgaaag cgcagtccat catgtcttta gcgtgtgcag cagtttggat 360
agcttggtgg ttggggaaac tcaaatcaca gggcagatga aaaacgctta taaattcgct 420
tttgaagaga aattttgctc taaagattta acccgattgc tccattttgc tttcaaatgc 480
gccgctaaag tgcgcaattt aaccggcatt tccaagcaag gggtttccat ctcttcagtg 540
gcggtcaaag aagcgcttaa tatttttgaa aaagaaagga ttaaggataa aaaagccctt 600
gtgatagggc ttggcgagat ggctcaatta gtcatcaagc acctttтaaa caagcaattt 660
gaagcgctta tcttagggcg taatgcggct aaatttgaag atttcatcaa agaattagaa 720
gaacctaaaa aagtaagctt tcaaaatata gaaaatttaa acgcttatat caatgaatac 780
gaactgcttt tttgcgccac ttcttcgccg cattttatcg tgcaaaatcg catgttaaaa 840
gaaacgattt tcaggcgttt ttggtttgat ttagccgtgc cacggaatat tgaaaagccg 900
gtattggata atatttтctt atacagcgtt gatgatttag agcctatggt gagagaaaat 960
gtggaaaaca ggcaagagag cagaatgaga gcttatgaga ttgtagggct tgccacaatg 1020
gagttttacc aatggattca aagtttagaa gtagagcctg tgattaagga tttaagggaa 1080

ttggctagga tttcagccca aaaagaattg caaaaagcgc ttaaaaaacg ctatgtgcct 1140
aaagaatacg aaaacaacat tgaaaagatc ttgcacaacg ctttcaacac ttttttgcat 1200
aaccctacca tcgccttaaa aaagaacgct caaaaagaag aatccgatgt gcttgtgggt 1260
gcgattaaaa acttgtttaa tttagacaaa tctaacgcta accatgccca gaatttgaat 1320
ctctataaat gcgaatatta cgaggaa 1347

Seq ID 28
atgttcattg tagcggtttt gatgctggcg tttttaatct ttgtccatga attagggcat 60
ttcactatcg ctaggatttg tggggtgaag gtagaagtct ttagcattgg ttttggtaaa 120
aaactctgtt tttttaagct ttttggcacg caattcgctt tgtctttgat cccgcttggg 180
ggctatgtga aattaaaggg catggataaa gaagaaaatg ggatgaatga aaccacggat 240
gacagctatg cgcaaaaaag ccctttttcaa aagctatgga tactatttgg gggggcgttt 300
tttaattttc tttttgcgat tttagtgtat tttttttctgg cattgggtgg ggaaaaagtc 360
ttactgcccg tcattggcga tttagacaaa aacgcgctag aagctgggct attaaagggg 420
gataaaatcc tttctatcaa ccataaaaaa atagcgagtt ttagagagat tagaagcgta 480
gtggcgcgtg ctagaggcga gttggtttta gaaatagagc gaaaccatca ggttttagaa 540
aaacgactga cccccaaaat cgtagcggta ataagcgatt ctaatgatcc taatgaaatg 600
atccggtata aagcgatagg catcaagcca gacatgcaaa aaatgggcgt tgtttcttat 660
tctttgtttc aagcgtttga aaaggccttg agtcggttta aagagggcgt tgttttgatc 720
gtggattctt taaggcgttt gattatggga agctcttcag ttaaggaatt gagcggggtg 780
gtaggcattg tgggagcgtt aagccatgcc aatagtttga gcatgctttt gttgtttggg 840
gcgtttttgt ccatcaattt agggatttta aacttactac ccattccagc cttagatggg 900
gcgcaaatgc taggggttgt ttttaaaaat atttttcata tcactttgcc aacacccata 960
caaaatgcgt tgtggctagc gggggtgggg tttttggttt ttatcatgtt tttagggctt 1020
ttcaatgatc tcactcgttt gcta 1044

Seq ID 29
atgctgttaa aaaacgcttc gttttatgat gatgaagttt taaaaagagc ggatatccgc 60
ttaaaagatt ccctcattac agagattaaa gaaaacttaa gccctattaa taatgaagaa 120
gtgattgagt gcagggattt attcgtgctg ccaagcttca ttgatttgag cgttactggt 180
ttggagggtt atgaaaattt aaaacaaaag gcttttaaag ggggggtagg gttactcaat 240
gtttttaatt gcgatcaaag cggcattaaa aacatcatgg caattaaaaa caaccaacta 300
gctgacatcg ccacgcttaa aaataaaggg ggggaaattt taatcgcgcc atctgacgct 360
tttttagaac tcattagcca ctacgccaaa tcctacaact tgcctctttt aatctcttta 420
gaaaattctt ttgaagccct aaatagtggg gaattagcct atgaattggg gcaaaatttt 480
gtggaaaatg cgtttgaaaa cacgcgcttg gtgcgtttca tggaagtttc tagagcgtta 540
caaatccctg tgcttttaga taaagtgaat agtatcacca cgctcaaact catcaaagcc 600
tttaatgatt taggggcgaa attacaagcc caaacgccct taagccattt agttttagat 660
gagagcgtgt atgaagatta tgagccacga tttaaaatcg ctcctccttt aagggataaa 720
gaaagccaaa acgccctaaa agaagcccta aaaaataacg aaatcgccat gctcacaagc 780
cttcatgctt ctaaaaattc taacgcacag ctttttgaag aaagcgcttt tgggtgtgag 840
agcatagagg acgcttttag cgtggcttat acttttttag ttcaaaaaaa ggttatcagc 900
ttccaacaac tcattaaagt catggcgatt aaccaagcga agtttttaaa actcaatgca 960
ggcgaggtta aagaaaacca attagccaat ttgatgatcg tggatttaaa cgctcaaaca 1020
agagtgagta atcaaaattc gccctttttat ggtttggaat tgtatggcga agtgcaaaga 1080
atgatcttaa aagggcaaac cacatttatt aaggagaatg catgcaagaa atca 1134

Seq ID 30
ttgaaaatag cgattgtcag gctttcagcg cttggggata ttatcgtgag cgcggtgttt 60
ttggcggtga ttaaagagtg tctgcctaac gcccaaatag aatggttcgt ggatgaaaga 120
tttagtgcga ttttagagca ttccccctat attgataaat tacaccccat cgctttaaaa 180
agtgcactca aaaccttgaa tcctttgaag attttcaaac tttttaaatc tttaagggct 240
tatgaatacg atataatcat tgacatgcaa ggcctagtca aatccgctct catcacgcaa 300
atgttgaaag cccctaaaaa agtcggcttt gattacgctt cggctagaga gggtttgagc 360
atgttttttt actcgcaaaa agtttctatc gcttatgatg agcctgtttt aaagcgcaat 420
ttcacgctcc tttctcatgc cctaaacttg ccccaaaaag aaatttcaaa agaaatttca 480
gagagcttaa gctctagggc taaagcgttt tcttaccagc cttctccaaa aattgatgcg 540
ttaaatttga ataagaataa gccaaaaatc ctttttattt tagaaacttc taaaatcaat 600
aaaacttacc ccatagagcg ttttaaagaa ttagcgttaa ttttagaaaa ttttcaaatt 660
tgcttgttat ggcatgctga tgaatataaa gccactacgc tttatcacgc tttaaaacac 720
caacgcgatg tgttattgct ccccaaactc actttaaacg aggttaaggc gttgctcttt 780
aaaatggatt tgattattgg gggcgatacg ggcatcacgc atttagcatg ggcgttgcaa 840
aaacccagca tcacccttta tggcaacacg cccatggagc gttttaaatt agaaagcccg 900
atcaatgttt cgctcaccgg taattcaaac gccaactacc ataaaaagga tttttctatc 960
caaaatatag agcctaaaaa aattaaagaa tgcgttttaa acatcttaaa ggaaaaagaa 1020

Seq ID 31
atgaaaaagt ttaaaaagaa accaaaaagt atcaaacgat cgcatcaaaa tcaaaaaaca 60

atcttaaagc gtcctttatg gcttatgcct ttactcatca gcgggtttgc tagtggggtg 120
tatgcgaata atctgtggga tttgttaaac ccaaaagtgg ggggtgagta tgtgcattgg 180
gttaagggca gtcagtattg tgcatggtgg gaatttgctg ggtgtttaaa gaatgtatgg 240
ggggcaaatc ataaaggcta tgatgctgga aacgccgcta actatttgtc ttctcaaaac 300
tatcaagcta tttcggtggg tagtgggaat gaaacgggga cttatagttt aagcggtttt 360
accaattatg ttgggggcaa tctcacgatc aatctaggca atagcgttgt tttagattta 420
agcggttcta atagtttcac ttcgtatcaa ggttataatc aaggcaaaga tgatgtaaca 480
tttacggttg gcgcaatcaa tttaaacggc actttagaag tgggtaatcg tgtgggatcg 540
ggagctggca cgcacaccgg cacagccact ttaaacttga acgctaataa ggtcaatatc 600
aattccaata tcaacgcgta taaaacttcg caagtgaata taggcaacgc taacagcgtt 660
attaccattg gttcggtttc tttgagtggg gatgtttgca gttctttagc tagcgttggg 720
ataggggcta attgctccac ttctgggcct agctattctt ttaaagggac gactaacgct 780
actaacacgg cgtttagtaa tgcaagcggc agtttcactt ttgaagagaa cgccactttt 840
agcggggcga aatggaatgg ggggacttat acctttaata aagagtttag cgctaccaat 900
aacaccgcct ttagtagcgg tagttttaat tttaaaggtg taagctcttt taatggtact 960
tcgtttagta acgcttctta tacttttgac aatcaagcca ctttccaaaa cagctccttt 1020
aatgggggga cttttacttt taataaccaa actaatccaa ctaacaacgc tcagcacccc 1080
caaattcaaa acagctcttt tagtggtaac gctaccactc ttaagggctt tgtgaatttc 1140
cagcaagcct ttaacaattc aaaccaccaa ctaacgatcc aaaacgcttc ctttaataac 1200
gccacttta acaataccgg taaaatcact atagaaaaag atgcgagttt taataacacg 1260
acattcaaca cttctgttga tacaaacaac atgagtgtta ccggtggcgt tactttaagc 1320
ggtaaaaatg acttgaaaaa tggctcaacc cttgattttg ggagttctaa aatcactctc 1380
gctcaaggga cgactttcaa cctcacaagt ttaggcagtg agaagagcgt aacgatttta 1440
aattctagcg gtgggatcac ttatagtaac cttttaaacc atgcaatcaa cggcttgaca 1500
agtgccttaa aaacgaacga aagcctttca aatccgcaaa gtttcgctca aggtttgtgg 1560
gatataatca cttacaatgg ggttaccggg cagcttttga atgaaaacgc tgcaacatct 1620
aaacccactg actcttcgcc ctctaaatcc tctacaaact ctacgcaagt ctatcaagtg 1680
ggttacaaaa taggggatac tatctacaaa ctgcaagaaa ctttcagcca caattccatt 1740
attattcagg ctttagagag cgggacttac acgccacccc ctgtcattaa cggctccaaa 1800
tttgacttat ccgcttcaaa ttatatcaat gctgacatgc cttggtatga ccataaatat 1860
tacatcccta aatcccaaaa ttttacagag agcgggactt attacttgcc gagcgtccaa 1920
atatggggga gctacactaa ctcgtttaaa caaactttta gcgcaaatgg tagtaatctg 1980
gtgattgggt ataactcaac atggactgat cataatgtct cttctagcgg cacggtgtct 2040
tttggggaca cttcagggag cgctcttaat gggcattgcg gaccttggcc gtattaccaa 2100
tgcacaggca cgactaacgg cacttatagc gcctatcatg tgtatatcac agcgaatctg 2160
cgttctggca atcgtatagg caccggtggg gcagctaatc taatctttaa tggggtagat 2220
agtatcaata tcgctaacgc taccatcacg caacataacg ccggaatcta ttcaagctct 2280
atgacttttt ccacgcaaag catggataat tcgcagaatt tgaatggtct aaattctaac 2340
ggcaaacttt cggtgtatgg caccactttc actaacgaag ctaaagatgg gaaattcatt 2400
ttcaatgcag ggcaagcggt ttttgaaaac accaacttta atggagggag ttaccaattc 2460
agcggcgata gcttgaattt ttcaaacaac aaccagttca atagcggttc gtttgaaatt 2520
agcgcaaaaa acgcttcgtt caataacgct aactttaaca acagcgcttc ttttaatttc 2580
aataattcta acgcgaccac ttcgtttgtg ggggatttca ctaacgctaa ttcaaatttg 2640
caaatcgccg ggaacgctgt ttttgggaac tctactaatg gctctcaaaa taccgctaat 2700
tttaataata ccggctctgt taatatttca gggaatgcaa cctttgataa tgtggtgttt 2760
aatggcccta cgaacacgag cgtgaaaggg caggttactt taaataacat cactttaaaa 2820
aacctgaacg ccccttttgtc ttttggcgat gggacgatta cttttaacgc tcattcggtg 2880
attaatattg ctgaatctat cactaatggc aaccctatca ctcttgtaag ctcttctaaa 2940
gaaattgaat acaacaacgc tttcagtaaa aatctatggc agctcatcaa ctaccaaggg 3000
catggggcaa gcagtgaaaa gctcgtctct agcgcgggta atggcgttta tgatgtggtg 3060
tattctttca ataaccaaac ctacaatttc caagaggttt tttcacaaaa cagcatttct 3120
atccggcgtt tgggcgttaa catggtgttt gattatgtgg atatggaaaa atcggatcat 3180
ttatattatc aaaacgctct cggttttatg acctacatgc ctaatagcta taacaataat 3240
ttagggaatg caaacaacac catttactat tacgacaaga gcattgattt ttatgcgagc 3300
gggaaaactc tattcactaa agcggaattt tctcaaacat tcaccgggca aaacagcgcg 3360
atcgtttttg gggctaaaag catatggacg agcttaagcg atgcaccgca gtctaacacc 3420
atcattcgct ttggggacaa taagggagca gggagtaatg atgcgagcgg gcattgctgg 3480
aatttgcaat gcataggctt tattacaggg cattatgaag cgcaaaagat ttacatcacc 3540
ggtagcattg aaagcgggaa tcgcatttct agcggtgggg gcgcgagcct taattttaac 3600
gggcttcaag gcattctttt aacgaacgcg actttgtata accgcgccgc tggcacgcaa 3660
agctcgtcta tgaattttat ctctaacagc gcgaacattc aggctcaaaa ctcctatttt 3720
atagacgata ccgcacaaaa tggcggtaac cctaatttca gtttcaacgc tttgaatctg 3780
gatttttcta acagctcttt tagaggctat gtggggaaaa cgcaatctgt ttttaaattc 3840
aatgccaaga atgcgatcag tttcaccaac agcacgaatt taagctctgg tttgtatcaa 3900
atgcaagcta aaagcgtgtt gtttgacaat tccaatttaa gcgtttcagt ggggacaagc 3960
agtattaaag ccaatgcgat caatctttct caaaatgcct ctattaatgc gagcaaccat 4020
tcaaccttag aacttcaagg cgatttgaat gtgaacgaca ccagctcgct caacctcaac 4080
caaagcacga ttaatgtttc caataacgcc acgatcaacg attatgcgag cttgattgcg 4140

agtaatggct ctcaccttaa ttttaacggg gcggttaatt tcaattcagc gaatattact 4200
acgagtttga ataattcctc tatcgtgttt aaggggcgg tctctttagg agggcagttt 4260
aatttaagca ataactcttc tttagatttc caaggctcta gcgctatcac ctctaacacg 4320
gcgtttaatt tctatgataa cgcttttttct caaagcccca tcactttcca tcaagccctt 4380
gacattaaag cgcccttaag tttgggaggc aacctttaa accctaacaa cagcagcgtg 4440
ctggatttaa aaaacagcca gcttgttttt ggcgatcaag ggagtttgaa tatcgctaac 4500
attgatttac taagcgatct aaatgataat aaaaatcgtg tgtataacat cattcaagcg 4560
gacatgaata gtaattggta tgagcgtatc agcttctttg gcatgcacat caatgacggg 4620
atttatgatg ctaaaaacca aacttatagt ttcactaacc cccttaataa cgccctaaaa 4680
atcaccgaga gctttaaaga caaccaacta agcgttacgc tctctcaaat cccgggtatt 4740
aaaaacacgc tctataacat tggctctgaa atttttaact accaaaaagt ttataacaac 4800
gctaatggcg tgtattctta tagcgatgat gcacaaggcg tgttttatct cacaagcaac 4860
gtgaaaggct attacaaccc taaccaatcc tatcaagcca gcggcagtaa caacaccacg 4920
aaaaataata atctaacctc tgaatcttct atcatctcgc aaacctataa cgcgcaaggc 4980
aaccctatta gcgcgttgca catctataac aagggctata atttcaacaa tatcaaagcg 5040
ttagggcaaa tggctctcaa actctaccct gaaatcaaaa aggtattagg gaatgatttt 5100
tcgccctcaa gtttgaacgc tttaaactct aatgcgctaa accaacttac caaactcatc 5160
acgcctaacg actggaaaaa cattaacgag ttgattgata acgcaaacaa ttcggtggtg 5220
caaaatttca ataacggcac tttgattgtg ggagcgactc aaatagggca aacagacacc 5280
aatagcgcgg ttgtttttgg gggcttgggc tatcaaacac cttgtgatta tactgatatt 5340
gtgtgccaaa aatttagagg cacttattta ggacagcttt tagagtccag ctcggctgat 5400
ttgggctata ttgacacgac ttttaacgct aaagaaattt atcttaccgg cactttaggg 5460
agcgggaacg catgggggac tgggggggagc gcgagcgtaa cttttaacag ccaaacttcg 5520
ctcattctca atcaggctaa tatcgtaagc tcgcaaaccg atgggatctt tagcatgctg 5580
ggtcaagagg gtattaataa ggttttcaat caagccgggc tcgctaatat tttgggcgaa 5640
gtggcggtgc aatccatcaa caaagccggg ggattaggga atttgatagt aaatacgcta 5700
gggagtaata gcgtgattgg ggggtattta acgcctgaac aaaaaaatca aaccctaagc 5760
cagcttttag ggcagaataa ctttgataat ctcatgaacg atagcggttt gaatacggcg 5820
attaaggatt tgatcagaca aaaattaggc ttttggaccg ggctagtggg gggattagcc 5880
ggactagggg gcattgattt gcaaaaccct gaaaagctta taggcagcat gtcaatcaat 5940
gatttattga gtaaaaaagg gttgttcaat cagatcaccg gctttatttc cgctaacgat 6000
atagggcaag tcataagcgt aatgttgcaa gatattgtca aaccgagcaa cgctttaaaa 6060
aacgatgtag cggctttagg caagcaaatg attggcgaat ttttaggcca agacacgctc 6120
aattctttag aaagcttgtt gcaaaaccag cagattaaaa gcgttttaga caaagtccta 6180
gcggctaaag gtttagggcc tatttatgaa caaggcttgg gggatttgat acctaatctt 6240
ggtaaaaaag ggcttttcgc tccttatggc ttgagtcaag tgtggcaaaa aggggatttt 6300
agtttcaacg cacaaggcaa tgtttttgtg caaaattcca ctttctctaa cgccaatgga 6360
ggcacgctct cttttaacgc aggaaattcg ctcatttttg ccggaaacaa tcatattgca 6420
ttcactaacc acgctggaac tcttcaatta ttgtccgatc aagtttctaa cattaacatc 6480
accacgctta acgctagcaa cggccttaag attaacgccg ctaataacaa tgtttctgtg 6540
tctcaaggca atctgtttgt cagcgctagc tgcgcgcaac aaagcgatcc aactacagct 6600
aatattgcaa acccttgcgc gcttagcgcc caaagcacga atggcgcttc ttctaataat 6660
gcgtcaaata acgcgccaat cgccttgagt aataacgatg aaagcttgat ggttgcggcg 6720
aatgatttca atttttcagg caatatttac gctaatgggg tggttgattt ttcaaagatt 6780
aaaggctctg caaacattaa aaacctgtat ctttacaata acgctcaatt ccaagccaac 6840
aatctcacta tttccaatca agcggtgtta gaaaaaaacg ccagctttgt aacgaataat 6900
ttaaacattc aaggagcgtt taacaacaac gccacgcaaa aaatagaggt gcttcaaaat 6960
ttagtgatcg cttcaaacgc ttctttaagc accgggattt atgggttaga agtaggggggg 7020
gctttgaata attctggagc gatccatttt aatttagaaa atacccaaac gccaacgccg 7080
ctcattcaag cagaggggat cattaacctc aacaccaccc aaacgccttt tatgaatgtc 7140
aataacagca tggccaataa tacgacttac actttattaa aaagcagccg ttacattgat 7200
tacaatatca accccaacag cttgcaatcg tatttgaatc tctacacttt aatcaatatc 7260
aacgggaacc acatagagga aaaaaacggc gcattgactt atttgggcca acgggttttg 7320
ttgcaagata aggggttatt gttaagcgta gcgctgccca actcaaacaa cgcttctcaa 7380
aacaacattt taagcctttc tgtcctttat aaccaagtta aaatgtcttg cggcgataaa 7440
gcgatggatt ttaccccccc taccttacaa gattacattg tgggcattca agggcaaagc 7500
gcgctcaatc aaattgaagc tgttgggggg aacgctatca agtggctttc aacattgatg 7560
atggagacta aagaaaaccc gtttttgcg ccgatttatt taaaaaacca ctctttgaat 7620
gaaatcttag gcgtaacaaa agatcttcaa aacaccgcaa gcttgatttc taaccctaat 7680
tttagagata acgctaccaa tcttttagaa ttggcgagtt acacccaaca aaccagccgt 7740
ttaacaaaac tctctgattt tagatctaga gagggagagt ctgatttttc tttgttagag 7800
cttaaaaaca agcgttttag cgatcctaat ccagaggttt ttgtcaaata ctctcaactt 7860
agcaaacacc caaataacct ttgggttcaa ggggtgggag gagcgagctt tatttctggg 7920
ggcaatggca cgctttatgg cttgaatgcg ggctatgaca ggttggttaa aaatgtgatc 7980
cttgggggtt atgtggctta tggctatagc gactttaatg ggaacatcat gcattctttg 8040
ggtaataatg tggatgtggg gatgtatgcg agggcttttt taaaaaggaa cgaattcact 8100
ttgagcgcga atgaaactta tggaggcaat gcaactagta tcaattcttc taattctttg 8160
ctctctgtgt tgaaccaacg ctacaactac aacacctgga caacgagcgt gaacgggaat 8220

tacggctatg atttcatgtt caaacaaaaa agcgtggtgc taaaacctca agtgggtttg 8280
agctatcatt tcataggtct aagtgggatg aaaggcaatg atgccgctta caaacaattc 8340
ctcatgcatt caaacccctc taacgaatcg gttttaacgc tcaacatggg gttggagagc 8400
cgtaaatatt ttggtaaaaa ttcctattat tttgtaacgg cgagactagg tagggatctt 8460
ttgatcaaat ctaaaggcag caatacggtg cgttttgtgg gcgaaaacac tttattgtat 8520
cgcaaggggg aagtttttaa cacttttgcg agcgtgatta caggggggcga aatgcatttg 8580
tggcgtttgg tgtatgtgaa tgcgggggtg gggcttaaga tgggcttgca ataccaagat 8640
attaatataa ccgggaatgt gggcatgcga gtggcgttt 8679

Seq ID 32
atgtttgaaa aaattaccct agcgcataag gacttgtttt caaggttttt aagcgctcaa 60
aaaatcgttt tatcagatgt gagttttacg aattgctttt tatggcagca cgcaaggctc 120
attcaagtgg cggtgattag ggattgtttg gtgattcaaa ccacttatga aaatcaaaaa 180
ccctttttatt tctatcctat cggtaagaat gcgtttgaat gcgtaaaaga gcttttgaaa 240
ttagaaaaaa atttaagatt ccactccctg actttagagc aaaaagacga tttgaaagac 300
aattttgtag gggtgtttga tttcacttac aaccgagaca ggagcgatta cgtttattct 360
attgaagaat tgatcgcttt aaaagggaaa aaataccata agaaaaaaaa ccacctaaac 420
cagtttttaa ccaatcatgc gaattttgtt tatgaaaaaa tttctcctca aaataaaaag 480
gaagttttag aagcttctca agcgtggttt ttagaaagcc aaaccgatga tatagggcta 540
atcaatgaaa ataagggcat tcaaagcgtg ttagaaaatt atgaaagctt ggatgtaaag 600
gggggggctta ttagggttaa tggggaaata gcctcgttta gttttggaga agttttaaac 660
gaagagagcg cgctcatcca cattgaaaaa gcccgcacag atattgcagg cgcgtatcag 720
atcatcaacc agcagttgct tttgaatgaa tttagtcatt taacttacgc taacagagaa 780
gaagatctag gattagaggg tttaagaagg tctaaaatga gctataaccc ggtgtttttg 840
atagacaaat acgaagccgt tgctaaaaat 870

Seq ID 33
atgcgcgtta cctttggctc aaaatacaac caaatgaata actaccaaaa cgctttacaa 60
aataaaatca acgacgctaa cacgcagatc gcttcagggc taaaaatccg ttatggttat 120
caaaacagcg acattaacaa ccagaattta aaattccaat acgaagaaaa caccttagat 180
caaggcattg atgtggcgca aaacgcttac acttcaacgc tcaataccga caaagccttg 240
caagaatttt ctaaaacgat ggaggcgttt aaaaccaaac tcatccaatc cgctaacgat 300
gtgcattcag aaacttctcg cgccgctatc gctaacgatt tagaacgctt aaaagagcat 360
atgataaatg tcgctaacac ttctataggg ggggaatttt tatttggggg cagtaaggtg 420
gatagacccc ccattgatag taatgggaaa taccatggca atggcgaaga tttaaacgtg 480
cttattagct ctgataacct tgtgccttat aatatcagcg ggcaagattt gtttttaggc 540
accgataaag acaaacacaa actcattacc accaacatta aattattcaa tcaaaacaag 600
ctccaccctg atgtgatgga cgctttagag cattcttcat tgcctgagga agtttttatt 660
aaacccagcg ataccttgcg agaactcatc ggcgataacg ataaagaccc caccaatgac 720
cctaaagagt ttttttattt gcaaggcgtt aggcctgatg gctccagttt taaagaaaaa 780
ttcgcgttgg ataaagccta tcaaaaccaa gagagtgcct ctaaagtgag cgatttgttg 840
gataaaatcg ctcacgctta cgggaacact tcgcaaaata aagtcgtgga tgtgagtttg 900
aacaattggg ggcaaattga gatcaaaaac ctaacccccg gcagtgaaaa tttggatttt 960
catttgattt ctagcgatgg ggattttgac gatttagacg ccttgcgttc gagcggtaaa 1020
agggttactg aatacatcaa aagtgcgttt gtaacggata ggagtttgag ccaagttaaa 1080
gcggtgccta acatgtataa tcccaaggtg cttgaagtcc ctagcgtgtt tgtcactaaa 1140
gacaatgttt tagccaacaa aaacactaaa ttgagcgaga tttttggcga tagcgtggaa 1200
actttaaaaa tcaatgccag ccgtttggac gaaacaagcg ctattaaaat cccaaacctc 1260
cctgtttatt tggacattcc cattctttta gacgtgaaaa attctacgat taaagatttg 1320
aaagacgcga tcaaaaaacg cttcaataat gaagtggatg tggaaattga aacaaacggg 1380
cgtttgagga ttattgacaa ttcttctaaa gaatcgccta tttctttggc tttaagcgcc 1440
ctagatgcta aaggactaga agtggccggt atccctacta ataacgcgag cgaataccaa 1500
aaaacctact tcaataaaga aggggcaaaa ttagaaagca atgtcgctca aaccgctcaa 1560
aatggcgcag ctaatggctc tactaaactg agtgaagccg ctaaggggag tttagaaaat 1620
agcgttttta acatgaaatt aaacgatgtg aatggcttat ttttggaagc gcaaatgaac 1680
ttggataata atggggcttt tttgagcctc cctaatggca ttaaaatccc gctttatgac 1740
cccacaagcg ctgatattca agcgtctaaa cccaatgaag tcacttacag gcaacttatg 1800
gatgcgatga gtatcgcgct caattacagc aatactgacc cagccatcta ccaacaaatc 1860
agcgataacc ccacttccaa agaaagcaag gagcgcttta ttggattgtt aaaacaagct 1920
aaagacaacc tttctgttaa tttgaatgaa gagggaaaag tcattatcca agataacatg 1980
cattccaaca ccaaaatgca gttcatgctt tttgataaag acgcgaatga tttttctcaa 2040
aacgccttgc acagcgacaa accaagcctt aaattaaacg ctaataacgc tctcattatt 2100
gacaagccca gcgtgaattt ttttgatcaa ttagaaaata ccatcacttc tgtaagaaaa 2160
gggatttatc gcccggacgc tttaggggat acttattcta gcgatatgcg taatttaggc 2220
attcaaaacg gcatcaccct tatagatcac ttgagcgatc acatagaaaa aatgatcgct 2280
aaaaacggtg ctcatggcaa ggcgtttgag aacattatca ggcgtaatga agttttaaaa 2340
acgcaagttc aaagcattcg tggggaaacg accggcacgg atatggcaga aacttacaac 2400
aaattttcca atctcactaa caactataac gctgttttgg cttccacgaa caaaatcaat 2460

aatttgtctt taacgaaata cttg 2484

Seq ID 34

atggatagag ccaaatttat attcgttaca gggggtgtgt taagctctct agggaaaggg 60
atttcatctt cttcaatcgc tacgctttta cagcattgca attaccaggt ttctattttg 120
aagatcgacc cttatatcaa tattgatcca ggcaccatga gccctttaga gcatggggaa 180
gtgtttgtaa ctagcgatgg cgctgaaacg gatttagaca tagggcatta tgaacgcttt 240
ttgaacagga atttaacgag gttgaataat ttcactactg ggcagatttt ttcaagcgtg 300
atagaaaatg aaaggaaagg ggaatattta ggcaaaacca ttcaaatcgt cccccatgta 360
accgatgaaa tcaaaaggcg cattaaaagc gcggctaagg ggttggattt tttaatcgtg 420
gaagtgggcg gaaccgtggg cgatatggag ggcatgtttt atttggaagc gatccgccag 480
cttaaattgg aattagggaa tgaaaaagtc atcaatgtgc atgtaaccct gatcccctat 540
atccaaacca ctaacgaact aaaaaccaaa cccacgcaac attccgtcca agaattaaga 600
cgccttggcg taacccctca aatcattttg gcgcgatcgc ctaagccttt ggataaagag 660
ttgaaaaata aaatcgcttt gagttgcgat gtggagcaag acagcgtgat tgtcgccaca 720
gacactaaaa gcatttacgc atgccctatt cttttcttgc aagaaggcat tttaaccccc 780
attgccagac gctttaattt gaataaacta caccccaaaa tggcggcttg gaacacttta 840
gtagaaaaga ttatcgctcc taaacacaaa gtcaaaattg gttttgtggg caagtattta 900
agcttgaaag aatcttataa atccttgatt gaagccctaa tccatgcggg cgcgcatctg 960
gatacgcaag tcaatattga atggctggat agcgagaatt ttaatgaaaa gacggattta 1020
gagggcgttg atgcgatttt agtgcctggg ggctttggag aaaggggat tgagggcaaa 1080
atttgcgcca ttcaaagggc taggttagaa aaactcccct ttttagggat ttgtttgggc 1140
atgcaattag cgatcgttga attttgtcgc aatgttttgg gtttaaaagg ggctaactct 1200
acggagttta accaacgctg cgaataccct gtggtgtatt tgattggaga ttttatggat 1260
caaaaccacc aaaaacaggt gcgcacctat aattcgcctt taggaggcac catgcgatta 1320
ggcgaatacg aatgcgaaat tatgccaaac agcttgttag aaaaagctta taaaaagcct 1380
agcattaaag aaagacaccg ccatcgttat gaaatcaacc ccaaataccg ccaagagtgg 1440
gaaaataagg gcttgaaagt ggtgggtttt ggatcgaatc atttgattga agcgattgaa 1500
ttagaagatc acccgttctt tgtgggggtg caattccacc cagaattcac ctccaggttg 1560
caaagcccta accctattat tttagatttc attaagagcg ctctttctaa atcc 1614

Seq ID 35

ttggatttaa aggtattatt gcaacggatt gttgattttt tcatcaagct caataaaaag 60
caaaaaatcg ccctgattgc agctggggtt ttgatcacgg ctttgcttgt gtttttattg 120
ctctatccct ttaaagaaaa agactacacg caaggggtt atggggtttt atttgaaggt 180
ttagactcta gcgataacgc tttaatctta cagcacctcc agcaaaacca aatcccttat 240
aaagtctcaa aggacgacac catccttatc cctaaagata aagtgtatga agaaaggatc 300
actctggctt ctcaagggat ccctaaaacg agtaaagtgg gctttgaaat ctttgacact 360
aaagactttg gagcgactga ttttgatcaa aatatcaaac tcattcgcgc cattgagggg 420
gaattgtcgc gcacgattga aagtttaaac cccattttga aagccaatgt gcatattgca 480
atccctaaag acagcgtgtt tgtggctaaa gaagtccctc ctagcgcttc ggtgatgctc 540
aaactcaagc ctgacatgaa gctttcaccc actcaaattt tagggattaa aaatttaatc 600
gctgcagctg tgcctaaact cacgatagaa aatgtgaaaa tcgtgaatga aaatggcgaa 660
tcaataggcg aaggcgatat actagaaaac tccaaagaat tagccctaga gcaattgcat 720
tacaaacaaa attttgaaaa cattctagaa aataagattg tcaatatctt agcccctatt 780
gtgggggta aaaacaaggt ggttgcaagg gtcaatgcag agtttgattt cagccaaaag 840
aaaagcacta aagagacttt tgatcccaat aatgtcgtaa ggagcgagca aaatttagaa 900
gaaaaaaaag aaggcgcttc taaaaaacaa gtcggtggcg tgcctggggt tgtgagcaat 960
atcgggcctg tgcaaggatt gaaagacaat aaagagccag aaaaatacga aaagtctcaa 1020
aacacaacca attatgaagt gggtaaaacc attagcgaga ttaagggcga gtttggcact 1080
ttagtgcgtt tgaatgcggc ggttgtggtg gatggcaagt ataaaatcgc gcttaaagat 1140
ggggtaaaca ctttagaata cgagcctttg agcgatgaat cgcttcaaaa aatcaacgct 1200
ctagtcaaac aagccattgg ctataatcaa aatagaggcg atgatgtggc ggtgagcaat 1260
tttgagttta accctatggc acctgtgatt gataacgcta ctttgagcga aaaaatcatg 1320
cacaaaactc aaaaaatctt aggctcattc acgcccttaa tcaagtatat tttagtgttt 1380
atagtgctat ttatttttcta taaaaaagtg attgtgcctt tcagcgaacg catgctagaa 1440
gtggtgcctg atgaagataa ggaagtgaaa tccatgtttg aagaaatgga tgaagaagaa 1500
gatgaattga acaaactggg cgatttgagg aaaaaagtag aagatcaatt agggcttaat 1560
gcaagcttta gcgaagaaga agtaagatac gaaatcatct tagaaaagat tagagggact 1620
cttaaagaac gccctgatga aatcgcaatg ctctttaaac tcctaatcaa agatgaaatc 1680
tcttcagacg gcgcgaaagg t 1701

Seq ID 36

atgtatgttg aaaaaattct ccagtcttta cagaaaaaat acccttatca aaaagagttc 60
catcaagccg tctatgaagc tatcacttct ttaaaacccc ttttagacag cgataaaagt 120
tatgaaaagc atgcgatttt agagcgtttg attgagcctg aaagggagat ttttttagg 180
gtgtgttggc tagatgataa caatcaaatc caagtcaatc gggggtgtag ggttgagttt 240
aattcggcta ttggccctta taaggggggt ttgagattcc accctagcgt gaatgaaagc 300

gtgatcaagt ttttaggctt tgagcaagtg ttgaaaaatt cgctcaccac tttggctatg 360
gggggcgcta agggggggag cgattttgac cctaaaggga agagcgagca tgagatcatg 420
cgtttttgcc aagcgttcat gaatgaatta taccgccata ttggagccac gactgatgtg 480
ccagctgggg atattggagt gggcgaaaga gagattggct atctgtttgg gcaatacaaa 540
aaattagtca atcgttttga gggcgtattg accggtaaag gactcactta tggagggagc 600
ttgtgcagaa aagaagctac cggttatggg tgcgtgtatt ttgctgaaga aatgttgcaa 660
gaaaggaaca gctctttaga gggtaaggtt tgcagcgttt ctgggagcgg gaatgtcgca 720
atttatacca ttgaaaaatt gcttcaaata ggagctaaac cggtaacggc gagcgattct 780
aatggcatga tttatgacaa agacggcatt gatttagagc ttttgaaaga aattaaagaa 840
gtgcgtcgtg ggaggatcaa agaatacgct ttagaaaaaa agagcgcgga atacacccca 900
acagaaaatt accccaaagg ggggaatgcg gtgtggcatg tgccttgttt tgcggctttt 960
cctagtgcga ccgagaatga attgagcgtt ttagacgcca aaaccctcct ttctaatggg 1020
tgtaaatgcg tggctgaagg ggcgaacatg ccctcaagca atgaagcgat tggattgttt 1080
ttgcaggcta agatttctta tggtataggc aaggcggcta atgctggggg ggtgagcgtg 1140
agcggcttgg aaatggcaca aaacgcaagc atgcaccctt ggagttttga agtggtggat 1200
gcgaaattgc accatattat gaaagagatt tataagaatg tctctcaaac cgctaaagag 1260
tttaaagacc ctactaattt tgtattaggg gccaatatcg ctggttttag aaaagtagcg 1320
tctgcgatga tagcgcaagg ggtt 1344

Seq ID 37
atggatgatt tgcaagaaat aatggaagac ttcttgattg aagcctttga aatgaacgag 60
caattggatc aggatttagt ggaattggag cataaccctg aggatttgga cttgctcaat 120
cgcattttta gagtcgccca caccattaaa ggctctagct cgtttttgaa tcttaacatt 180
ctcacgcacc tcacgcacaa catggaagat gtcttgaatc gcgccagaaa gggcgaaatc 240
aaaatcacgc ctgatattat ggatgtcgtg ttgcgctcca ttgatttgat gaaaaccttg 300
ctcgtaacga ttagagatac cggctctgat actaataacg gcaaggaaaa cgagattgaa 360
gaagcggtca aacaacttca agccatcacg agtcaaaatt tagagagtgc taaagaaagg 420
actacagaag ccccccaaaa agaaaataaa gaagagacga aagaagaagc gaaagaagaa 480
aataaagaaa acaaggcaaa agcccctact gcagaaaaca catcaagcga taacccgcta 540
gccgatgagc cggatttgga ttacgctaac atgagcgctg aagaagtgga agcagagatt 600
gaacggctgc tgaacaaacg ccaagaagcc gataaagaac gaagagctca aaaaaaacaa 660
gaagccaaac ccaaacaaga agttacccca acaaaagaaa cccccaaagc ccctaaaacc 720
gaaactaaag ctaaggctaa agccgatact gaagaaaata aagccccctc tattggcgtg 780
gagcaaaccg ttagggtgga tgtgcgccgc ttggatcact tgatgaattt aatcggcgag 840
cttgtgttag ggaagaatcg cttgatcagg atttatagcg atgtggaaga acgctatgat 900
ggggaaaagt ttttagagga attaaaccag gtggtctctt ctatttcagc ggtaacgaca 960
gacttgcagc ttgcggtgat gaaaacacgg atgcaaccag tgggtaaggt gttcaataaa 1020
ttccctcgca tggtaaggga tttgagccgg gaattaggca agagcattga attgatcatt 1080
gagggcgaag aaaccgaatt agacaaatcc attgtagaag agattggcga tccgctcatt 1140
cacattatcc gcaactcatg cgatcatggg attgagcctt tagaagaaag acgaaagctt 1200
aacaagcctg aaaccggtaa agtgcaattg agcgcgtata atgagggtaa ccacattgtg 1260
attaaaatct ctgatgatgg caaagggtta gaccctgtga tgcttaaaga aaaagcgatt 1320
gaaaaagggg tgattagcga aagagacgct gaaggcatga gcgataggga agcgtttaac 1380
ctcattttca agccaggctt ttctaccgca aaagtcgttt ccaatgtctc aggcaggggt 1440
gttggcatgg atgtggtgaa aaccaatatt gaaaagctca atgggatcat tgaaattgat 1500
tcagaagtgg gggtaggcac gactcaaaag cttaaaatcc ctctcacttt ggctatcatt 1560
caagctttac tcgtgggcgt tcaagaagaa tattacgcta tcccgctttc ttcagtgtta 1620
gaaaccgtgc gcatcagcca ggatgaaatt tacaccgttg atggcaagag cgtgttgcgt 1680
ttgagagatg aggtgctttc tttggtgcgc ctttctgata tttttaaagt agatgctatt 1740
ttggaatcca actcagatgt gtatgtggtt atcattggct tggctgatca aaaaattggc 1800
gtgatcgtgg attatttaat cggtcaagaa gaagtggtca ttaaatcttt aggttactat 1860
cttaaaaaca ctagaggcat tgctggtgct acggtgagag gcgatgggaa aatcaccctt 1920
attgtagatg tgggggcgat gatggatatg gcaaaaagca tcaaggtcaa tatcactacc 1980
ttaatgaacg aatccgaaaa cacgaagagc aaaaattccc ctagcgatta tattgtctta 2040
gcgattgatg acagcagcac ggatagagcg attatccgca aatgtttaaa accattaggc 2100
atcacgcttt tagaggcgac taacgggtta gagggcttag aaatgcttaa aaatggcgat 2160
aagattccgg acgctatttt agtggatatt gaaatgccta aaatggacgg ctacactttc 2220
gcttctgaag tgcgtaaata caataaattc aaaaacctgc ctttgatcgc agtaaccagt 2280
cgggtaacta aaaccgatag gatgcgtggc gttgaatccg gcatgactga atacatcacc 2340
aaaccttata gcggtgaata tttaaccacc gtagtgaagc gcagcattaa attagaagga 2400
gaccaatcg 2409

Seq ID 38
gtgatagagc ttgacattaa cgctagcgat aaatcgctct cacacagagc cgttattttt 60
agcctgctcg ctcaaaaacc ttgtttcgtg cggaattttt taatgggaga agattgttta 120
agctctttag aaatcgctca aaatttaggg gctaaagtgg aaaataccgc caaaaattct 180
tttaaaatca caccccaac aactataaag gagcctaaca agattttaaa ttgcaacaat 240
tctggcacaa ccatgcgttt atacagcggg cttttaagcg ctcaaaaagg gcttttttgtt 300

ttaagcgggg acaattcctt aaacgcacgc cccatgaaaa gaatcattga gcctttgaag 360
gcttttgggg caaaaatttt agggagagag gataaccatt tcgccccctt agtgatctta 420
gggagtccgt taaaagcttg ccattatgaa agccctatcg cttcagctca agtcaaaagc 480
gcttttattt taagcgcctt acaagctcaa ggcgcaagca cttataaaga aagcgagctt 540
agccgtaacc acacagaaat catgcttaaa agtttgggag ctgatattca caatcaagac 600
ggcgttttaa aaatttcacc cctagaaaaa cccctagaag cctttgattt tacgatagct 660
aatgatccgt ctagcgcgtt ttttttcgcc ctcgcttgcg cgattacgcc aaaaagccgc 720
cttcttttaa aaaatgtctt gctcaacccc actcgcatag aagcttttga agttttgaaa 780
aaaatgggtg cttccataga gtatgcgatt cagtccaaag atttagaaat gattggcgat 840
atttatgtag agcatgcccc tttaaaagcg atcaatattg atcaaaatat cgccagtctt 900
attgatgaaa tccccgcttt aagtatcgct atgctttttg caaaaggcaa aagcatggtt 960
aaaaacgcta aagatttacg agctaaagaa agcgacagga ttaaagcggt tgtttctaat 1020
ttcaaagctt tagggattga gtgcgaagag tttgaagatg ggttttatgt agagggatta 1080
gaagatataa gcccattaaa acagcgcttt tctaggatta agccccccct tatcaaaagc 1140
ttcaatgacc acaggattgc gatgagtttt gctgttttaa ctttagcgtt gcctttagaa 1200
attgataatt tagaatgcgc aaacatttct ttcccgcaat tcaaacacct actcaatcaa 1260
ttcaaaaaag ggagtcttaa tggaaat 1287

Seq ID 39
ttggatattt tagatttgaa caaagcgcaa gcggtgcaac aaaatgaaca agaggtagag 60
gataaagagc gagagtctaa agagccggtg gttttagaag atttgagcgc tttagcgtgg 120
cttgaattag aagagtttag ccgcctttca gggcttccta aagaaaggat tttggaatta 180
gtgaatcttg gtaaaatcaa gagcaaaata agcagcaaca agcttttaat tgatgcgagc 240
agcgggacaa acgctttaat caaaaaggta gaaaatagtt tgatttctat ggatatgaac 300
gggcgttctt tagaacctgt gtttgtggaa aagaccatta acacgatttt aaacttgcat 360
gataaggtca ttggcgctaa agatgaaacg atttcagcct ttaaaaatga aaacatgttt 420
ttaaaagacg ctttaatctc tatgcaagaa gtctatgaag aagataaaaa aaccattgat 480
cttttgcgcg atgaactcaa tcaagcgaga gaagaaattg aatttatgaa gaggaaatac 540
cgcttgatgt gggggaaagt cgctgacatg agcagcgtga ataaaaag 588

Seq ID 40
atgattttag tattagattt tgggagtcaa tacacacagc tgattgctag aagattgaga 60
gagagaggga tttatacaga aatagtccct ttttttgaaa gcatagaaaa cattcaaaaa 120
aaagccccca aaggtttgat tttgagtggg gggccagcga gcgtgtatgc taaagacgct 180
tacaagccta gtgggaaaat ctttgatttg aatgtgccga ttttagggat ttgctacggc 240
atgcagtatt tggtggattt ttttgggggg gtagtggttg gtgcgaatga gcaagaattt 300
ggtaaggctg ttttagaaat cactcaaaat tctgtgattt ttgaaggcgt gaagattaaa 360
agccttgtgt ggatgagcca tatggataaa gtcatagaac tgcctaaagg ctttactacc 420
cttgcaaaaa gccctaattc cccccattgc gcgattgaaa acggcaagat ttttggcttg 480
caattccacc cagaagtcgt tcaaagcgaa gaaggggtta agattttaga aaattttgcc 540
cttttagttt gcggctgtga aaaaacttgg gggatgcagc atttcgctca aagagaaatc 600
gcacgattga aagaaaaaat cgctaacgct aaggttttgt gcgcggtgag tgggggcgtg 660
gattctacgg tggtcgctac gctgttgcac agagccatta aggataattt gatcgctgtt 720
tttgtggatc atggcttgtt gcgtaaaaat gaaaaagaaa gggtgcaagc gatgtttaag 780
gacttgaaaa tccctttaaa cacgatagac gctaaagaag tctttttgtc taaattaaag 840
ggcgtgagcg agcctgaatt gaagcgaaaa atcatcggcg agacctttat tgaagtgttt 900
gaaaaagaag ccaaaaagca ccatttaaaa ggcaaaattg aatttttagc ccaaggcact 960
ttataccctg atgtgattga atccgtgagc gttaaagggc cttcaaaagt gatcaaaacc 1020
catcataatg tgggcggact gcctgaatgg atggatttta aactcataga gcctttaagg 1080
gagttgttta aagatgaggt gcgcttactg ggtaaagaat tgggcgttag tcaggatttt 1140
ttaatgcgcc acccttttcc agggcctggg cttgctgtaa ggattttagg cgaaatcagt 1200
gagagtaaga tcaaacgctt gcaagaagcg gattttattt ttatagagga acttaaaaaa 1260
gccaatttgt atgacaaggt ttggcaagct ttttgcgtgc tgttgaatgt caattctgtg 1320
ggggttatgg gggataaccg cacttatgaa aacgctattt gcttaagagc ggtaaatgcg 1380
agcgatggca tgacggcgag cttttcattt ttagagcatt ctttttaga aaaggtttct 1440
aaccgtatca ctaatgaagt gagcggtatc aatagggtgg tgtatgacat tacctctaaa 1500
ccaccaggaa cgattgaatg ggaa 1524

Seq ID 41
atgaaagtca ataagggttt taaattccgc ttgtatccca ctaaagaaca acaagataag 60
ttgcaacact gcttttttgt ctataatcaa gcttataata ttggcttgaa tgaactgcaa 120
gagcaatatg aaaccaacaa agattcacca cctaaagaaa gaaaatacaa aaaatcaagc 180
gaattagaca atgcgatcaa acaatgcttg agagctaggg acttgccctt tagcgctgtg 240
atagcccaac aagcacgcat gaatgttgaa agggctttaa aagatgcttt taaagttaaa 300
aacagaggct ttcctaaatt caaaaactct aaatccgcca aacaatcttt ttcgtggaac 360
aatcaaggct tctctatcaa agagagcgat gatgagtgct tcaagacatt cactctgatg 420
aaaatgcctt tactcatgcg catgcataga agacttcccc ctaattttaa agtgaaacaa 480
attagtatct cttgcagcca tagaaaatat tttgttagct ttagcgtgga atacgaacaa 540

gacattactc ccataaaaaa cactaaaaat ggtgtggggc tagatttgaa tatccttgat 600
acagcttgtt cttgtgagat aaacaaccat gacaaactaa cggactttaa gcaataccaa 660
acagacatga aagaattact agggatagaa atagatgaag agctggatac taaacgactt 720
atccctactt attccaaatt gtattcttta aaaaaatact ctaaaaaatt taaaagatta 780
caaagaaaac aaagccgtag gtgt 804

Seq ID 42
atgttagaaa gcgcccttaa atattgcaag gaaaaagcca tagacctttt agtagggttt 60
gtgccaaaaa cctattctat ggcacaagag tgcaatattt taggcttgta tgatgatgct 120
ttcattatta ccaaacaaga aaatctagta ggcattatat ccttacaagg actaagctat 180
tctaatttaa tgcaaaaaga cttagagggc tattttgatg ctagacaaaa tgttctcaac 240
accattagta aagacattca attaagaatt gtggctaaaa ggcgtaagga atttatcaat 300
caaagtccaa atattgacaa tatttatgcc aaagctatta tcacacaatt tgaaagcaag 360
ggaatctata aaacagagta ttttttagtg tttgaaacta tcacttctaa tgtcaagtct 420
ttctttgaaa aaaagaaatt ggaaatgact acttcaatta atgaagagtt agaagaaagc 480
tctaaagaag ataaacaaga gaatgaaaat agctccaatg aaactcattc aaacacaagc 540
tctaaaaaag acaagaaaaa caagttcaaa aaaaagataa cctttagcac caaaagtaaa 600
agagccttac tcattcaaac catagaaaga gtaaaaaacg ctcttaaaga atttaaaccc 660
actttactaa attctaaaga agtattaaat ttctacgcag aatacatcaa tggcaaatac 720
atcgccttta atcctaaatt aaagcgatta agcgatagct atattgcatc taatgtgcat 780
tttaagaaag attactttgt cattgaattt caaaatcaaa acacctttg tgcgtgtgtg 840
gggattaagg cttatgagag cgaagaaatt tcttcgctcc ctatatctac tcttttacac 900
acccaaattg aactagattt aatctttcat atccgctctt tagggcaatt tgaaagcctg 960
aatttttaa aaactaagaa aaagctcacg ctttctaaaa tagtaaaagc tgatattgat 1020
aattatatag aattagtgca agccaatcgt ttgagcatgc aagagtgtgc tttaaactta 1080
gttataaggg ctaaaagtaa agctaaatta gacaagtctt taaaagagat tttatccttg 1140
cttaataatg ctggactagg cagtgttaca gaaactatag ggctaaaacc atcttatttt 1200
tcattcttcc caaataacgc caatatcaac cctagaatga gacatcaaac ttcccaagtc 1260
atagcatctt tgattttgtt tgagaaaaat aatacaggtt ttagagcaaa ttcttggggg 1320
gatatgccct tatctgtgtt taagaaccta gaccatagcc cttatttgtt taattttcat 1380
aatcaagaag tcaaacataa gggcgtgtta gcccacaatg tcgcacgagt agtgggacat 1440
accatgatta taggagcaac aggtgctggt aaaaccacac tcattagcta tttgatgatg 1500
agtgccttaa aatattctaa cattgatatt ttagctcttg atagactaaa tggtttgtat 1560
tcctttacca agtattttga tgggatttat aatcaaggcg aaaactttca tattaaccct 1620
ttttcattag aagatagcgc aactaataga gccttttttat tgcattttta tgcccaaatg 1680
gcaaaagtgg atagttatga tgaccataag gataaagtag aagatagaac agccctttta 1740
aatgctattg atacgatgta tagaaattat aacgatgaag tcaaacaagc caaatttagc 1800
aaccaagaat taccccttcc ttttgattta aaagagtttg tcaatgccat tgctaaaacc 1860
aatacagaca ttttagatag tagttttgaa gactatttaa aatcttcctt attttctagc 1920
cgaatggata gtctagattt taaaactcgt attagcacca taaataccga tagcatttta 1980
cataatgatg atgacgctgg gcttttagcc tactatgtct ttcataagat gattgacaga 2040
gccttaaaaa tcaatcgtgg gtttttatgc tttattgatg agtttaagtc ttacgctcaa 2100
aatgaaatga tgaataaaaa aatcaatgaa atcattactc aagctagaaa ggctaatggg 2160
gtgattgttc tagccttaca agacattaac caactaagcg aagtgagaaa cgctcaaagc 2220
tttataaaaa atatggggca attgattttg tatccccaaa gaaatattga taccaaagat 2280
ttaaacgata aatttggcat tagactaagc gatacagaaa aacatttttt agaaaacacc 2340
gccgttaatg aatacaaagt cttactcaaa aacatgaatg atggctcatc taacattata 2400
gatgtgagcc taagttcttt gggtaattac ctacaaatct ttagctctaa ttctagcatg 2460
gtagaacaca ttgataatct cattaagcat taccctaaaa cttggcgaga agtctttgtg 2520
agtaacaaac acgaaaattt tgatgacaaa aaacacttag aaaaggtgct taaa 2574

Seq ID 43
atgaaaaata ttagaaatat cgctgtaatc gcgcatgttg atcatgggaa aaccactcta 60
gtagatggct tactttctca atctggcaca tttagtgaga gggaaaaagt ggatgaaagg 120
gtgatggata gcaatgattt ggaaagagaa agagggatta ctatcctgtc taaaaacacc 180
gctatttatt acaaagacac taaaatcaat atcattgaca ctcccgggca tgctgatttt 240
gggggcgaag tggagcgcgt tttaaaaatg gtggatgggg tgttgctttt agtggacgct 300
caagaagggg tcatgcctca aactaaattc gtggttaaaa aggctttgag ttttgggatt 360
tgccctattg tggtggtgaa taaaattgat aagcctgccg ctgaaccgga cagagtggtg 420
gatgaagttt ttgacttgtt cgtagccatg ggggctagcg ataagcaatt ggatttccct 480
gtggtgtatg ccgccgcacg agatggctat gcgatgaaaa gtttagacga tgaaaagaaa 540
aatttagagc ctttgtttga aacgatttta gagcatgtgc caagccctag cgggagcgtt 600
gatgagcctt tgcaaatgca aattttcacg cttgattatg acaattatgt gggcaaaatc 660
ggtatcgcta gggtgtttaa tggctcggtt aaaaagaatg aaagcgtgct gttgatgaaa 720
agcgatggga gtaaagaaaa tggccgtatc actaagctta taggtttttt agggctggct 780
aggactgaga ttgaaaacgc ttatgcgggc gatattgtag cgattgccgg gtttaatgca 840
atggatgtgg gcgatagcgt cgttgatcct gctaacccca tgcctttaga tcccatgcat 900
ttagaagagc ctacgatgag cgtgtatttt gctgtcaatg attcaccctt agccgggtta 960

gaaggaaagc atgttactgc taataaattg aaagacaggc tcttaaaaga aatgcaaacc 1020
aatatcgcta tgaaatgcga agaaatgggc gagggcaagt ttaaagtgag tgggcgtggg 1080
gaattgcaaa tcactatttt agctgaaaac ttgcgccgtg aagggtttga atttagcatt 1140
tcacgccctg aagtcatcat taaagaagaa aatggcgtta aatgcgagcc ttttgagcat 1200
ttagtgattg acacgcccca agattttagt ggggctatca ttgagagatt gggcaaaaga 1260
aaagctgaga tgaaagcgat gaatcccatg agtgatggct atacaagatt agaatttgaa 1320
attcctgcaa gagggcttat cggttatagg agcgagtttt taaccgacac caagggcgaa 1380
ggcgtgatga atcatagctt tttagaattc cgccctttca gcgggagcgt ggaatcgcgc 1440
aaaaatgggg cgctaatcag catggaaaat ggcgaagcga ccgctttttc cctttcaat 1500
atccaagaaa gaggcacgct ttttatcaac ccccaaacga aggtttatgt gggcatggtc 1560
attggcgagc acagccggga taatgattta gatgtcaatc ctattaaatc caagcattta 1620
accaacatga gagcgagcgg gagcgatgat gcgatcaaac tcaccccgcc taggactatg 1680
gtgttagaaa gagcgttaga atggattgaa gaagatgaga ttttggaagt tacccccttg 1740
aatttaagga tcaggaaaaa gattttagac cctaacatga ggaaaagggc gaaaaaa 1797

Seq ID 44
atgaaaaaaa ttggtttgag cttgtgtttg gttttgagtt tgggtttttt aaaagcccat 60
gaagtgagcg ctgaagagat tgcggatatt ttctacaaac tcaacgccaa agagcctaaa 120
atgaaaatca accacactaa ggggtttttgc gctaaaggcg tgttcctccc taatgcgcaa 180
gcaaaaaagg atttagatgt gccattactc aatgaaaaag aaatccctgc gtctgtaagg 240
tattctttag gaggcgtggc aatggacgat aaaagcaaag ttaggggaat ggcgttaaaa 300
ttagaaaacc aaaacgctag ctggacaatg gtgatgctca atacagaaat caattttgcc 360
aaaaacccta acgaattcgc ccaatttttt gagatgagaa tccctaaaaa tggcaaggtg 420
gatgaagcaa gaatcaaaaa gctttatgaa gaagtcccct cttataggaa ttttgccgct 480
tacaccaaaa cgatagggat cagctcaagc gtggctaaca cgccttatta cagcgtgcat 540
gcgttcaggt ttaaagacaa aaaagggaag ttattacccg caagatggaa atttgtgcct 600
aaagagggca ttaagtatct taacccccaa gaattaaagc aaaaagattc aaattatctg 660
ctctctgcat tccaacaaca ccttaaaact aagcccatag aataccaaat gtatctggtg 720
tttgcgaata aaaatgatgc cactaacgac acgaccgcgc tttggaaagg taaacacaag 780
gaattattgg tggggacctt gaaagttgaa aaatacgaag gaatgggttg caataaagat 840
gtgtatttcc cagctgatct ccccaaaggc gtagaagccc ctactgatcc cttattccaa 900
atcaggaatg aagtttatgg gatcactttt agcagaaggc aa 942

Seq ID 45
atgttaaggc ttttgatagg acttcttcta atgagtttta taagcttgca atcagcctct 60
tggcaagaac ccttaagagt gagtatagaa tttgtggatt tgcctaaaaa aatcattcgt 120
tttccggctc atgatttgca agtgggggag tttggttttg tcgttactaa actttcagat 180
tatgaaatcg ttaattctga agtggtcatt attgccgttg aaaatggcgt cgcaacggct 240
aaattcagag cgtttgagtc tatgaaacaa aggcatttac ccactccaag aatggtcgct 300
agaaagggtg atttagtcta ttttaggcaa ttcaacaacc aagcgttttt aatcgctcct 360
aatgatgaac tctatgagca aatcagagcg actaacaccg atattaattt tattagttct 420
gatttgttgg ttacttttct gaatgggttt gacccaaaaa tcgctaattt aaggaaagcg 480
tgcaacgttt atagcgtggg ggtgatttat attgtaacca ccaacacgct caatatttta 540
agttgtgaga gttttgaaat tttagaaaaa agagagctgg atacaagcgg cgttactaaa 600
acttccacgc cgtttttttc tagggttgag ggtattgatg caggcacgct agggaaactt 660
ttttcaggca gtcagtctaa aaattacttc gcttactatg acgctttagt gaagaaagaa 720
aaacgcaaag aagtgaggat taaaaagagg gaagaaaaga ttgattctag agaaattaaa 780
cgagaaatca agcaagaggc cattaaagag cctaaaaaag ccaatcaagg cacacaaaac 840
gctcctactt tagaagagaa aaactaccaa aaagcagagc gcaaacttga tgctaaagaa 900
gaaaggcgtt atttgagaga tgaaaggaaa aaagccaaag ccaccaaaaa ggctatggaa 960
tttgaagaaa gagaaaaaga gcatgatgaa agggacgaac aagagactga aggaagaaga 1020
aaagctttag aaatggataa aggcgataaa aaagaagaaa gagtcaaacc caaagaaaat 1080
gagcgagaaa tcaagcaaga agccattaaa gagccaagtg atggaaataa cgccacccaa 1140
caaggcgaaa aacaaaacgc tcctaaagag aacaacgctc aaaaagaaga gaataaacca 1200
aattctaaag aagaaaaacg ccgcttgaaa gaagaaaaga aaaaagccaa agccgaacaa 1260
agagcgagag aatttgaaca aagagcgaga gagcatcaag aaagagatga aaaagagctt 1320
gaagagcgaa gaaaggcgct agaagcgggt aaaaaa 1356

Seq ID 46
atgtttaaag atttttatcg caccaccctc tctttttaa agcctttatt gcttttacta 60
gttttattat tgccgttttc actttgtata gctgatgaat atattagcat aagtgatgat 120
tgggatgaaa ttgtgcgaaa tcataagaca tattattttg aaaatggttt agaccatttt 180
aatcaaggcc aataccagca agcctttaaa gattttagat tggcgcaaga atacagcatc 240
gggcttggca gtgtttattt agccaaaatg tatttggagg gaaagggcgt gaaagtggat 300
tacaaaaaag cacaatttta tgcagaaaac gctatcaaag ggtatgggag cggattgtta 360
gggggtgctc ttattttagg acgcatgcaa gcagaaggct tagggatgaa aaaggatttg 420
aaacaagcgc tcaagactta taggcatgtg gttcgcatgt tttctaataa aagcacaaat 480
tttgctaaca attttagatt accaaacctt gcggaattta ctagtatgct tattggatcg 540

cgattcattg atctttcagg tttgagcgcg aatcctataa aatttggaaa gaaatttgga 600
atacttgtta agaaatccac tcaaatcaaa gataagacac ttctttggga agatattgct 660
gaaatttcaa gcaatattac tttactcaaa caacaaatgg gggagatcct ttataggatt 720
gggatcgctt ataaagaagg gcttggcact agaaagaaaa aggacagggc taaaaaattc 780
ctgcaaaaat ccgcagaatt tggctatgaa aaagccatgg aagctctg 828

Seq ID 47
atgactgaag acagattgag tgcagaagat aaaaagtttc tagaagtaga aagagcttta 60
aaagaagcgg cattaaatcc tctaaggcat gctactgaag aacttttgg tgatttttta 120
aaaatggaaa atatcactga gatttgttac aatgggaaca aggttgtatg ggttttaaaa 180
aataatggcg aatggcaacc atttgatgtg agagacagga aagcctttag cctgtctcgt 240
ttaatgcatt ttgctcggtg ttgtgcaagt tttaagaaaa aaacaataga caactatgaa 300
aatcctattt tgagcagcaa tttagcgaat ggtgaaaggg tgcagattgt cctttccccc 360
gttacagtta atgatgaaac catttccata tccataagga tacctagcaa aacaacctat 420
cctcatagct tctttgaaga gcaaggtttt tataatctac tagacaacaa agaacaagcg 480
atcagcgcga ttaaagatgg tattgctatt ggtaaaaatg tgattgtttg tggtggcaca 540
ggaagcggta aaacgactta tatcaaaagc atcatggagt ttatccctaa agaagaaagg 600
atcatatcca ttgaagacac cgaagagatt gtattcaaac accacaaaaa ctacacacag 660
ctttttttg gtgggaatat cacctctgct gattgcttaa agtcatgtct gagaatgcgg 720
cctgatagaa tcattttagg ggaactcaga agcagtgagg catacgattt ttataatgtg 780
ctttgtagcg gtcataaagg cacactaacc actctgcatg cagggagcag tgaagaagcg 840
tttatccgtt tggccaacat gagttcatct aatagcgcag caaggaatat caagtttgaa 900
agtcttattg agggctttaa agatttgatt gatatgattg tccatatcaa ccaccacaaa 960
cagtgtgatg aattttatat caaacacagg 990

Seq ID 48
atgaatgaag aaaacgataa acttgaaact tctaaaaaag cccaacaaga ttcaccccaa 60
gatttatcca atgaagaagc aacagaagcc aatcattttg aaaatctttt aaaagaatcc 120
aaagaaagct cagatcatca tcttgacaac cccacagaaa ctcaaaccca ttttgatgga 180
gacaagtcag aagaaaccca aactcaaatg gattctgaag gtaatgaaac ttcagaatct 240
agcaatggca gtctagcaga caagttattc aaaaaagcca gaaaattagt tgataataaa 300
aaacctttca ctcagcaaaa gaatttagat gaagaaaccc aagaactgaa cgaagaagac 360
gatcaagaaa ataatgagta tcaagaagaa actcaaacgg acttaattga tgatgaaact 420
tctaaaaaaa cccaacaaca ttcaccccaa gatttatcca atgaagaagc aacagaagcc 480
aatcattttg aaaatctttt aaaagaatcc aaagaaagct cagatcatca tcttgacaac 540
cccacagaaa ctcaaaccaa ttttgatgga gacaagtcag aagaaaccca aactcaaatg 600
gattctgaag gtaatgaaac ttcagaatct agcaatggca gtctagcaga caagttattc 660
aaaaaagcca gaaaattagt tgataataaa aaacctttca ctcagcaaaa gaatttagat 720
gaagaaaccc aagaactgaa cgaagaagac gatcaagaaa ataatgagta tcaagaagaa 780
actcaaacgg acttaattga tgatgaaact tctaaaaaaa cccaacaaca ttcaccccaa 840
gatttatcca atgaagaagc aacagaagcc aatcattttg aaaatctttt aaaagaatcc 900
aaagaaagct cagatcatca tcttgacaac cccacagaaa ctcaaaccaa ttttgatgga 960
gacaagtcag aagaaataac tgacgactct aacgatcaag agattatcaa aggaagcaaa 1020
aagaaatata ttattggtgg cattgtagtc gctgttctta tcgtgattat tttattttct 1080
agaagcattt ttcactactt catgcctttg gaagataaaa gctctcgttt tagcaaagac 1140
aggaatcttt atgtcaatga tgaaatccaa ataaggcaag agtataaccg attgctgaaa 1200
gaacggaatg aaaaaggcaa tatgatcgat aagaatcttt tcttcaatga cgatcccaat 1260
agaaccttat acaactattt gaatattgca gaaattgagg acaaaaaccc gttgagagcc 1320
ttttatgaat gtattagtaa tggtggcaac tatgaagaat gtttgaagct tatcaaagac 1380
aaaaaacttc aagatcagat gaaaaagact ctagaggctt ataacgactg catcaaaaat 1440
gccaaaactg aagaagaaag gatcaagtgt ttagatttaa tcaaagatga aaacctaaaa 1500
aaaagcttac tgaaccaaca aaaagttcaa gtggcgctag attgtttgaa aaacgctaaa 1560
accgatgaag aacgaaacga gtgcctaaaa ctcataaatg accctgagat tagagagaaa 1620
ttccgtaagg aattagagct tcaaaaagag cttcaagagt ataaggattg tatcaaaaac 1680
gccaaaacag aagctgagaa aaacaaatgc ttgaaaggct tgtctaaaga agctatagag 1740
agattgaaac agcaagcgct agattgtttg aaaaacgcta aaaccgatga agaacgaaac 1800
gagtgcttga aaaatattcc ccaagacttg caaaaagaac tattagctga tatgagcgtc 1860
aaggcttaca aggattgcgt atcaaaagct agaaatgaaa aagagaaaca agaatgcgag 1920
aaattgctca cgcctgaagc gaggaaaaag ttagaacaac aggttctaga ttgtttgaaa 1980
aacgctaaaa ccgatgaaga acgaaaaaag tgtttgaaag atctccctaa agacttacaa 2040
agcgatattc tagccaaaga gagcctgaaa gcttataaag actgcgtatc tcaagccaaa 2100
accgaagctg agaaaaaaga atgcgagaaa ttactcaccc ctgaagcgaa aaaactttta 2160
gaagaagaag ccaaagagag cgttaaggct tatttggatt gcgtatctca agccaaaacc 2220
gaagctgaga aaaaagaatg cgagaaattg ctcacccctg aagcgaaaaa aaagttagaa 2280
gaagctaaaa aaagcgttaa agcttacttg gattgcgtat caagagctag gaatgaaaaa 2340
gagaaaaaag aatgcgagaa attgctcacc cctgaagcga aaaaactttt agagcaacaa 2400
gcactagatt gtttgaaaaa cgctaaaacc gataaagaac gaaaaaagtg tttgaaagat 2460
ctccctaaag acttgcagaa aaaggtttta gctaaagaaa gcgttaaagc ttacttggat 2520

tgcgtatctc aagccaaaac tgaagctgag aaaaaagaat gcgagaaatt actcacccct 2580
gaagcgagaa aacttttaga agaagctaaa aaaagcgtta aggcttattt ggattgcgta 2640
tctcaagcca aaactgaagc tgagaaaaaa gaatgcgaga aattactcac ccctgaagcg 2700
agaaaacttt tagaagaaga mgccaaagag agcgttaaag cttacttgga ttgcgtatct 2760
caagccaaaa acgaagctga gaaaaaagaa tgcgagaaat tgctcaccct tgaatcgaaa 2820
aaaaagttag aagaagctaa aaaaagcgtt aaggcttatt tggattgcgt atctcaagcc 2880
aaaaccgaag ctgagaaaaa agaatgcgaa aaattgctca cgcctgaagc gaaaaaactt 2940
ttagagcaac aagcgctaga ttgtttgaaa aacgctaaaa ccgaagctga taaaaaaagg 3000
tgtgtcaaag atctccctaa agacttgcag aaaaaggttt tagccaaaga gagcctgaaa 3060
gcttataaag actgcgtatc aaaagctagg aatgaaaaag agaaaaaaga atgcgagaaa 3120
ttactcaccc ctgaagcgaa aaaactttta gaagaagcta aaaaaagcgt taaggcttac 3180
ttggattgcg tatctcaagc caaaactgaa gctgagaaaa aagaatgcga gaaattactc 3240
acccctgaag cgagaaaact cttagaagaa gctaaagaga gcgttaaagc ttataaagac 3300
tgcgtatcaa aagctaggaa tgaaaaagag aaaaaagaat gcgagaaatt actcacgcct 3360
gaagcgaaaa aacttttaga gcaacaagtg ctagattgtt tgaaaaacgc taaaaccgaa 3420
gctgataaaa aaaggtgtgt caaagatctc cctaaagact tgcagaaaaa ggttttagct 3480
aaagagagcg ttaaggctta tttggactgc gtatcaagag ctaggaatga aaaagagaaa 3540
aaagaatgcg agaaattgct caccccctgaa gcgaaaaaac ttttagaaga agccaaagag 3600
agtcttaaag cttataaaga ctgcctctct caagctagaa atgaagaaga aaggagagct 3660
tgcgagaaac tactcacgcc tgaagcgaga aaactcttag agcaagaagt taagaaaagc 3720
attaaggctt atttggactg cgtatcaaga gctaggaatg aaaaagagaa aaaagaatgc 3780
gagaaattac tcacgcctga agcgagaaaa tttttagcga agcaagtgct aaattgtttg 3840
gaaaaagctg gaaatgaaga agaaagaaaa gcatgtctta aaaatctccc taaagactta 3900
caggaaaata ttttagctaa agagagtctt aaagcttata aagactgcct ctctcaagct 3960
agaaatgaag aagaaaggag agcttgcgag aaactactca cgcctgaagc gagaaaactc 4020
ttagagcaag aagttaagaa aagcgttaag gcttatttgg actgcgtatc aagagctagg 4080
aatgaaaaag agaaaaaaga atgcgagaaa ttactcacgc ctgaagcgag aaaatttta 4140
gcgaaagaac tccaacaaaa agataaagcg atcaaagatt gcttgaaaaa cgccgatcct 4200
aacgacagag cggctatcat gaagtgtttg gatggtttga gcgatgaaga gaagctcaaa 4260
tacctgcaag aagctagaga aaaggctgtt gcggattgtt tggctatggc taaaaccgat 4320
gaagaaaaaa ggaaatgcca aaacctttat agcgatttga tccaagaaat ccaaaataaa 4380
aggacacaaa acaaacaaaa tcaattgagt aaaacagaaa ggttgcatca agcaagcgag 4440
tgcttggata acttagatga ccctactgat caagaggcca tagagcaatg tttagagggc 4500
ttgagcgata gtgaaagggc gctaattcta ggaattaaac gacaagctga tgaagtggat 4560
ctgatttata gcgatctaag aaaccgtaaa acctttgata acatggcggc taaaggttat 4620
ccattgttac caatggattt caaaaatggc ggcgatattg ccactattaa cgccactaat 4680
gttgatgcgg acaaaatagc tagcgataat cctatttatg cttccataga gcctgatatt 4740
gccaagcaat acgaaacaga aaaaaccatt aaggataaga atttagaagc taaattagct 4800
aaggctttag gtggcaataa aaaagatgac gataaagaaa aaagtaaaaa atccacagca 4860
gaagctaaag cagaaaacaa taagatagac aaagatgtcg cagaaactgc caagaatatc 4920
agtgaaatcg ctcttaagaa caaaaaagaa aagagtgggg aatttgtaga tgaaaatggt 4980
aatcccattg atgacaaaaa gaaagcagaa aaacaagatg aaacaagccc tgtcaaacag 5040
gcctttatag gcaagagtga tcccacattt gttttagcgc aatacacccc cattgaaatc 5100
actctgactt ctaaagtaga tgccactctc acaggtatag tgagtggggt tgtagccaaa 5160
gatgtatgga acatgaacgg cactatgatc ttattagaca aaggcactaa ggtgtatggg 5220
aattatcaaa gcgtgaaagg tggcacaccc attatgacac gcttaatgat agtctttact 5280
aaagccatta cgcctgatgg tgtgataata cctctagcaa acgctcaagc agcaggcatg 5340
ttgggtgaag caggggtaga tggctatgtg aataatcact ttatgaagcg cataggcttt 5400
gctgtgatag caagcgtggt taatagcttc ttgcaaactg cgcctatcat agctctagat 5460
aaactcatag gccttggcaa aggtagaagt gaaaggacac ctgaatttaa ttacgctttg 5520
ggtcaagcta tcaatggtag catgcaaagt tcagctcaga tgtctaatca aattctaggg 5580
caactgatga atatcccccc aagtttttac aaaaacgagg gcgatagtat taagattctc 5640
acaatggacg atattgattt tagcggtgtg tatgatgtta aaattactaa caaatctgtg 5700
gtagatgaaa ttatcaaaca aagcaccaaa actttgtcta gagaacatga agaaatcacc 5760
acaagcccca aaggtggcaa t 5781

Seq ID 49
gtgaaatgtt ttttaagcat attttctttc ttgacttttt gtggtttgtc tctgaatggc 60
acagaagtag taataacgct tgaacccgcc ttaaaagcca ttcaggcgga cgcacaagcc 120
aaacaaaaaa ccgctcaagc tgaattaaaa gccatagaag ctcagtctag tgccaaagaa 180
aaagccattc aagcgcaaat agagggagaa ttgaggactc agcttgcaac catgagtgct 240
atgttaaaag gggctaatgg cgttattaat ggtgtcaatg gcatgacagg ggggtttttt 300
gcaggttcag acatcttgct tggcgtcatg gaagggtatt caagcgcgct tagtgcattg 360
gggggaatg ttaaaatgat cgtggaaaaa caaaaaatta acacccaaac agaaatccaa 420
aacatgcaaa tcgcgctcca aaaaaataac gaaataatca agctcaaaat gaaccagcaa 480
aacgctctct tagaagcgtt aaaaaatagc tttgaaccga gcgttactct aaaaacacaa 540
atggaaatgc tttctcaagc tctaggaagt tcttctgaca acgctcaata catcgcttac 600
aatacgattg gtatcaaggc gtttgaagaa accttaaaag gttttgaaac atggttgaaa 660

gtggctatgc aaaaagcgac ccttattgat tataattccc taacgggtca ggctttgttt 720
caaagtgcca tctatgcgcc tgctcttagt ttttttcaa gcatgggtgc accatttgga 780
atcattgaaa cattcactct agcgcccaca aaatgcccct atcttgatgg gctaaaaatt 840
tcagcatgcc ttatggaaca ggttattcag aattacagaa tgattgtagc ccttattcaa 900
aataaactga gtgatgcaga ttttcaaaat atcgcttatt tgaatgggat caatggagaa 960
atcaaaacct taaaaggatc agtagatttg aacgcgctca tagaagttgc tatcttaaac 1020
gcagaaaatc atttaaacta tatagagaat cttgaaaaaa aagccgacct ttgggaagaa 1080
caactgaaat tagaaagaga aacgacagca agaaacattg ctagctctaa agttattgtc 1140
aaa 1143

Seq ID 50
atggcaggta cacaagctat atatgaatca tcttctgcag gattcttatc ggaaatttcc 60
tcaatcatct caagcacaag tggtgttgca gggccatttg caggaatagt agcgggtgct 120
atgtcagcag cgattattcc tattgttgtg ggatttacta atccgcaaat gaccgctatc 180
atgacccaat acaatcagag catcgctgaa gccgtaagca tgcctatgaa agctgctaac 240
caacaataca accaattgta tcaaggtttt aacgatcaaa gcatggctgt ggggaacaat 300
atcttaaata tcagcaaatt aacaggggaa tttaacgtgc aaggcaacac gcaaggcgcg 360
caaattagtg ccgttaatag tcagattgca agcattttag cgagtaacac cacccctaaa 420
aatcctagcg ctattgaagc ttatgcgaca aatcaaatcg ctgttcctag tgtgccaaca 480
acggttgaaa tgatgagcgg tatcttaggc aatattacaa gcgcggcacc aaaatacgcc 540
ctagctctac aagagcaatt gcgttctcaa gcaagcaaca gctcaatgaa tgatacagcc 600
gattcccttg atagctgtac cgctttaggt gcacttgttg gctcatcaaa agtgtttttt 660
agttgcatgc aaatttctat gacgcccatg agtgtttcta tgcccactgt ttatgccaaa 720
taccaagcgt tascnactaa tgccctaact tcaggcacta atcctatgac cactcctgca 780
tgccctattg gggacaaagt tcttgccgtt tattgctatg ctgaaaaagt agcagaaatt 840
ttgagggaat actatataga atttgtgaaa aacaatacca atttgttgca aaacgcttct 900
caaatgatac ttaatcaatc aggattagct actagcacct atgacactca agcgatttct 960
aacataagct cgctatataa ttacaatata gtagcgaata aatctttttt gaaatcgcat 1020
ttgacttacc ttgattacat caaaaacaag cttaaggggc aaaaagatag ctacttaaca 1080
gaaagggtgc aaactaaaat aatcgtgaag 1110
"n" can be any base

Seq ID 51
atgaaaacga atttttataa aattaaatta ctatttgctt ggtgtcttat cattggcatg 60
tttaacgctc cgcttaatgc tgaccaaaac acggatataa aagatattag tcctgaagat 120
atggcactaa atagcgtggg gcttgtttct agagatcaac taaaaatага gatccctaaa 180
gaaaccctag aacaaaaagt ggccgtactc aatgactata atgataagaa tgttaatatc 240
aagtttgaca acataagttt agggagtttt caacctaatg ataatctagg tatcaatgcg 300
atgtggggca ttcaaaatct tctcatgagc caaatgatgg gcgattacgg tccaaacaat 360
cctttcatgt atggttatgc accaacatac tcagattcat cattttacc accgatctta 420
gggtat 426

Seq ID 52
gtgtttgtgg caagcaaaca agctgacgaa caaaaaaagc tagtcataga gcaagaggtt 60
caaaagcgcc aatttaaaaa aatagaagaa cttaaagcag acatgcaaaa gggtgtcaat 120
ccctttttta aagtcttgtt tgatgggggg aataggttgt ttggtttccc tgaaactttc 180
atttattcct ctatatttat attgtttgta acaattgtac tatctgttat tctttttcaa 240
gcctatgaac ctgttttgat tgtagcgatt gttattgtgc ttgtagctct tggattcaag 300
aaagattata ggctttatca aagaatggag cgagcgatga aatttaaaaa acctttttg 360
tttaagggcg tgaaaaacaa agcgttcatg agcatttttt ccatgaagcc tagtaaagaa 420
atggctaatg acatccactt aaatccaaac agagaagaca ggcttgtgag cgctgcaaac 480
tcctatctag cgaataacta tgaatgtttt ttagatgatg gggtgatcct tactaacaac 540
tattctcttt taggcacaat caaattgggg ggcattgatt ttttaaccac ttccaaaaaa 600
gatctcatag agttacacgc ttctatttat agcgttttta ggaattttgt taccctgaa 660
ttcaaattct attttcacac tgttaaaaag aaaatcgtta ttgatgaaac caatagggac 720
tatagtctta ttttttctaa tgatttcatg cgagcctata atgagaagca aaagagagaa 780
agtttttatg atattagttt ttatctcacc atagagcaag atttattaga cactctcaat 840
gaacccgtta tgaataaaaa gcattttgca gacaataatt ttgaagagtt tcaaaggatt 900
attagagcca agcttgaaaa cttcaaggat aggatagagc tcatagaaga gctattgagt 960
aaataccacc ccattagatt aaaagaatac actaaagatg gcgttattta ctccaaacaa 1020
tgcgagtttt ataatttcct tgtgggaatg aatgaagccc cttttatttg caacagaaaa 1080
gacttgtatc tcaaggaaaa aatgcatggt ggggtgaaag aagtttattt tgccaataag 1140
catggaaaaa tcttaaatga cgatttgagt gaaaaatatt ttagcgctat tgagattagt 1200
gaatacgccc ctaaatcaca aagcgatttg tttgataaaa tcaacgccct agacagcgaa 1260
tttattttca tgcatgctta ttcgcctaaa aactcacagg ttttaaagga caaactagct 1320
ttcacctcta gaagaattat tattagtgga ggctctaaag agcagggcat gactttaggt 1380
tgcttgagcg aattagtggg taatggtgat attacgctag gcagttatgg taattcttta 1440
gtgttgtttg ctgatagctt tgaaaaaatg aaacaaagcg ttaaggaatg cgtctctagt 1500

cttaacgcta aaggtttttt agccaacgca gcgactttct ctatggaaaa ttacttttc 1560
gccaaacatt gctcttttat cacgcttcct tttatttttg atgtaacttc taataatttt 1620
gctgatttca tcgctatgag ggctatgagt tttgatggca atcaggagaa taacgcttgg 1680
ggcaatagtg tgatgacgct aaaaagcgag atcaattcgc ctttttatct gaacttccac 1740
atgcctactg attttggttc agcttcagca ggacacactt tgatacttgg ctcaaccggt 1800
tcaggtaaga cagtgtttat gtcaatgacc ttgaacgcta tggggcaatt tgttcacaat 1860
tttcctgcta atgtcagcaa agacaagcaa aagctcacta tggtttatat ggataaagat 1920
tatggcgctt atgggaatat tgtcgcaatg ggtggggagt atgtcaagat tgagctaggg 1980
acagatacag gattaaatcc ttttgcttgg gcggcttgtg tgcaaaaaac aaatgcaaca 2040
atggagcaaa aacaaacagc tatttctgtt gtcaaagagc ttgtgaaaaa cttagcaacc 2100
aaaagcgatg aaaaagatga gaatggcaac agcatctctt ttagcctagc agattctaat 2160
acgcttgcag cggcagtaac caaccttatc acaggagata tgaacctaga ttatcccatc 2220
actcaactta ttaatgcttt cgggaaagac cacaatgatc ctaatgggct tgtcgcgcga 2280
ttagcacctt tttgcaaatc aaccaatggt gaatttcaat ggctttttga taataaagca 2340
acggatcgct tagatttttc aaaaacgatt attggcgttg atgggtcaag tttcttagac 2400
aataatgatg tttcgccctt tatttgtttt tacctttcg ctcgtatcca agaggcaatg 2460
gatgggcgta gatttgtctt agatattgat gaagcttgga aatatttagg cgatccaaag 2520
gtcgcttatt ttgtaagaga catgctaaaa actgcaagga aaagaaacgc tattgtcaga 2580
cttgcgactc aaagcatcac tgatcttttg gcttgcccta ttgctgatac gattagagaa 2640
caatgcccta caaagatttt tttgagaaac gatgggggca atctttctga ttaccaaaga 2700
ttggctaatg ttacagaaaa agaatttgaa atcatcacta agggactaga taggaaaatt 2760
ctctacaaac aggatggaag ccctagcgtt atcgctagtt ttaatttgag gggcattcct 2820
aaagaatatt tgaaaatttt atccacagat actgtatttg tcaaagaaat tgacaagatt 2880
atccaaaacc atagtatcat agataaatat caggccttga ggcaaatgta tcaacaaata 2940
aaggagtat 2949

Seq ID 53
ttgatcaata ataatagtaa taaaaaactg agaggctttt ttgtgaaagt tctcttaagt 60
ctcgttgttt tcagttcgta tgggttagca aatgacgata aagaagccaa aaaagaagtg 120
ctagaaaaag aaaaaaacac tcccaatggg cttgtttata cgaatttaga ttttgatagt 180
ttcaaggcga ctatcaaaaa tttgaaagac aagaaagtaa ctttcaaaga agtcaatccc 240
gatattatca aagatgaagt ttttgacttc gtgattgtca atagagtcct taaaaaaata 300
aaggatttga agcattacga tccagttatt gaaaaaatct ttgatgaaaa gggtaaagaa 360
atgggattga atgtggaatt gcagatcaat cctgaagtga aagacttttt tacttttaaa 420
agcatcagca cgaccaacaa acaacgctgc tttctatcgt tgcgcgggga aacaagagaa 480
attttatgcg atgataagct gtataatgtt ttattggccg tattcaattc ttatgaccct 540
aatgatcttt tgaaacatat tagcaccgta gagtctctca aaaaaatctt ttatacgatt 600
acatgtgaag cggtatatct a 621

Seq ID 54
atgactaacg aaactattga tcaaacaaga acaccagatc aaacacaaag ccaaacagct 60
tttgatccgc aacaatttat caataatctt caagtggctt ttattaaagt tgataatgtt 120
gtcgcttcat ttgatcctga tcaaaaacca atcgttgata agaacgatag ggataacagg 180
caagcttttg atggaatctc gcaattaagg gaagaatact ccaataaagc gatcaaaaat 240
cctaccaaaa agaatcagta tttttcagac tttatcgata agagcaatga tttaatcaac 300
aaagacaatc tcattgatgt agaatcttcc acaaagagct ttcagaaatt tggggatcag 360
cgttaccaaa ttttcacaag ttgggtgtcc catcaaaaag atccgtctaa aatcaacacc 420
cgatcgatcc gaaattttat ggaaaatatc atacaacccc ctatccctga tgataaagaa 480
aaagcagagt ttttgaaatc tgccaaacaa tcttttgcag gaatcattat agggaatcaa 540
atccgaacgg atcaaaagtt catgggcgtg tttgatgaat ccttgaaaga aaggcaagaa 600
gcagaaaaaa atggagggcc tactggtggg gattggttgg atatttttct ctcatttata 660
tttaacaaaa aacaatcttc cgatgtcaaa gaagcaatca atcaagaacc agttccccat 720
gtccaaccag atatagccac tactaccacc gacatacaag gcttaccgcc tgaagctagg 780
gatttacttg atgaaagggg taatttttct aaattcactc ttggcgatat ggaaatgtta 840
gatgttgagg gagtcgctga cattgatcct aattacaagt tcaatcaatt attgattcac 900
aataacgctc tgtcttctgt gttaatgggg agtcataatg gcatagaacc tgaaaaagtt 960
tcattattgt atgcgggcaa tggtggtttt ggagacaaac acgattggaa cgccaccgtt 1020
ggttataaag accaacaagg taacaatgtg gctacactca ttaatgtgca tatgaaaaac 1080
ggcagtggct tagtcatagc aggtggtgag aaagggatta ataaccctag tttttatctc 1140
tacaaagaag accaactcac aggctcacaa cgagcattga gtcaagaaga gatccgaaac 1200
aaagtagatt tcatggaatt tcttgcacaa aataatacta aattagacaa cttgagcgag 1260
aaagagaaag aaaaattcca aaatgagatt gaagattttc aaaaagactc taaggcttat 1320
ttagacgccc tagggaatga tcgtattgct tttgtttcta aaaaagacac aaaacattca 1380
gctttaatta ctgagtttaa taatggggat ttgagctaca ctctcaaaga ttatgggaaa 1440
aaagcagata aagctttaga tagggagaaa aatgttactc ttcaaggtag cctaaaacat 1500
gatggcgtga tgtttgttga ttattctaat ttcaaataca ccaacgcctc caagaatccc 1560
aataagggtg taggcgctac gaatggcgtt tcccatttag aagcaggctt taacaaggta 1620
gctgtcttta atttgcctga tttaaataat ctcgctatca ctagtttcgt aaggcggaat 1680

```
ttagagaata aactaaccgc taaaggattg tccctacaag aagctaataa gctcatcaaa  1740
gacttttga gcagcaacaa agaattggct ggaaaagctt taaacttcaa taaagctgta  1800
gctgaagcta aaagcacagg caactatgac gaggtgaaaa aagctcagaa agatcttgaa  1860
aaatccctaa ggaaacgaga gcatttggag aaagaagtag agaaaaaatt ggagagcaaa  1920
agcggcaaca aaaataaaat ggaagcaaaa gctcaagcta acagccaaaa agatgagatt  1980
tttgcgttga tcaataaaga ggctaatagg gatgcaagag caatcgctta cactcaaaat  2040
cttaaaggca tcaaaaggga attgtctgat aaacttgaaa aaatcagcaa ggatttgaaa  2100
gactttagta aatcttttga tgaattcaaa aatggcaaaa ataaggattt cagcaaggca  2160
gaagaaacgc taaaagccct taaaggctcg gtgaaagatt taggtatcaa tccagaatgg  2220
atttcaaaag ttgaaaacct taatgcagct ttgaatgaat tcaaaaatgg caaaaataag  2280
gatttcagca aggtaacgca agcaaaaagc gaccttgaaa attccgttaa agatgtgatc  2340
atcaatcaaa aggtaacgga taaagttgac aatctcaatc aagcggtatc agtggctaaa  2400
gcaatgggcg atttcagtag ggtagagcaa gtgttagccg atctcaaaaa cttctcaaag  2460
gagcaattgg ctcaacaagc tcaaaaaaat gaagatttca atactggaaa aaattctgaa  2520
ctataccaat ccgttaagaa tagtgtaaat aaaaccctag tcggtaatgg gttatctgga  2580
atagaggcca cagctctcgc caaaaatttt tcggatatca agaaagaatt gaatgagaaa  2640
tttaaaaatt tcaataacaa taataatgga ctcaaaaaca gcacagaacc catttatgct  2700
aaagttaata aaaagaaaac aggacaagta gctagccctg aagaacccat ttatactcaa  2760
gttgctaaaa aggtaaatgc aaaaattgac cgactcaatc aaatagcaag tggtttgggt  2820
ggtgtagggc aagcagcggg cttccctttg aaaaggcatg ataaagttga tgatctcagt  2880
aaggtagggc tttcagctag ccctgaaccc atttacgcta cgattgatga tctcggcgga  2940
cctttccctt tgaaaaggca tgataaagtt gatgatctca gtaaggtagg gcgatcaagg  3000
aatcaagaat tggctcagaa aattgacaat ctcaatcaag cggtatcaga agctaaagca  3060
ggtttttttg gcaacctaga gcaaacgata gacaagctca aagattctac aaaaaagaat  3120
gttatgaatc tatatgttga aagtgcaaaa aaagtgcctg ctagtttgtc agcgaaattg  3180
gacaattatg ctattaacag ccacacacgc attaatagca atatccaaaa tggagcaatc  3240
aatgaaaaag cgaccggtat gctaacgcaa aaaaaccctg agtggcttaa gctcgtgaat  3300
gataagatag ttgcgcataa tgtgggaagc gtttctttgt cagagtatga taaaattggc  3360
ttcaaccaga agaatatgaa agattattct gattcgttca agttttccac caagttgaac  3420
aatgctgtaa aagacattaa gtctggcttt acgcactttt tagccaatgc attttctaca  3480
ggatattact gcttggcgag ggaaaatgcg gagcatggaa tcaaaaatgt taatacaaaa  3540
ggtggtttcc aaaaatct                                               3558
```

Seq ID 55

```
gtggcaataa acacctttt aaaacattct tttttagtct gtttgttagc ggttaattct    60
tacgcttttg attggaacat ttttaaatac aatctgggtt tcaatatgtt catcatggac   120
catgaaggct caacgcctta ttgggtcaat actaacacca atcttaaaac ccgtttgact   180
ccaaattttg ggatccaatt ttatacaaga ggtgtggagc aaagcttgac tgtgggggcg   240
tatttttttc aaaacttcca taactacagc actaattttc cctaccgttg ggggcctact   300
atgtattata aggctagagg gaagcgtttt actttttatg gagggatttt ccctaggaaa   360
aacctcttag gaaggtatgg tttgaatatt tttgcccctt attattggtt tatagatcca   420
aacgctagag ggtttttatt gcaatttcaa aaccattatt cgccttcaaa accctattat   480
gggcatgcgg agttcatgct agattggttt ggaggcaatt gttacaacac ttgtaagttt   540
gggagaaacc cttatgggaa cgcaatggac aggtttcaaa tgaacggctc tgtcgcttat   600
aatttcttta aggatttatt gggtattgga gggtattttg tcttgttcca taacgaagac   660
aaataccttt taaatggggc tgatggcatg cagtttaatg aaaaaaaagc gattgataac   720
agtgcgattt atttactgga tcgcctttat tataatgctt acattagcac aagcctttta   780
gacatcgccc cctttatgga aaaactcagc gctaaatttg gcatggtttc tgaagcgagc   840
cgattgagaa acagagagaa agaagtgccc tttatcaata gcgtgggcgg gcaatttgat   900
gtggagatcc aatacaaagg ctttggcatc cacaatttat ttttcttcgc caagacccca   960
gagatgcctt tttataacca ataccagtat gttgaaatgt attgcacgcc ttcgtattgc  1020
cccacgccta tttatcgtgg cgtgccattc tttcaagcga acatgtataa ccgttttgat  1080
ttctattaca actggaaaaa cgacttcgca tcggtccgca tcaatttcgt gcttaatgcg  1140
atgcgtgggg gctttgatag gagcttgcct tggtcagaat cttaccaagt gtatatgacg  1200
gttgcttttg atccttataa ccttattaac aaaattgcca gaaaaaag               1248
```

Seq ID 56

```
atgatgattt tcattgatgc atgttttaga aaggaaacgc cttacacgcc catttggatg    60
atgaggcaag cggggcgtta ccttagcgaa taccaagaga gccgtaaaaa agcggggagt   120
ttcttggaat tgtgtaaaaa tagcgatcta gccacagaag ttaccttaca gccggtagag   180
attttaggcg tggatgcggc tattttgttt agcgatattt tagtagtgcc tttggaaatg   240
ggcttgaatt tggagtttat ccccaaaaag gggccgcatt ttttagagac gattacggat   300
ttaaaaagcg tggaaagcct aaaagtaggg gcttataaac aactaaacta tgtctatgat   360
acgatttctc aaacgcgcca aaagctttct agagagaaag cgttaatcgg tttttgcgga   420
tcgccttgga ctttagcgac ttacatgata gaaggcgagg ggagcaaatc gtatgccaaa   480
agcaagaaaa tgctttatag cgagcctgaa gttttaaaag cgcttttaga aaaattaagc   540
cttgaattga tagagtattt gagccttcaa atccaagcag gggtcaatgc agtgatgatc   600
tttgactcat gggctagcgc tttagaaaaa gaagcgtatt tgaaattcag ttgggattat   660
```

ttgaaaaaaa tctctaaaga gcttaaaaaa cgctatgcgc atatcccagt tatccttttc 720
cctaaaggga ttggcgctta tttggatagc atagatgggg aatttgatgt gtttggcgtg 780
gattggggca cgcctttaac tgcggcaaaa aagattttag gcggtaagta tgttttgcaa 840
gggaatttag aacccacccg cctttatgat aaaaacgctt tagaagaagg ggttgaaacg 900
attctaaaag tcatgggcaa tcaagggcat atttttaatt tagggcatgg gatgttgccg 960
gatttaccca gagaaaacgc caaatattta gtgcaattag tgcatgctaa aaccagacga 1020

Seq ID 57
atgtataaaa cagcgattaa tcgtcctatt acgaccttaa tgtttgcttt ggcgattgtc 60
ttttttggga ctatggggtt taaaaaattg agcgtggcgc ttttccctaa aattgatttg 120
cctacggtgg tggttactac gacttatcct ggggctagcg ctgaaatcat agagagtaag 180
gtaaccgata agattgaaga agcggtgatg gggattgatg ggatcaaaaa ggttacttcc 240
acgagttcta aaaatgtgag tatcgtcgtc attgaatttg agttagaaaa acctaatgaa 300
gaagccttaa acgatgtggt gaataaaatt tcttcggtgc gttttgatga ctctaacatt 360
aaaaaaccct ctatcaataa atttgatacc gacagccaag ccattatttc attgtttgtg 420
agcagttcaa gcgtgccggc tacaaccctt aatgactacg ctaaaaacac catcaaaccc 480
atgctccaaa aaatcaatgg ggtaggggge gtgcagctca acggctttag ggagcgccag 540
attaggattt atgcaaatcc cactttgatg aataaataca acctgactta tgcggatctt 600
ttcagcacgc ttaaagcgga gaatgtggaa attgatgggg ggcgcattgt caatagccaa 660
agggaatttt ctattttaat caatgcgaat agttatagcg ttgcggatgt ggaaaagatt 720
caagtgggta atcatgtgcg tcttggcgat attgcaaaaa ttgaaatcgg tttggaagaa 780
gacaacactt ttgcgagctt taaagacaaa cccggtgtga ttttagaaat ccaaaagatt 840
gccggagcga atgaaattga aatcgtagat agggtgtatg aagctttaaa gcgcattcaa 900
gccattagcc ctaactatga aatcagaccc tttttagaca ccacgggcta tatccgcacc 960
tctattgaag acgtgaaatt tgatctagtt ttaggggcga ttttagcggt tttagtggtg 1020
tttgcgttct tgcgtaacgg cacgatcacc ctcgtttcag cgatctctat ccctatttct 1080
atcatgggga cttttgcgct catccaatgg atgggctttt cattaaacat gctcaccatg 1140
gtggctttaa cgttggcgat agggattatc attgatgatg cgatcgtggt gattgaaaac 1200
atccataaaa agctagaaat gggcatgagt aaacgaaaag cgagctatga gggggtgaga 1260
gaaattggct ttgctctagt ggcgatttca gcgatgctgc tctctgtttt tgtgcctata 1320
gggaacatga aaggcattat tgggcgtttt tttcaaagtt ttgggatcac ggtggcttta 1380
gcgatcgctc tatcgtatgt ggtggtcgtt acgattatcc ccatggtaag ctcagtcgtg 1440
gtcaatccca ggcattctcg tttttatgtg tggagtgagc ctttttttaa ggctttagag 1500
tctcgttata ccaagttgct ccaatgggta ttaaaccaca agatcattat ctctatagcg 1560
gtggttttgg tgtttgtggg atcgcttttt gtggcttcta agattggtat ggagttcatg 1620
ctgaaagaag atagggggag gtttttggtg tggcttaagg ctaaaccggg cgtgagcata 1680
gattacatga cacaaaagag taagatcttt caaaaagcga ttgaaaaaca tgctgaagtg 1740
gaattcacca ccttgcaagt gggttatggc accacacaaa acccttttaa ggctaagatt 1800
tttgtgcaac tcaagccttt aaaagagcgt aaaaaagagc atcaattggg gcaatttgag 1860
ttgatgagcg ttttaaggaa agagttgaga agcttgcctg aagctaaagg tttagatact 1920
attaatcttt ctgaagttac tcttataggg ggcggtgggg atagttcgcc cttccaaacc 1980
tttgtgtttt cccattctca agaagcggtg gataaaagcg tggagaattt gaaaaaattc 2040
ttattagaaa gccctgaatt aaaaggcaag gttgaaagct atcatacaag cacgagcgaa 2100
tcgcaaccgc aattgcaact caaaatctta agacaaaacg ctaacaaata cggcgtgagc 2160
gctcaaacca ttggatcagt ggtgagctct gctttttctg ggacttctca agcgagcgtg 2220
ttcaaagaag atggcaaaga atacgacatg atcattagag tgcctgatga caagcgcgtt 2280
tctgtagaag acatcaaacg cttgcaagtg cgtaacaaat acgataaatt gatgtttttа 2340
gacgctttag tggaaatcac agaaactaaa agcccgtcca gtatttctcg ctataaccgc 2400
caacgcagcg ttacggtgct tgctgagcct aataggaatg cgggcgtttc tttaggcgag 2460
attttaacgc aagtgagcaa aaacactaaa gaatggttgg ttgaaggggc gaattacaga 2520
tttaccggag aagcggataa cgccaaagag agcaacgggg agtttttagt cgctttagcg 2580
acagcgtttg tgctgattta tatgatttta gcggcgttgt atgagtccat tttagagcct 2640
tttatcatca tggttaccat gcctttaagt ttttcagggg cgttttttgc tctaggttta 2700
gtccatcagc ctttgagcat gttctctatg ataggcttga ttttgctcat tggtatggtg 2760
ggtaaaaacg ccacgctttt aattgatgtg gcgaatgaag agcgtaaaaa aggtttgaat 2820
atccaagagg ccatttttatt tgccggcaaa acccgtctaa gaccgatttt aatgacgacc 2880
attgcgatgg tttgcgggat gctgccttta gcgttggcga gtggggatgg agcggcgatg 2940
aaatccccta tagggattgc gatgagtggg ggcttgatga tttctatggt gttaagctta 3000
ctcattgtgc cggtgtttta tcgtttgctc gctcccatag acgacaaaat caagcggttt 3060
tatcaaaacc aaaaaacttt agaa 3084

Seq ID 58
atgaaaaaag tactcatcat taacggggcc aaagcgttcg ggagctctgg agggaaactc 60
aatgaaacct tgactgacca tgcaaaaaag actctagagt ctttggggct agaagtggat 120
actacgatcg tggataaagg ctatgaacat gctcaagaag tggagaaagt ctttagcgct 180
gatgcgacga tttggcaaat gcctggctgg tggatgggag agccttggat tgtgaaaaaa 240
tacattgatg aagtctttag cgtagggcat ggaaagcttt atgctagcga tggcagaagc 300
tcgcaaaacc ccactaaaaa ctacgggaaa gggggcttga tgcaaggcaa aaaatacatg 360

ttgagcttga cttggaacgc tcccattgaa gcctttaatg atcctagtga atttttgaa 420
ggggtgggtg tggatgttgt gtatttgcat ttgcataaag cgttccaatt tttagggctt 480
tcagcgttgc ccacttttat ttgcaacgat gtggtgaaaa acccccaagt ggagcagtat 540
cttaactctc tcaccacgca tttgcgccaa gcttttggca ag 582

Seq ID 59
ttggtttttg tttttctttt taaatgcgtt aatgaagaaa caagcctgaa ttttacgccc 60
cttttagagc gaatggcatg caatttgcaa gcgcgttttt atagcgttta taaggataat 120
accacttctt tctacctcca agcgagcgct gaaaccactt tagagttcgc gcaaaaactc 180
agcgaaattc tgccctttcc tttagatttt agctttttgt ctttaaagga aatcacagag 240
cctttagatg aaaatctttt ccaaacagca agcctttcaa agccccttt tatgaacgct 300
aaagagcatc aagatttttt agacaaaaat tcatctttgt atgccgatac tctgggcttg 360
attaaaaaca ccgcttttaa gggggatata atccatagcc ctaaagagct tatagattgc 420
ttaacccaat taaaaggcat gctcaaaacg caagatttta tccctatttt cacttctaga 480
gaggcgttat ccctttcttt aaaaaatccc tctccaagcg ttatttttag cgatctttct 540
agcgttttga gctgcactaa attgccttta gaggacgcta aatatttggc cagtttggaa 600
aaaccctcca tcaaagcccc attaaaaagc gtgtttaaag acactttcaa aaacgatgaa 660
atcatcgccc agctacccta tgaccccata ttgaatttat tgtgccatat tttacaagat 720
gaggggatag aatttgtttt tatgcatgaa agccgttctt gtgaagcgct tttgtattat 780
gaagcgcttt ttaaaacccc taaacgcttg atcacaccca ctaaaaaatt cgtgctagaa 840
aataattttt ctacctttcc ctttaaagat gaattagagt ttttaagcgc aacccccaat 900
tctatcgttt tgtatctcag tttcaagcgc cctacaaggt tgttattgca tgctaatggt 960
tctttaaaaa cgcttttaag cgtcagtttt gattttaaca aaatgtttaa cgcgctcaaa 1020
caagatgaaa aagcctccag aatgctacaa aactacgcca ctaaattccc tgatttttac 1080
gcgcgcattg tagagctttc taaatacgat ctaggggcg cgaatttatt ggatttttt 1140
tgcattttag ggtttgtttt gggctatagc gaggattttt gcacacagag cgttattcct 1200
ttggctaaag aatgcttacg ccctaaaggc cctaggattg attataaaat ccttaaagac 1260
aattctttga aaatggcttt aaacttttca aagatcatgc acagtgcgat gagtttcagg 1320
ctcgcaggcg tggaaaatga aattttgagt ttggggattt tggattcttt agcggagttt 1380
ttagggaatt tcatttggga taacgcgcaa aattttagcg ttcaagaagt aacgatcgct 1440
ggggatttct ttggcgaaaa agtgtttttg gatttgtttg tgcggtattt ccctaaaacc 1500
ctagcccttа aaacgcatgc atttttggat tatgaa 1536

Seq ID 60
attaaaaaat taattctatc ctctcttgtt ttcgcatgta tcaataccag cgttgaagct 60
ttagaaaatg acggctctaa accaaacgat ttgacttctc caaaagaagc ctctcaagaa 120
tctcaaaaaa atgaagctcc aaaaaatgaa gttcaaagaa atgaagctca aaaagaaacc 180
ccccaatcca atcaaacgcc taaagaaatg aaagtcaagt ccatttctta tgtcgggctt 240
tcttacatgt ctgacatgct cgctaatgaa attgtaaaga ttcgtgtggg cgatattgtg 300
gattctaaaa aaatagacac cgctgttttg gctttgttca atcaagggta ttttaaagac 360
gtttatgcca cttttgaagg cggcatatta gagtttcatt ttgatgaaaa agccaggatt 420
gccggggtag aaatcaaggg ttatgggact gaaaaggaaa aagacggctt aaaatcccaa 480
atggggatca aaaagggcga caccttgat gagcaaaaat tagagcatgc taaaacggct 540
ttaaaaaccg ctttagaggg gcagggctat tatgggagcg tggtggaggt gcgcacagaa 600
aaggtcagtg agggtgcatt attgatcgtg tttgatgtga atagggggga tagcatttat 660
atcaaacaat ccatttatga gggaagcgcg aaattaaaac gccgcatgat tgaatctttg 720
agtgcgaaca agcaacgaga tttcatgggc tggatgtggg gcttgaatga cgggaaattg 780
cgtttagatc aactagaata cgattctatg cgtatccaag atgtgtatat gcgtaggggt 840
tacttagacg ctcatatttc ttcgcctttt ttgaaaacgg atttttctac ccatgacgct 900
aagcttcatt ataaagtcaa agaggggatc caatacagga tttcagacat tttaatagag 960
attgacaacc cggtagtccc cttaaaaacc ttagaaaaag cgcttaaagt gaaaaggaaa 1020
gatgtcttta atattgagca tttaagagcg gatgcgcaaa ttttaaaaac cgaaatcgcc 1080
gataagggtt atgcgtttgc ggtggtgaag ccagacttgg ataaagatga aaaaaacggg 1140
cttgtgaaag tcatttatcg tattgaagtg ggcgatatgg tgtatatcaa tgatgtcatc 1200
atttcaggga accagcgcac gagcgatagg atcattagaa gggagttatt gttagggcct 1260
aaggataaat acaacttgac caaactgaga aattccgaaa attctttaag gcgtttagga 1320
ttcttctcta aagtcaaaat tgaagaaaaa agggttaata gctcactcat ggatttatta 1380
gtgagcgtag aagaggggcg tactgggcag ttgcaatttg ggttaggcta tggctcttat 1440
ggagggctta tgcttaatgg gagcgtgagc gaaagaaacc tttttggcac agggcaaagc 1500
atgagcttgt atgctaacat cgctacaggg gggggtagat cttatccggg catgccaaaa 1560
ggagcggggc gtatgtttgc cgggaatttg agcttgacta atccaaggat ttttgacagc 1620
tggtatagct ctacgatcaa cctttatgcg gattacagga taagctacca atacatccaa 1680
caaggcgggg gctttggggt gaatgtcggg cgcatgctgg gtaatagaac ccatgtgagc 1740
ttagggtata acttgaatgt taccaaactc cttggtttca gcagcccttt atacaaccgc 1800
tactattcct ctgttaatga agtggtttct ccaaggcaat gttctacccc cgcatcggtg 1860
attatcaatc gcttatcagg cggtaaaacc cccttacaac ctgaaagctg ttctagtcct 1920
ggagcgatca ccacttcacc agaaataaga ggtatttggg atagggatta ccatacgcct 1980
atcaccagct ctttcaccct tgatgtgagc tatgacaaca ccgatgatta ttacttccct 2040

agaaatgggg ttatctttag ttcctatgcg acgatgtctg gcttgccaag ctctggcacg 2100
ctcaattctt ggaacgggtt aggcgggaat gtccgtaaca ccaaagttta tggtaaattc 2160
gccgcttacc accatttgca aaaatattta ttgatagatt tgatcgctcg ctttaaaacg 2220
caaggaggtt atatctttag gtataacacc gatgattact tgcccttaaa ctccaccttc 2280
tacatggggg gcgtaaccac ggtgagaggc tttaggaacg gatcggttac tcctaaagat 2340
gagtttggct tgtggcttgg aggcgatggg atttttaccg cttctactga attgagctat 2400
ggggtgctaa aggcggctaa aatgcgctta gcgtggtttt ttgactttgg tttcttaacc 2460
tttaaaaccc caactagagg gagtttttc tataacgctc ctgttacgac agcgaatttt 2520
aaagattatg gcgttatagg ggctgggttt gaaagagcga cttggagggc ttccacaggc 2580
ttgcagattg aatggatttc gcccatgggg cctttggtgt tgattttccc tatagcgttt 2640
ttcaaccaat ggggcgatgg caatggcaag aaatgtaaag ggctatgctt caaccctaac 2700
atggacgatt acacgcaaca ctttgaattt tctatgggaa caaggttt 2748

Seq ID 61
atgaggaaaa ttttttctta tgttttgaag gctttgttgt ttattgggat tgtttatgca 60
gagccggaat ctaaagtgga agccttagaa gggaggaagc aagagtcttc tttggataaa 120
aaaatccgcc aagaattgaa gaataaggat ttgaaaaata aagaattgaa aaataaaaaa 180
gaagaaaaga aaaacaccga agaaaagaaa gaaacaaaag ccaagagaaa gcccagggca 240
gaagtccatc atggggatac caaaaatccc actcaaaaaa taacgcctcc taaaatcaaa 300
gagaacgcta aaggagttca aaatcaaggc gttcaaagca acgcgccaaa acttgaagaa 360
aaagacacaa cctctcaaac tcttgaaaaa aagggagcaa gccctagctc tcaattcaat 420
tccatttttg gtaatcctaa tgacgctgct aacaataccc ttgaagataa ggtcgtaggg 480
ggcatttctt tgcttgttaa tggttcgcct atcacgctgt atcaaatcca agaagagcaa 540
gaaaaatcta aagtgagcaa agctcaagca agggatcgtt tgatcgctga acgcattaaa 600
aaccaagaaa ttgagcgctt aaaaatccat gtagatgacg acaagctaga ccaagaaatg 660
gcgatgatgg cgcaacaaca aggcatggat ttggatcatt tcaaacaaat gcttatggct 720
gagggacatt ataaactcta tagggatcag cttaaggagc atttggaaat gcaagaattg 780
ttgcgtaata tcttactcac gaatgtggat accagctctg aaactaaaat gcgcgaatat 840
tacaacaaac acaaggagca attcagtatc cccactgaaa tagaaaccgt gcgctacact 900
tccaccaatc aagaggattt agaaagggcg atggcggatc ctaatttgga aattccaggg 960
gtgagtaagg ctaatgaaaa aatagagatg aaaaccttaa accctcaaat cgctcaagtc 1020
tttatttcgc atgagcaagg ctcttttacg cccgttatga atgggggtgg ggggcagttc 1080
atcacctttt atatcaagga aaaaaagggt aaaaacgaag tgagcttcag tcaggccaag 1140
caattcatcg cccaaaaatt agtggaagaa tctaaagata agattttaga agagcatttt 1200
gaaaaattgc gcgttaagtc taggattgtg atgattagag ag 1242

Seq ID 62
atgctttctg tcatcatact ggccgctggt aaaggcactc gcatgcgttc tagcctgcct 60
aaaactttac acaccatttg tggggagcct atgttgtttt acattttaga aacggctttt 120
tcaatcagcg atgatgtgca tcttatctta caccaccaac aagaacgcat taaagaagcg 180
gtgttggagc gttttaaggg cgtcattttt cacactcaaa ttgtggaaaa atattcaggg 240
acaggtgggg ctatcatgca aaaagataaa acgcctattt ctacgaaaca tgagcgggtt 300
ttgattttga atgcggacat gcctttaatc actaaagacg ctctcgcccc cttattagaa 360
agcaagaata acgctatagg cttactccat ttagctgacc ctaaaggtta tgggcgcgtt 420
gttttagaaa accatcaggt taaaaagatt gtagaagaaa aggacgctaa tgatgaagaa 480
aaagaaatta aaagcgtgaa tgctggcgtg tatgggtttg aaagggattt tttagaaaaa 540
tacttaccca agctccatga ccaaaacgcc caaaaagaat actacctcac ggatttaatc 600
gctctaggga tcaatgaaaa cgaaacaatt gacgctattt tcttaaaaga agagtgtttt 660
ttaggggtga atagccaaac agaaagggcg aaagctgaag aaatcatgct agaaagactg 720
cgcaaaaacg ccatggactt gggggtagtg atgcaattgc ctaatagcat ttatttagaa 780
aaaggcgtga gttttaaggg ggagtgcgtt ttagagcaag gggtgcgttt gattgggaat 840
tgtttgatag aaaacgcgca tattaaggct tatagcgtga tagaagagag ccagattgtt 900
aatagcagtg tggggccgtt tgcccatgcg cgccctaaaa gcgtgatttg taatagccat 960
gtggggaatt ttgtagagac taaaaacgct aaacttcaag gcactaaagc agggcatttg 1020
agctatttag gggattgtga gatagggaaa aacacaaatg taggggctgg cgtgatcact 1080
tgcaattacg atggtaaaaa gaaacaccaa acaatcatcg gtgaaaatgt ctttataggg 1140
agcgatagcc agctagtcgc ccccataaat atcggctcta atgtcttaat cggcagcggc 1200
accactatca ctaaagacat tcctagcggt tcgttgagcc tttcacgcgc ccctcaaacc 1260
aacattgaaa acgggtattt taagtttttt aagaaacct 1299

Seq ID 63
atgaaagaaa tcactatcgc ccttgtgggc cagcctaatg tggggaaatc gtccttaatc 60
aacgctttga gcaacgccca tttgaaagtg gggaattttg ccggggttac cgtggataaa 120
atggaagtgg gtttgatcca caaagagcat caaatcacta tcattgattt acctggcact 180
tacgcgctca atgacttcac cactgaagaa aaggttacta aagatttttt agaaaaaggg 240
caatacgatc tcattcttaa tgtggtggat tccaccaatt tagagcgtaa tttagcctta 300
agcgcgcagc tattagacac gaataaaaaa atgctactcg cactcaacat gtgggatgag 360
gcacaaaaag agggcattaa aatcaataca gaaaagcttt ctaaagaatt aggggttgtg 420

tgcgtgccaa caagtgcaag atccaaagaa gatcgcttga ataccgagct tttattagac 480
gaaattgtca ggctttattc tcaaaatact acaaataatg aaaacataaa agtcccgtct 540
caaagcttta aggagtcttt aaaatacagc cagagcgctc aaagaatcgc tcaattagtg 600
atcagtgaaa accaacaaaa cgcgagtttt gaacacactt ataagattga taagatttta 660
atgcacaagc gttatgggat tttcattttt ttagggttta tgtttatcat tttttccttg 720
agcttttaa taggggggg agtgcaaaaa gcgcttgaaa cagggtttaa atttttaagc 780
gatggcatca aagaaaatgt ggctaatgaa gatttagcgt ctttggtggg cgatggcatt 840
attgggggag tgggagcgac ggtttcattc ttgcctttaa ttgtggtgtt gtattttggg 900
atttctttac tagagacgac aggctatatg agtagggtag cgtttttgtt agatgggatc 960
ttgcataaat ttggcttaca tgggaagagt tttatccctt taatcaccgg ttttggctgc 1020
tcagtgcccg cttacatggc gacaagaacc ttacaaaact ataacgaacg actgatcacg 1080
ctttttgtga tcgggtttat gagctgctcg gcaaggctgc ctatttatgt gctgtttgta 1140
ggctcgtttt tcccttcttc aagtgctggg tttgtgctgt tttgcattta tattttgggg 1200
gcggttgtgg cgttagtgat ggccaaatta ctcaaattaa gcgtgtttaa aggacaaacc 1260
gaatctttta tcatggaaat gcccaaatac cgctttccca gttggagaat ggtctatttc 1320
agtatctaca ccaaatcgct ttcttacctt aaaaaggctg ggacttacat tttagtggga 1380
gcgattttaa tctggtttat gtctcaatac cctaaaagcg atgcggccat gaaagcttat 1440
aaacaagaaa gcttgttagt gaataaggat accactcttt caagcgaagc taaagaagaa 1500
aaattaaaag aattaaaaac agaattggat aaaaagaatt taaaaaatag cattgtagga 1560
agaggcgggg cgtatttaga aaaagtcttt agccctatgg attttgattg gcgtttgagt 1620
gtgtcgcttg taaccggatt tatggctaaa gaggtggtgg tttctacttt gggcgtgttg 1680
ttttctttag gggatcaaaa tgaaaaatct gacgctttta gagggatttt aagaaaagaa 1740
gtcagcgtgc ctagcggaat cgcttttatc gtgtttgtga tgttttatat cccttgtttt 1800
gcagcgacca ttacttttgg tagggaagcg ggagggataa agtttgtagc gtatttattc 1860
atcttcacaa ccgttgtagc gtatgcgttt tccttgatag ctttttatgc gactcaaatt 1920
ttggtt 1926

Seq ID 64
atggcaaatt tattgaaaaa cggcaaaact ttaaaacaag ctagagatga aatcctagcc 60
aggacagaaa aaacagggca ttataatggt ctcaaaaaac tagagtttaa agaaagagat 120
ccgattggtt atgagaagat gttctctaaa ttaagaggcg gtatcgtgca tgccagagaa 180
acggctaaaa ggattgcggc aagccctatt gttgagcaag agggagaatt gtgcttcacg 240
ctttataacg ctgtgggcga tagcgtgctg acttctacag gtatcattat ccatgtaggg 300
actatgggat cagctatcaa atacatggta gagaataatt gggaagataa cccaggcatc 360
aatgacaagg atattttcac caataacgac tgcgcgattg ggaatgtgca cccatgcgat 420
attatgactc ttgtgcctat tttccacgat gaaaaattga ttgggtgggt aggcggcgtt 480
acgcatgtga ttgataccgg ttcggttact ccaggatcga tgagcactgg acaggttcaa 540
agatttgggg atggatacat gatcacttgc cgtaagacag gagcgaatga tgaaagcttt 600
aaagattggt tgcatgaatc tcaaagatcg gttcgcacgc ctaaatattg gattctagat 660
gaaaggacta ggattgcagg atgccatatg attagggatt tagtgatgga agtcattaaa 720
gaagacggca ttgattctta catgcgattt attgatgagg tgattgaaga ggggagaaga 780
ggccttatct ctaggattaa atccatgacc ataccaggca agtatagaaa ggtagcgttt 840
gtggatgtgc cttatgcgca taaggatatt ggcgtgtgct ctgagtttgc taagctagac 900
acgatcatgc actctcctgt ggaaatcact atcaataaag acgctacatg gaaattggat 960
tttgatggcg cgtctaggtg gggatggcac tctttcaatt gcaaccaagt gtcttttact 1020
agcggtattt gggtgatgat gactcaaacg ctgataccca cttctcgcat caacgatggc 1080
gcttattttg cgactcaatt cagactcaaa aaagggactt ggatgaatcc agatgacagg 1140
cgcaccgggc atgcttatgc gtggcacttc ttggtatcag gctggagcgc tttgtggaga 1200
ggcttgtctc aagcgtatta cagccgaggg tatttagaag aggtcaattc cgggaacgct 1260
aacacttcca attggctgca aggtggcggt atcaaccaag atggagaaat ccatgcggtg 1320
aatagctttg agacgagttc ttgtgggact ggagcttgtg cgataaaaga cggcttaaat 1380
cacgcagcgg ctatttggaa cccagagggc gatatgggcg atgttgaaat ttgggaaatg 1440
gcagagcctc ttctttattt aggcaggaat gtcaaagcca ataccggtgg gtatgggaaa 1500
tatcgaggcg gtaacgggtt tgaaacctta agaatggtgt ggggtgcgca tgattggacc 1560
atgttcttta tgggtaatgg ctatatgaat agcgattggg gtatgatggg aggctatcca 1620
gcggctagtg gttataggtt tgaagcgcac aacaccgatt tgaaaaacag gattaaaaat 1680
aacgccagct tgcctttggg gggcgatttt aacccaactg atcgcgatta tgaaaagcac 1740
atttctcatg cgtctcaagt caaaagggat aagcaatgca tcaccactga aaactgcttt 1800
gacaattacg acttgtattt gaattacatc aaaggcggtc ctggatttgg cgatccgatt 1860
gaaagggatt tgaatgcgat tttagaagat ctcaacagca aacagctatt gccagaatac 1920
gcttacaagg tttatggcgc agtggtgagt caaaataaag acggcgtgtg ggtcggcgat 1980
gaagccaaaa cgaaagccag aagaaaagaa attcttgaaa acagaaaggc tagatccata 2040
ccggtaaaac aatggatgga gcaagaaaga aacgctatcc ttgaaaaaga ggcttccaaa 2100
caggttaagc acatgtatgc gactagcttt gatctctcgc ctaagttttt gaatgatttt 2160
aaaacattct ggaacttgcc aaagaattgg agcgtgaaag aagatgagct tggcgtattc 2220
acctatggat ctaaatacag gatggatttg agcaaattgc ctgatgtgcg cacagttctg 2280
ttggttgatg agaaa 2295

Seq ID 65

```
atgcaagata attcagtcaa tgaaacaaaa aatattgtag aagtggggat tgattcttct     60
attgaagaga gctatttagc ttattccatg agcgtgatca tagggcgcgc tttaccggac    120
gctagagatg gcttaaagcc cgtgcatagg cgtattttgt atgcgatgca tgaattaggc    180
cttacttcaa aagtcgctta caaaaaaagc gctaggatcg tgggtgatgt gattggtaaa    240
taccaccccc atggcgataa tgcggtttat gatgcgctag tgagaatggc gcaagatttt    300
tccatgcgtt tggaattagt ggatgggcag ggcaactttg gctctattga tggcgataac    360
gccgcagcga tgcgttacac tgaagccaga atgactaagg cgagtgaaga aattttaagg    420
gatattgata aagacaccat tgattttgtg cctaattatg acgatacctt aaaagagcca    480
gatattttac caagccgtct gcctaacctt ttagtcaatg gggctaatgg gatcgctgtg    540
gggatggcga cttctatccc ccctcacagg atggatgaaa tcatagacgc tttagtgcat    600
gtcttagaaa accctaacgc tggattagat gaaatcttag aatttgtcaa agggcctgat    660
tttcccactg gtgggatcat ttatggcaag gcgggtatta ttgaagccta taaaacgggg    720
cgaggacgcg tgaaagtgcg ggccaaagtg catgtggaaa aaacaaaaaa taaagaaatc    780
atcgttttag atgaaatgcc ttttcaaacc aataaagcca aattagtgga acaaatcagc    840
gatttagcgc gagaaaagca aattgaaggc attagtgaag tgcgcgatga gagcgataga    900
gagggcatta gagtggtgat tgaattaaaa agagacgcga tgagtgaaat tgtcttaaac    960
cacctctaca aactcaccac tatggaaacc acttttagca tcattttact cgctatttac   1020
aataaagagc ctaagatttt cacgctttta gagttgttgc acctttttctt aaaccacaga   1080
aaaaccatta ttataagacg cacgattttt gaattagaaa aggctaaggc cagagcgcat   1140
attttagagg gctatttgat cgcactagac aatattgatg aaatcgtgcg actcattaaa   1200
acaagccaaa gcccagaagc ggctaaaaac gccttaatgg agcgtttcac tttgagcgag   1260
attcaaagca aggccatttt agaaatgcgt ttgcaacgct taacaggcct tgaaagggat   1320
aagatcaaag aagaatacca aaacttgttg gagcttattg atgatctcaa tggcatttta   1380
aagagcgaag atcgcttgaa tggagtcgtc aaaacagagc ttttagaagt caaagagcaa   1440
ttttcttctc caaggcgcac tgaaattcaa gaatcttatg aaaatattga catagaagat   1500
ttgatcgcta atgagcctat ggtagtgagc atgagttata aaggctatgt gaaaagagtg   1560
gatttaaaag cttatgaaaa gcaaaatcgt ggtggtaaag gcaagctttc aggcagcact   1620
tatgaagacg atttcattga aaacttttttt gtggctaaca cgcatgatat tttgctcttt   1680
atcaccaata aggggcaatt gtatcatttg aaagtctata aaatcccaga agcgagccgg   1740
atcgctatgg gtaaagccat tgtaaattta atctcgctcg ctccggatga aaagatcatg   1800
gcgactctaa gcaccaaaga ctttagcgat gaacgctctt tggccttctt cacgaaaaat   1860
ggcgtggtga agcgcaccaa tttgagcgaa tttgaaagca acaggagttg tggtatcaga   1920
gcgattgttt tagatgaagg cgatgaatta gtgagcgcaa aagttgtgga taaaaacgct   1980
aagcatttgc tcatcgcatc gcatttgggc attttcatta aattcccttt agaagaggtg   2040
cgcgagatcg gaagaactac tcgtggggtt ataggcatca agctgaatga aaacgatttt   2100
gttgtcggtg cggtcgttat tagcgatgat ggcaacaagc ttttgagcgt gagtgaaaac   2160
gggcttggca agcaaacttt agccgaagcg tatagagggc aatctcgtgg aggtaagggg   2220
gtcattggca tgaagctcac tcaaaaaacc ggcaatctag tgggcgttat cagcgtggat   2280
gatgaaaatt tggatttgat gatccttact gcaagcgcaa aaatgatcag agtttctatt   2340
aaagatatta gagaaaccgg aagaaacgct agtggggtaa agctcataaa caccgccgat   2400
aaagtcatgt atgtcaattc ttgccctaaa gaagaagagc cagaaaattt agaaacctct   2460
tcggcacaaa atttgtttga g                                             2481
```

Seq ID 66

```
atggaattta tgaaaaagtt tgtagcttta gggcttctat ccgcagtttt aagctcttcg     60
ttgttagccg aaggtgatgg tgtttatata gggactaatt atcagcttgg acaagcccgt    120
ttgaatagta atatttataa tacaggggat tgcacaggga gtgttgtagg ttgccccccа    180
ggtcttaccg ctaataagca taatccagga ggcaccaata tcaattggca tgctaaatac    240
gctaatgggg ctttgaatgg tcttgggttg aatgtgggtt ataagaagtt cttccagttc    300
aagtcttttg atatgacaag caagtggttt ggttttagag tgtatgggct ttttgattat    360
gggcatgcca ctttaggcaa gcaagtttat gcacctaata aaatccagtt ggatatggtc    420
tcttggggtg tggggagcga tttgttagct gatattattg ataacgataa cgcttctttt    480
ggtatttttg gtggggtcgc tatcggcggt aacacttgga aaagctcagc ggcaaactat    540
tggaaagagc aaatcattga agctaagggt cctgatgttt gtacccctac ttattgtaac    600
cctaacgctc cttatagcac caaaacttca accgtcgctt ttcaggtatg gttgaatttt    660
ggggtgagag ccaatattta caagcataat ggcgtagagt ttggcgtgag agtgccgcta    720
ctcatcaaca agtttttgag tgcgggtcct aacgctacta atctttatta ccatttgaaa    780
cgggattatt cgctttattt agggtataac tacacttttt                          819
```

Seq ID 67

```
atggcgatct tacgcgcaaa ccttagccct aaaaacaaat taaacgccac tttaaaaggg     60
tggctcccca ttttacaaag cgagcttgaa gatttagaag aagtgttgaa acaaaacgct    120
ttagataacc ccttaatcaa aattgaaaac aaacgcatca aaaattttag cgatcgcttt    180
agcgctaaaa agagtagcga tcatttagaa aatttcgcaa ccgcatctaa aagccttttt    240
gaaaccttag aagctcaaat cattcccccc ctctttccta ctgaaacctc tcaaaaaatc    300
gctatggata ttatcagcgg gttgaataat gaggggtatt ttgaagaaaa tattgaagaa    360
agggctagaa ttttaggggt agagagcgaa gtttatgaaa aagtgcgcaa gcgttttagt    420
```

taccttaatc ccgctggcat tggtgctaaa gatgtgaaag agagcttttt attccagtta 480
gagagtaggg aattagacga taatgagctt tatgaagaaa cgcgaaaaat cattttaaat 540
ttagaaaaac accatgaatt ttctaaagat ttttattatg aaaaggcttt aaagatttta 600
aaatccttta aaaaccccca agccattgag tttttagaaa aagaaataga agtcattcct 660
gaacttttta ttgtagaagt ggataatgga atcatcgtgc gtttgaatga tgagagctac 720
ccgacaatca gtttggaaga aaatcgcttt aaggatagcg gctatttaaa agaaaaatta 780
aaagaggcta aagatttgat tgatgcgcta aatttgagaa aagccacgat ttataaaatc 840
ggtctgatgc ttttagagta tcaatacgat ttttttaagg gtaaggaatt acgcccttta 900
aagctattag atttagccaa tgagtttaac cactctgtaa gcacgatttc aagggccatt 960
tctaataaat atttggcatg cgaaaggggg gttttcccca ttaagcattt ctttagcatc 1020
gccttagaca atagcgagac ttcaaacgct gtgattaaag actatctttt agaattgatc 1080
aaaaacgaag acaaaaaaga gcctttgagc gacgctaaga ttttagaact cattgaagaa 1140
aaattccatt tgaaaatggt aagaagaacg atcaccaaat accgccaact gctcaacatc 1200
gcctcttcaa gcgaaaggaa aaggctctat ttgatgcgcg ct 1242

Seq ID 68
atgcaagttt tagcgttaaa ataccgcccc aaacatttta gcgagctagt cggtcaagag 60
agcgtggcta aaacgctttc tttagcccta gacaaccagc gtttggctaa cgcttattta 120
ttcagcgggt taagaggctc agggaaaacc agctcttcta ggatttttgc tagggcttta 180
atgtgtgaag aagggccaaa ggctgtgcct tgcgatactt gcatccaatg ccagagcgct 240
ttaaacaacc accacataga tattatagaa atggatgggg cgtctaatag ggggattgat 300
gatgtccgta atctcataga gcaaacgcgc tacaaaccaa gctttgggcg ctataaaatc 360
tttatcattg atgaagtgca tatgttcacc accgaagcgt ttaacgcgct tttaaagact 420
ttagaagagc ctcctagcca tgtgaaattc cttttagcga caacagacgc cttgaaactg 480
cccgctacca tactcagccg cacccagcat ttcaggttta aaaaaatccc tgaaaattcc 540
gttatttctc atttaaaaac cattttagaa aaagaacaag tgagttatga aacaagcgcg 600
ttagaaaaac tggctcacag cgggcaaggg agcctaaggg atacgatcac tcttttagaa 660
caagccatca attattgcga taacgctatc acagaaagca aggtggctga aatgttagga 720
gcgattgaca gaagcgtttt agaagatttt ttccaaagcc taatcaacca agatgaagcg 780
cgattaaaag agcgttatgc cattttagaa aattatgaaa ccgagagcgt tttagaagaa 840
atgatgcttt ttttgaaagc gaaattattg agccctgatt tttattctat ccttttgata 900
gagcgctttt ttaaaatcat tatgagcagt ttgagccttt taaaagaagg ggcaaatgcc 960
agttttgtgc tgttgttatt gaaaatgaaa ttcaaagaag ctttgaaatt caaagcccta 1020
gacgatgcga ttttggaatt agagcaaacc cctttcaatc aaaaccctag cataagctat 1080
aacgccccta aacaagaatc taaaaatata gaaaaaagag aaaaaataga acaaatagaa 1140
agaatagagg gaacagaaaa aagagaaaaa ctagaaaaaa aagagaacgc agaaaccccg 1200
caaactccca tgctttcagc taaagatcgc atttttcaca acctttttcaa acaagttcaa 1260
acattggttt atgagcgcaa ttatgagtta ggggcggtgt ttgaaaaaaa tatccgtttc 1320
attgattttg acagccagac taaaaccttg acttgggagt ctttagccac tgataaggat 1380
aaggagcttt taagagaacg atttaaaatc gtgaaaagta tcgttgatgg ggtttttggc 1440
aagggcgaaa gtatcaaaat cgctttaaaa aatcattcag aaaataaaag cactttagaa 1500
gtggttaaag agcttaaatt cccttattca aagcccaaac caaccactga aacgacggct 1560
gaaacgaaag aaaaagaaac taaagaaaaa gagattcaag aaaacgacac taaagagatt 1620
caagaagtcc aaccaaaaca agcccctaca gcgttgcaag aattcatggc taaccactct 1680
gagctgattg aagagattaa gagcgagttt gaaatcaaaa gcgtggaatt gtta 1734

Seq ID 69
atgagaatat ttttgaaatt gttgattctt ttatttttgtt tgaaggggca ggttatggct 60
caaaatttac ccaccattgc tttactggcg acaggggggga cgattgcagg gagtggtgcg 120
agcgcgagtt tgggtagtta taagagtggt gagttgggca tcaaagagct tttgaaggct 180
atccctagtc ttaacagact cgctcgcatt caaggggagc agatttctaa catcggctca 240
caagacatga atgaagaggt atggttcaag ctcgccaaac gtgcccaaga attgctagat 300
gatagccgta ttcaaggcgt ggtcatcacg catggcacgg acactttaga agagagcgcg 360
tatttttaa acttagtttt acgctccaca aaaccggtcg tgctggtggg agcgatgcgt 420
aatgctgctt ctttgagcgc ggatggggct ttgaatttat ataatgctgt gagcgtagcg 480
ctcaatgaaa aaagtgcgaa taaaggcgtg ttagtggtga tggacgataa tatttttagc 540
gctagagaag tgattaaaac gcacaccacc cacacttcca cctttaaagc cttaaatagc 600
ggcgcgatag ggagcgtgta ttatggcaaa acgcgctatt acatgcagcc tttgagaaaa 660
cacaccacag agagcgaatt ttccctttca caactcaaaa ccccctgcc taaagtggat 720
attatttaca cgcatgctgg catgacccct gatttattcc aagcgagcct aaactcgcat 780
gcaaaaggcg ttgtgatagc cggggtgggt aatgggaatg tgagcgctgg gtttttaaaa 840
gcgatgcaag aagcgagcca aatgggggtg gttattgttc gttctagcag ggtaaatagc 900
ggtgagatta cttcaggcga gattgatgac aaggccttca tcacaagcga caatttaaac 960
ccccaaaaag ctagggtgct tttacaactc gctttaacta aaacaaataa taaagaaaaa 1020
atccaagaaa tgtttgaaga gtat 1044

Seq ID 70
atggacttta aaaataaaaa atggcttttt ctagcccctt tagcaggcta tacggatttg 60

cctttcagga gcgtggtgaa aaaatttggc gtggatgtta ccacgagcga aatggtgagc 120
tcgcattcgt tggtgtatgc gtttgataaa acttctaaaa tgttggaaaa atccccttta 180
gaagatcatt tcatggcgca aatttcaggc tctaaagaaa gcgtagtcaa agaagcggtg 240
gagaaaatca acgctttaga gcatgtgaat gggattgatt ttaattgcgg ttgtcccgct 300
cctaaagtgg ctaatcatgg taatggtagt gggttattga aggatttaaa ccacttagtg 360
aagcttttaa aaaccatcag agaaaacact agtaaaaaaa tcacaagcgt gaaagtgcgt 420
ttaggctttg aaaagaaaat ccctaaagaa atcgctcatg ccctaaatga cgcaccggtg 480
gattatgtgg tggtgcatgg gaggacacga agcgataaat accaaaaaga caaaatagat 540
tacgaaagca tcgctttaat gaaaaagatt ttaaaaaagc cggtgatagc caatggcgaa 600
attgacagcg tgaaaaaggc ttttgaagtt ttacaaatca ctcaagcgga tgggctaatg 660
atagggcgag cggccttaag agccccatgg atattttggc aaatcagaaa caacaccaca 720
aaattacccg cagtcgtgaa aaaagacctg gttttagaac attttgataa aatggtggag 780
ttttatgggg atatgggggt aatcatgttt aggaaaaatt tgcatgctta cgctaagggc 840
gaaatgcaag cgagcgcgtt tcgtaactgc gtcaataccc ttacagaaat aaagagcatg 900
cgagagagca tagaggaatt ttttaatcaa gaaatgttgc aaagtgaagt gccgttatgg 960
gtagaattga atcaaaaaag cgtt 984

Seq ID 71
atggcaatag gttcattaag ctcattaggg cttggcagta aggttttgaa ttacgatgtg 60
attgacaagc ttaaggacgc tgatgaaaag gcgttaatcg ccccccttaga caagaaaatg 120
gagcaaaatg ttgaaaaaca aaaagccctt gtagaaatta aaacgctcct ttcagctcta 180
aaaggcccgg ttaaaacgct ttcagattat tccacttata tcagccgaaa aagcaatgtt 240
acaggcgatg cgttgagtgc gagcgtgggg gttggcgtgc ctattcaaga tattaaagtg 300
gatgtgcaaa atttagcgca aggcgatatt aacgaattgg gggcgaaatt ttcttcaaga 360
gacgatattt ttagccaagt ggataccacg ctcaagtttt acacacaaaa caaagactac 420
gccgttaata ttaaagcagg aatgacttta ggcgatgtgg ctcaaagcat cacggacgct 480
accaatggcg aagtgatggg tattgtgatg aaaacaggag ggaatgaccc ctaccaatta 540
atggtgaata ccaaaaacac cggcgaagac aaccgagtct attttggctc acacctccaa 600
tccacgctca ctaacaaaaa cgccctttct ttgggggttg atgggagcgg aaaaagtgaa 660
gtgagtttga atttaaaggg ggctgatggg aacatgcatg aagtccccat catgctagaa 720
ctccctgaaa gcgcttctat caaacaaaaa aacaccgcaa tccaaaaagc gatggagcag 780
gctttagaaa atgaccctaa ttttaaaaat ttgatcgcta atggggatat ttccatagac 840
actcttcatg gaggggaatc tttaatcatt aatgacaggc gtgggggaaa cattgaagtt 900
aaagggagta aggctaaaga gcttgggttt ttacaaacca ccacccaaga aagcgattta 960
ttaaaaagct ctcgcacgat aaaagagggt aaattagaag gggtggtcag tttgaatggc 1020
caaaaactgg atttgagtgc tttaaccaaa gagagcaaca ccagtgaaga aaacacagac 1080
gctatcattc aagcgatcaa cgctaaggaa ggcttgagtg cgttcaaaaa cgccgaaggc 1140
aagcttgtga tcaattctaa aaccggaatg ctaacgatta agggcgagga cgctttaggc 1200
aaggccagtt tgaaagattt gggtttaaat gctggcatgg tgcaatctta tgaagcttca 1260
caaaacacgc tttttatgtc taaaaatttg caaaaagcga gcgattcagc attcacttat 1320
aatggggtga gcatcacacg ccccactaat gaggtcaatg atgtgattag tggggttaat 1380
atcactttgg agcaaaccac agagcctaat aaacctgcca ttatcagcgt gagtagggac 1440
aatcaagcca ttatagacag ccttactgaa tttgtcaaag cctataatga gcttatccct 1500
aaactggatg aagacactcg ttatgacgct gacactaaaa tcgctgggat ttttaacggc 1560
gtgggcgata ttcgcgcgat tcgatcttct cttaataatg tgttttctta tagcgtgcat 1620
acggataatg gggtagaaag cttgatgaaa tacgggctta gtttagacga taagggcgtg 1680
atgagtttgg atgaggctaa attgagtagt gcgctaaatt ctaaccctaa agcgactcaa 1740
gatttttttct atgggagtga tagtaaggat atgggggggca gagaaatcca ccaagagggc 1800
atttttttcta aattcaatca agtcatcgct aatctcatag atggagggaa cgctaaatta 1860
aagatttatg aagattccct agacagagac gctaaaagcc tgactaaaga caaagaaaac 1920
gctcaagagc ttttaaaaac ccgctacaac attatggcgg acgttttgcc gcttatgata 1980
gccaaatctc taaagccaat caaaaattca attccgtgca aa 2022

Seq ID 72
atgcaaattg caacagcaat atggaaaaca agaatttggc aactccaaac ccattttgat 60
aaaaaagaag cgcatttgaa gcatttagaa gcacaacaca aagaatttgt aagagatgaa 120
aaacgctatt tagaaaagga aaaaaaagag cttgaaaaag aacgccaaat tttagaacaa 180
gaaaaagaaa attttaaaaa acagcgcgct gtttgtaaag aatctcaagc caaagcgcta 240
gacgcgatgc tcaattacat ggcttatact aaagatgaaa ttaaaagcat gattttagag 300
caattagaag aagaattaga agcccaaaaa agcgccttaa tcaggcgtta tgaaaaagaa 360
gccaaagaag agggcaagaa aaaatcgtat gccattttag cggaagcgac agcccgtttt 420
gcgggtaatt atgcggcaga gaatttaaca actcgtattg ctttgccttg ctcagattat 480
atcggtcgtg tgataggcaa agacgggaaa aatattgaag cgtttaaaaa ggtcagcggg 540
gtggatatag aatttagcga agatagcagc gaattgtgtt tgtccagttt caatctttat 600
cggcgtgaag tagcgagcga gacgcttaaa attttaatag aagacggccg tatccagcct 660
aacaggattg aagaggttta tcatagagtc gcgcgcaacc tggaaaaaga attgctttct 720
gaaggggaga gcgtggtgtt agaattagag cttggagcta tggaagatga gcttaaaatt 780
ttaataggca aaatgcgtta tcgctccagt tttgggcaaa acgccttaca gcattctaaa 840

gaagtcgctc ttttagccgg cttgattgca gagcagcttg gggggataa aaaactcgct 900
agaagagccg gtattttgca tgatattggt aaagcgctca cccaagagct tgggagagat 960
catgtgaatt taggggttga ggtgtgcaag cgccataaag aagatccggt tgtgatcaat 1020
gcgatttatg cccaccatgg gcatgaagag attttgagcg tggagtgcgc gagcgtgtgc 1080
gcggctgatg cgctttcagc agggcgtcct ggggctagga gaaagagcga tgaagaatac 1140
gctaaacgca tgcaagcttt agaagagatc gcgctagaat ttgatggggt ggaaaaagcg 1200
tatgcgatgg agagtgggcg agaattaaga gtgattgtca aatccaacca agtcagggac 1260
aatcaagtgc ctattattgc cagaaagatc gctaaaaaga tagaagagag cgctcagtat 1320
gtgggcgaag tgggcgtgca agtggtgcga gaaagccgtt tcaaaacgac cgctacgctc 1380
aagcaa 1386

Seq ID 73
atgcccatgc gtttgcacac tgccttttt ggtattaatt cattgcttgt tgcctctctt 60
ttgataagcg gttgcagtct ctttaaaaag cgtaacacta acgcccagct aatcccccct 120
tcagctaatg gcttgcaagc ccccatttat ccccccaacca atttcacccc tagaaagagc 180
attcagcctc tcccaagccc tcgccttgag aataacgatc agcccgtcat tagttctaac 240
cccactaacg ctatccctaa caccccccatt ctcacgccta ataatgtcat tgaattgaac 300
gcatgggcat gggcgtggct ccagaatcca ccatttcacc ctctcaagcc ctggctc 357

Seq ID 74
atggaaaaca acccaaacaa taaccaagcg tcattagaac gcaacgaatt gcacaacacc 60
atttggaaag tggctaacga attgagaggc tcagtggatg gctgggattt taagcaatac 120
gttttaggca ttctttttta ccgctacatt tcagaaaaca tgactcatta catcaataaa 180
gaagagcgaa agcgcgatcc gagttttgat tacgctaaat taagcgatga aaaggccgag 240
cgtggaagaa aacaccttat tgaacaaaaa ggctttttca tcccgccaag cgctttattt 300
tgtaatgcgc taaaaaacgc gtgccataac gaagatctca atgtaacctt acaaaatatt 360
tttaacgaaa tagaaaaatc tagccttggc actccatcag aagaaaatgt caaaggcttg 420
tttgcggatt tagatgtcaa tagcaataaa ttagggagct ctcatcaaaa tagggtggaa 480
aaattgacta aaatccttga agccataggg ggcatgcaat taggcgatta tttaaaaagc 540
gggattgatg tttttggcga cgcttatgaa tatttaatgg ccatgtatgc gagcaacgcc 600
ggcaaaagcg gaggggaatt tttcaccccc caagaagtga gcgaactgct cgctaaaatc 660
accctacacg gccaagagag cgtcaataaa gtttatgacc catgctgtgg gagtgggagc 720
ttactcttac aattttctaa agtgttaggc gataaaaatg tctcaaaagg gtattttggg 780
caagaaatca atttgaccac ttacaacctt tgccgtatca acatgttttt gcatgacatc 840
aattattcta aattccatat tgcgcacggg gacacgcttt tagacccaaa acatgaagac 900
gatgagcctt ttgatgcgat cgtttccaac cctccttatt ccactaaatg ggtgggcgat 960
agcaacccca ttttaatcaa cgatgagcgc tttagcccgg ctggtgtgct agcgcccaaa 1020
aacgccgccg atctcgcatt cactatgcac atgctttctt atttatccaa tagcggcacg 1080
gctgcgatcg tggaatttcc cggggtgctt tataggggaa acgctgaagc aaaaatcaga 1140
gaatatttag tcaaagagaa tgtcattgac tgcgtgatcg ctttaccaga caacctcttt 1200
tttggaacga gtatcgctac ttgcatttta gtgcttaaga aaaacaaaca agacgacacc 1260
acgcttttta ttgatgcgag taaggaattt gtcaaagagg gcaagaaaaa caagctcaaa 1320
gagcgcaacc gagaaaagat tttgcaaacc tatattgaaa gaaaagagat taagcatttt 1380
tgcgccctag ctaatattga gaaaatcaaa gaaaacgatt acaatctctc cgtgaatcgc 1440
tatgtggagc aagaagacac caaagaagcc attgacatta aagcgcttaa tagtgagatt 1500
gctcaaatcg tagaaaagca aagcgcttta aggaaccgtc ttgaatccat catcaaagag 1560
ttagaagggg ggcaaaatgc a 1581

Seq ID 75
atgctacaaa ccatcaactt aacgcaacgc tatgcgacta aaaaattgtt tgaaaacgtg 60
aatatcaagc tggataaaaa caaacgctac gggcttattg gggctaatgg cgcaggaaag 120
tccacttttt taaagatttt aagcaagagc attgattgta gcagtgggga agtcatcatt 180
acaagcggca tgaaaatggg ggttttaggg caggatcaat acgcttttga agatttgagc 240
cttaaagatg cggttttgat aggcaacaag cgtttgtatg acgctatcaa agaaaaagag 300
cgcttataca ccgaaggcga tttgagcgat gataaagtga atgccagatt aggggagtta 360
gaaaccattt gcgtggaaga agatcccatg tatgaatgcg aagtggcgat tgaaaaaatc 420
ctagaagatt taggcattcc tagctctaaa cacaacgatt tgatgaaaac cctgccaagc 480
agcgataaat ttaaaatcct tctcgctcaa gtcttgttcc ctaaaccgga tattttgctt 540
ttagatgagc cgaccaacaa cctggattta aacgccattg aatggctaga aaacaacctc 600
aaacgccatg aaggcacgat ggtcgtcatt agccatgaca ggcatttttt aaatgcggta 660
tgcacgcata ttttggattt ggatttccac agcgtgcgcg aatttagcgg gaattatgac 720
gattggtata tcgcttccac tctgatcgct aaacagcaag aggccgaacg caataaaaaa 780
ctcaaagaaa aagaagagct agaaaaattc atcgcgcgct ttagcgctaa cgcttctaaa 840
gccaagcaag ccaccagccg ccaaaaacaa ctggataaat tagacattca aagtttagcg 900
gtatctagca ggagggatcc tagcattatt tttaaaccca aacgcaccat tggtaatgaa 960
gccttagagt gcgaaaacat ctctaaaagt tatgacgacc aaatcgtttt aaatcaagtg 1020
agcttgaaag tgatgcctaa agacaagatc gccctcatag ggccaaacgg cgtgggtaaa 1080
tccacgcttt gtaaaattct agtagaagaa ttaaagccgg ataagggcgt ggtgaaatgg 1140

ggggcgacgg tttcaaaagg ctatttccct caaaacgtga gcgaagaaat tagcggggaa 1200
gagaccttgt atcaatggct ctttaacttc aataaaaaga ttgaaagcgc tgaggttagg 1260
aacgctttag ggaggatgct gtttaatggc gaagagcaag aaaaatgcgt gaacgcttta 1320
agtgggggcg aaaaacaccg aatggtttta tccaagctca tgctagaggg ggggaatttt 1380
ttagtcttag atgagccaac caaccatttg gatttagaag cgattatcgc tttaggcgaa 1440
gcgctcttta aatttgatgg ggcgctgatt tgcgtaagcc atgacagaga gctcattgat 1500
gcgtatgcta ataggatcat tgaattagtc ccaagcccta aaggcgcttc aatcattgat 1560
tttaaaggca gttatgaaga gtatttggcg agcaaaaaa 1599

Seq ID 76
atgaataaac catttttaat cttactcata gccctaattg tctttagcgg ctgtaacatg 60
agaaaatatt tcaaacccgc taaacaccaa attaaaggcg aagcgtattt ccctaaccat 120
ttgcaagaaa gtatcgtttc gtctaatcgt tatggagcca ttttgaaaaa tggagcggtt 180
ataggcgata aaggtttaac gcagctaaga atcggtaaga acttcaatta cgaaagcagt 240
tttttaaatg agagtcaagg gtttttttatt cttgcgcaag attgtttgaa caagattgat 300
aaaaaaacaa acaaaagcaa ggtggctaag actgaagaaa cggaattgaa attaaagggc 360
gttgaagcgg aagtccaaga taaagtctgt catcaagtgg aattgattag caataaccct 420
aacgccagcc aacaatctat cgttattcct ttggagactt ttgccttgag cgcaagcgtt 480
aaagggaatc ttttagcggt ggtgttagcg gacaattcag cgaacttata cgacatcact 540
tctcaaaaat tgctttttag tgagaaaggt tccccaagca ccacgatcaa ttctttaatg 600
gcgatgccta tttttatgga tacggtcgtg gtgttcccca tgctagatgg gcgcttgttg 660
gtcgtggatt atgtgcacgg aaaccctacg cctattagaa acattgttat cagcagcgat 720
aagtttttta acaatatcac ctaccttatc gtagatggca ataacatgat cgcttctaca 780
gggaaaagga tactctcagt agtgagcggt caagagttca actatgatgg ggatattgtg 840
gatttgcttt atgataaggg gactttatat gtgctcacgc tagacgggca gattttgcaa 900
atggataaga gtttgaggga attaaacagc gtgaaactgc cttcgtcgct caacacgatt 960
gtattaaacc ataataaatt gtattcttta gaaaaacgag ggtatgtgat agaggtggat 1020
ttaaatgatt ttgattcgta taatgtctat aaaacgccaa ctataggcag ttttaagttt 1080
ttttcatcta atcgtttgga taaaggggtg ttttatgata aaaatcgggt gtattacgat 1140
cgctactatt tagattataa cgattttaaa ccaaaacttt atcccgttgt ggaaaaatcg 1200
gcatctaaaa aatctcaaaa aggcgaaaaa gggaacgctc ctatttattt gcaagaaagg 1260
cataaagcta aagaaaataa acagccttta gaagaaaaca aagttaaacc aagaaatagc 1320
gggtttgaag aagaagaggt taaaaccaga aggcctgagc ctattaggga tcaaaataac 1380
gccacccaac aaggcgaaac aaaaaacaat gaaagtaaaa acgctcctgt cttaaaagaa 1440
aacgccgcta aaaaagaagt gccaaaacca aattctaaag aagaaaaacg ccgcttgaaa 1500
gaagaaaaga aaaaagccaa agccgaacaa agagcgagag aatttgaaca aagagcgaga 1560
gagcatcaag aaagagatga aaaagagctt gaagaaagaa gaaaagcttt agaaatgaat 1620
aagaag 1626

Seq ID 77
atgaaacgaa gggattttat taaaacgact actttaggcg ctacaggtgc tgttttagga 60
gcacagattt tgcaggcaga agaaagtaaa gggagtgttg caaaatataa aatagaagct 120
caatacagca ttgattttga ttctgcagaa cacacttcac ttttcattcc catgccgagt 180
gttgtagcga gcaatgtgca tttacaaggc aatcatgcta gctataaaag catgctcaat 240
tttggagtgc cttatttgca agtggatttt ttaaaaagca ctcaaaaaaa gcaagtccat 300
ttgtcttatg agatcgctag ctatcaattg aatgagcgtt tgtttgaaac gagcgatttt 360
gtagcaatgg ggcgttatga aagagacgat gcgagcgtgg ctaacattgc caaccagctt 420
aagggaacaa cccctaaaga aagcgttcgc aatttttatg cgttcatcaa gcatgagatg 480
cctaagagac agaaggcttt agagggtaaa gaaaatttac ctaagcgtga gagtttgccc 540
tggtttgcaa ccatttcaaa agagagcatg tttgtgtcct tatgccatgc gtgcgggatt 600
aaaagcgctg aagtgcaagg cttgaaactg ggtcaaaaca gcgtggtgaa aaacgctcct 660
agagtggaag tgtatttgaa agattcattt ctagcgtttg attttcaaaa taatcacaag 720
gaagttttta tcccgttgaa tcgtcataaa gacatgcagt tagattctgc cttattggcg 780
acttttggcg atgcttttgc ccttgtggat ggtagggatt taggcaatta cgagagcaaa 840
ctttttgaaa aaagagtgtc ctatacgatt gtc 873

Seq ID 78
atggttaata aagatgtgaa acaaaccact gcttttggcg ctcccgtttg ggatgacaac 60
aatgtgatta cggccggccc tagaggtcct gttttattac aaagcacttg gtttttggaa 120
aagttagcgg cgtttgacag agaaagaatc cctgaaaggg tggtgcatgc taaaggaagc 180
ggagcttatg gcactttcac tgtgactaaa gacatcacta aatacactaa agcgaaaatt 240
ttctctaaag tgggcaaaaa aaccgaatgc ttcttcagat tttctactgt ggctggtgaa 300
agaggcagtg cggatgcggt gagagaccct agaggttttg cgatgaagta ttacactgaa 360
gaaggtaact gggatttagt ggggaacaac acgcctgttt tctttatccg tgatgcgatc 420
aaattccctg atttcatcca cactcaaaaa cgagatcctc aaaccaattt gcctaaccat 480
gacatggtat gggatttttg gagtaatgtt cctgaaagct tataccaagt aacatgggtt 540
atgagcgata ggggtattcc taaatctttc cgccacatgg atggttttgg cagccacact 600
ttcagtctta tcaacgcgaa aggcgaacgc ttttgggtga aattccactt tcacaccatg 660

caaggcgtta agcatttgac taacgaagaa gccgcagaag ttaggaagta tgatccggat 720
tccaatcaaa gggatttatt caatgcgatc gctagagggg atttcccaaa atggaaatta 780
agcattcaag tgatgccaga agaagatgct aagaagtatc gattccatcc gtttgatgta 840
actaaaattt ggtatctcca agattatcca ttgatggaag tgggcattgt ggagttgaat 900
aaaaatcctg aaaactattt cgcagaagtg gaacaagcgg cattcagtcc ggctaatgtc 960
gttcctggaa ttggctatag ccctgatagg atgttacaag ggcgcttgtt ctcttatgga 1020
gacacacacc gctaccgctt aggcgttaat tatcctcaaa taccggttaa taaaccaaga 1080
tgcccattcc actcttctag cagagatggt tacatgcaaa acggatacta cggctcttta 1140
caaaactata cgcctagctc attgcctggc tataaagaag ataagagcgc gagagatcct 1200
aagttcaact tagctcatat tgagaaagag tttgaagtgt ggaattggga ttacagagct 1260
gatgatagcg attactacac ccaaccaggt gattactacc gctcattgcc agctgatgaa 1320
aaagaaaggt tgcatgacac tattggagag tctttagctc atgttaccca taaggaaatt 1380
gtggataaac aattggagca tttcaagaaa gctgacccca aatacgctga gggagttaaa 1440
aaagctcttg aaaaacacca aaaaatgatg aaagacatgc atggaaaaga catgcaccac 1500
acaaaaaaga aaaag 1515

Seq ID 79
atgtttttaa gagtataccc aaagcttaga tacgctttat gtttcccccc actcgctgag 60
acttgctata gcgaagagcg gactttaaat aaggttacca cccaagctaa aaggattttc 120
acttacaaca atgagtttaa agtaacttct aaagaactag atcaacgcca aagcaatgaa 180
gtcaaggact tgtttaggac taaccctgat gtgaatgtgg gcggagggag cgtgatgggg 240
cagaaaatct atgtgagagg cgttgaagac aggcttttaa gggttacagt ggatggggct 300
gcacaaaatg gcaatatcta ccaccaccaa ggcaacaccg tgattgaccc tggcatgctc 360
aaaagcgtgg aagttaccaa aggcgcggcg aatgcgagcg cggggccagg agcgattgcg 420
ggagtgatta aaatggagac taaaggagcg gctgatttta tccctagggg gaaaaattat 480
gctgccagtg gggcggtgag tttttatacc aattttggcg atcgagagac tttcagatcg 540
gcttatcaaa acgcgcattt tgatattatc gcttactaca cgcaccaaaa catcttctat 600
tatagaagcg gcgctacagc gatgaaaaac cttttcaatc ccacacaagc cgataaagag 660
ccaggaactc ctagcgagca aaacaacgct ttgattaaaa tgaatggtta tttgagcgac 720
agagacacgc tcactttcag ctggaacatg acacgagata acgctacacg ccctttaagg 780
agtaacgcta tagggttagc ctatccttgt gaagcccccc ttagtcctga tagttctcaa 840
gggtgtccta atgtgttaga tagtttcaca agatacatgt atcactctat taatagtgcc 900
aacaatcttt ccttacaata caaaagggaa gcgggaaatt cttttggcga cccacgatta 960
gattttaccc tttatacaag catcaggaac gctcagtttg atcccctatt tgatcctaat 1020
ggcgtttatg ctaaattccc cacttcttta gcgagcgcat gggaaaaaga aaattaccca 1080
tgcgttgaag gcgcttattg caccccaagc ttttcagatg tggataaacc aagctcacag 1140
cctaggaatt tgtttttaaa caacaccggc ttaaacctta aagtcgcgca tgtgattgat 1200
gaagccacag acagcctttt tgaatacgga ttcaactacc aaaatttgag cgtttttgac 1260
gctcgcatcc ctaaatcaga attatacagg cctaatcaag tttatactga tgataaagga 1320
caaaaacaaa tcgcttgctc tcttgtgaat aataacccca atgaccccac tctgtgccaa 1380
agagggaaag cgaacgggaa tatttatgga ggctacgtgc aagcgaatta ctcgcctcat 1440
aaaatcatca cttttggagc cggggtaagg tgggacgctt acacgcttta tgataaagac 1500
tggaaccacc gctacactca aggctttagc cctagcgcgg ctcttgtgct aagccccatt 1560
gagcctttat ctttaaaaat cacttattct caagttacaa gaggggtgat gccaggagat 1620
ggcgtgtaca tgcgtcaaaa cgatttacga tacgccaaaa acatcaagcc tgaagtgggc 1680
tctaacgctg aatttaatat tgattattca agccagtatt ttagcgggag ggctgcggcg 1740
ttttatcagg ctttggataa tttcatctca caatacgcac aaaatttgat tgtaaccaat 1800
ttgagtcaag cgattcgtat ttatggctat gaagtgggtg ggactttcag atacaagggc 1860
gtgagtttga atgtaggggt ctcgcgcacc tggcccacca ctaggggtta tttaatggcg 1920
gatagctatg agcttgccgc aagcaccggt aatgttttta tcatcaaatt ggattacacc 1980
atccccaaaa cagggatcaa tcttgcatgg cttagccgct ttgttaccgg tttagattat 2040
tgcgggtttg atatttactt gcctgattat gggacggctg agaaacccaa aacccctacc 2100
gatttagcca aatgcggatc tcaattaggg ttagtgcata tgcataaacc gggctatggc 2160
gtgagtaatt tttatatcaa ttggagtcct aaaaccaaaa gccgctggaa gggtttgttg 2220
ctttcagccg tgtttaataa tgttttcaac aaattctatg tggatcaaac aagcccttat 2280
gtcatgagcc cggatatgcc aggcactgac gctgttaaaa gagcgatcgc tgagcctggg 2340
tttaacgcgc gttttgaagt ggcttacaaa tgg 2373

Seq ID 80
atggaaatac aacaaacaca ccgcaaaatc aatcgccctt tggtttctct cgctttagta 60
ggagcgttag tcagcatcac accgcaacaa agtcatgccg ccttttcac aaccgtgatc 120
attccagcca ttgttggggg gattgctaca ggcgctgctg taggaacggt ctcagggctt 180
cttggctggg ggctaaaaca agccgaagaa gccaataaaa ccccagataa acccgataaa 240
gtttggcgca ttcaagcagg aaaaggcttt aatgaattcc ctaacaagga atacgactta 300
tacagatccc tactatctag taagattgat ggaggctggg attgggggaa tgccgctacg 360
cattattggg tcaaaggcgg gcaatggaac aagcttgaag tggatatgaa agacgctgta 420
gggacttata atctctcagg gctaagaaac tttactggtg gggatttaga tgtcaatatg 480
caaaaagcca ctttgcgctt gggccaattc aatggcaatt ctttcacaag ctataaggat 540

agcgctgatc gcaccacgag agtggatttc aacgctaaaa atatcttaat tgataatttt 600
ttagaaatca ataatcgtgt gggttctgga gccgggagga aagccagctc tacggtttta 660
actttgcaag cttcagaagg gattactagc agtaaaaatg cggaaatttc tctttatgat 720
ggcgccacgc tcaatttggc ttcaaacagc gttaaattaa tgggtaatgt gtggatgggc 780
cgtttgcaat atgtgggagc gtatttggcc ccttcataca gcacgataaa cacttcaaaa 840
gtgacagggg aagtgaattt taaccatctc actgtgggcg atcacaacgc cgctcaagca 900
ggcattatcg ctagtaacaa gactcatatt ggcacactgg atttgtggca aagcgcggga 960
ctaaacatta tcgcccctcc agaaggcggt tataaggata aacctaagga taaacctagt 1020
aacaccacgc aaaataatgc taacaacaac caacaaaaca gcgctcaaaa caatagtaac 1080
actcaggtta ttaacccacc caatagcgcg caaaaaacag aaattcaacc cacgcaagtc 1140
attgatgggc cttttgctgg tggcaaagac acggttgtca atattgatcg catcaacact 1200
aacgctgatg gcacgattaa agtgggaggg tataaagctt ctcttaccac caatgcggct 1260
catttgcata tcggcaaagg cggtatcaat ctgtccaatc aagcgagcgg gcgcaccctt 1320
ttagtggaaa atctaaccgg gaatatcacc gttgatgggc ctttaagagt gaataatcaa 1380
gtgggtggtt atgctttggc aggatcaagc gcgaattttg agtttaaggc tggtacggat 1440
accaaaaacg gcacagccac ttttaataac gatattagtt tgggaagatt tgtgaattta 1500
aaagtggatg ctcatacagc taattttaaa ggtattgata ctggtaatgg tggtttcaac 1560
accttagatt ttagtggcgt tacaggtaag gtcaatatca acaagctcat tacggcttcc 1620
actaatgtgg ccgttaaaaa cttcaacatt aatgaattgg ttgttaagac caatggggtg 1680
agtgtggggg aatacactca ttttagcgaa gatataggca gtcaatcgcg catcaatacc 1740
gtgcgtttgg aaactggcac taggtcaatc ttttctgggg gtgtcaaatt taaaagcggt 1800
gaaaaactgg ttatagatga gttttactat agcccttgga attatttga cgctaggaat 1860
attaaaaatg ttgaaatcac cagaaaattc gcttcttcaa ccccagaaaa cccttggggc 1920
acatcaaagc ttatgtttaa taatctaacc ctgggtcaaa atgcggtcat ggactatagt 1980
caattttcaa atttaaccat tcaggggat ttcatcaaca atcaaggcac tatcaattat 2040
ttggtccgag gcgggcaagt agccaccttg aatgtaggca atgcggcagc tatgttcttt 2100
agtaataatg tggatagcgc gactgggttt taccaaccgc tcatgaagat taacagcgct 2160
caagatctca ttaaaaataa agaacatgtc ttattgaaag cgaaaatcat cggttatggc 2220
aatgtttctt taggcactaa cagcattagt aatgttaatc taatagagca attcaaagag 2280
cgcctagccc tttacaacaa caataaccgc atggatattt gtgtggtgcg aaatactgat 2340
gacattaaag catgcgggac ggctatcggc aatcaaagca tggtgaataa ccccgacaat 2400
tacaagtatc ttatcggtaa agcatggaag aacataggga tcagcaaaac agctaatggc 2460
tctaaaattt cggtgtatta tttaggcaat tctacgccta ctgagaaagg tggcaatacc 2520
acaaatttac ctacaaacac cactagcaat gtgcgttctg ccaacaacgc ccttgcgcaa 2580
aacgctcctt tcgctcaacc tagcgccact cctaatttag tcgctatcaa tcagcatgat 2640
tttggcacca ttgaaagcgt gtttgaattg gctaaccgct ctaaagatat tgacacgctt 2700
tatgctaact caggcgcgca aggcagggat ctcttacaaa ccttattgat tgatagccat 2760
gatgcgggtt atgccagaca aatgattgat aacacaagca ccggtgaaat caccaagcaa 2820
ttgaatgcgg ccactaccac tttaaacaac atagccagtt tagagcataa gacaagcagc 2880
ttacaaactt tgagcttgag taatgcgatg atcttaaatt ctcgtttagt caatctctcc 2940
agaaggcaca ccaataatat tgactcattc gcccaacgct tacaagcttt aaaagaccaa 3000
aaattcgctt ctttagaaag cgcggcggaa gtgttgtatc aatttgcccc taaatatgaa 3060
aaacctacca atgtttgggc taacgctatt gggggaacga gcttgaataa tggcggcaac 3120
gcttcattgt atggcacaag tgcgggcgta gatgcctacc ttaatgggga agtggaagcc 3180
attgtgggcg gttttggaag ctatggttat agctctttta ataatcaagc gaactctctt 3240
aactctggag ccaataacac taattttggc gtgtatagcc gtatctttgc taaccagcat 3300
gaatttgatt ttgaagctca aggggcgcta gggagtgatc aatcaagctt gaatttcaaa 3360
agcgctctat tgcgagattt gaatcaaagc tataattact tagcctatag cgctgcaaca 3420
agagcgagct atggttatga ctttgcattt tttaggaacg ctttggtgtt aaaaccaagc 3480
gtgggcgtga gctataacca tttaggttca accaacttta aaagcaatag caatcaagtg 3540
gctttgaaaa atggctctag cagtcagcat ttattcaacg ctagcgctaa tgtggaagcg 3600
cgctattatt atggggacac ttcatacttc tatatgaacg ctggagtttt acaagaattt 3660
gctaactttg gttctagcaa tgcggtatct ttaaacacct ttaaagtgaa tgccgcacac 3720
aatcctttaa gtacccatgc cagagtgatg atgggtgggg aattaaaatt agctaaagaa 3780
gtgtttttga atttgggctt tgtttatttg cacaatttga tttccaatat aggccatttc 3840
gcttccaatt taggaatgag gtatagtttc 3870

Seq ID 81
atgcctcaaa tacaatcatc gcattccaat cattttgatt tcactataga cacggcggat 60
cgcactaaat tattgatgag ctatttagtc gtgcctacaa cggctaattt caacaatgtc 120
atgcatgggg gggaattatt gaatttattg gataaagtgg cttatgtgtg ttcgactcgt 180
tattgcgcta aaggaacggt cactttaagc gtggatgggg ttacttttaa ataccccatt 240
cctgtaggga atttgctcac ttttttagcc agcatcaatt atgtgggcaa cacctcgtgc 300
gaagtgggga ttaaggtttt gagcgaagac attaaaactc gtgaaatcac gcacacgaac 360
tcatgttatt tcaccatggt ggctgtagaa aatggcaaac ccacccccat gcctaaatac 420
gagcctaaaa cagaggttga aatccgccgt tatgaagggg ctttaaagcg caaggaaatg 480
cgcacacgag ggtatttaaa aagcgggaaa cacgagggtg tt 522

Seq ID 82

```
ttgaataatt tagacattaa aactttaggg caggttttca cccctaaaaa gatagtggat      60
ttcatgctca ctctcaaaca caatcatggg agtgttttag aaccgagtgc tggcgatggg     120
agtttttaa agcgcttaaa aaaggccgta aggattgaaa tcgatcctaa aatctgccct      180
aaaaatgccc tttgcatgga ctttttttgac taccctttag aaaatcaatt tgacaccatt    240
attggtaacc cgccctatgt caagcacaag gatattgcgc caagcaccaa agaaaaactc     300
cattacagcc tttttgatga aaggagtaat ctctacttgt ttttcataga aaaagcgatc     360
aagcatttaa aacctaaagg cgaattgatt ttcatcaccc caagggattt tttaaaatcc     420
acttctagcg tgaaattaaa cgaatggatt tataaagaag gcacgataac gcatttttt      480
gaactgggcg atcaaaaggt tttcccaaac gccatgccta attgcgtgat ttttcgtttt     540
tgtaagggta atttcagtag aatcaccaac gatggtttgc aatttttgtg caaaaaaggc     600
attttgtatt tcctcaacca atcttacacg caaaaattaa gcgaggtttt taaggttaaa     660
gtgggggcag tgagcgggtg cgataagatt tttaaaaatg aaaaatacgg gaatttagaa     720
tttgtcacct caatcacgaa aagaaccaat gctttagaaa aaatggtttt tgtcaatgag     780
cctaatgatt atttactcca gcataaagac agcttaatgc aaagaaagat taaaaaattc     840
aatgaaaata actggtttga gtgggggaga atgcatcaca tatcccctaa aaaacgcatt     900
tatgtcaacg ccaaaacgca ccaaaaaaac ccctttttta tccaccaatg ccctaattat     960
gacggctcta ttttagcgct attcccttat aaccaaaacc tggacttaca aaatctctgc    1020
gacaaactca acgctatcaa ctggcaagaa ttaggctttg tgtgcggcgg gcgttttttg    1080
ttttcgcagc gctctttaga aaacgcgctt ttgcctaaag acttttaaa tctagga        1137
```

Seq ID 83

```
atgaaacaaa atttaaagcc attcaaaatg attaaggaaa atttaatgac acaatctcaa      60
aaagtaagat tcttagcccc tttaagccta gcgttaagct tgagcttcaa tccagtgggc     120
gctgaagaag atgggggctt tatgaccttt gggtatgaat taggtcaggt ggtccaacaa     180
gtgaaaaacc cgggtaaaat caaagccgaa gaattagccg gcttgttaaa ctctaatacg     240
acaaacaaca ccaataccaa tattgcaggc acaggaggca atgtcgccgg gactttgggc     300
aacctcttta tgaaccaact aggcaatttg attgatttgt atcccatttt gaacactaaa     360
aatatccatc aatgtggtac tactaataat ggtagtagta gtgcgaccac tgcagccgct     420
actactaaca atggcctttg tttccaaggt aacctggatc tttataacga aatggttggc     480
tctatcaaaa ctttgagtca aaacatcagc aagaacatct ttcaaggcaa caacaacacc     540
acgagccaaa acctctccaa ccagctcagt gagcttaaca ccgctagcgt ttatttgact     600
tacatgaact ccttcttaaa cgctaacaac caagcgggtg ggatttttca aaacaacact     660
aatcaagctt atggaaatgg tgttaccgct caacaaatcg cttatatcct aaagcaagct     720
tcaatcacta tggggccaag cggtgatagc ggggctgccg cagcgttttt ggacgccgct     780
ttagcgcaac atgttttcaa ctccgctaac gccgggaacg atttgagcgc taaggaattc     840
actagcttgg tgcaaaacat cgtcaataat tctcaaaacg ctttaacgct agccaacaac     900
gctaacatca gcaattcaac cggctatcaa gtgagctatg gcgggcatat tgatcaagcg     960
cgctctaccc aactgttaaa caacaccaca aacactttgg ctaaagttac cgctctaaac    1020
aacgagctta aagctaaccc atggcttggg aatttcgctg ccggtaacag ctctcaagtg    1080
aatgcgttta acgggtttat cactaaaatc ggttataagc aattctttgg ggaaaacaag    1140
aatgtgggct tacgctacta cggcttcttc agctataatg gcgcgggcgt gggtaatggc    1200
cccacttaca atcaagtcaa tctgctcact tatggggtgg ggactgatgt gctttacaat    1260
gtgtttagcc gctcttttgg tagccgaagt cttaatgcgg gcttctttgg ggggatccaa    1320
ctcgcagggg atacttacat cagcacgcta agaaacagcc ctcaacttgc gaatagaccc    1380
acagcgacga aattccaatt cttgtttgat gtggggttac gcatgaactt tggtatcttg    1440
aaaaaagact tgaaaagcca taaccagcat tctatagaaa tcggtgtgca aatccctacg    1500
atttacaaca cttattataa agctggcggc gctgaagtga aatacttccg cccttatagc    1560
gtgtattggg tctatggcta cgccttc                                       1587
```

Seq ID 84

```
atggcgttta aaaaggccag gttgatttcc aagtttattt caaagggatc tttcaaattg      60
aataagatct caaagaaaat tttcacattg aatcaaatct taaaatgtga aaagcccttа     120
aaacgccata aaaaagcttt aaaacctatt aaaaagctct ctaatcgcaa caaatctttt     180
ttaaaagctt cggttttatt gataggagcg ttaggggggt tatcccacct aagggctaac     240
gaatgccgtt attggtcatg gtcgtcttgg agttaccaag ataatattga aagcggtcct     300
aattcgccca cgcacaactc ttattgcctt tttagtagca ctcaaggctc tgggacttat     360
tatttaaaca ctcttaccac ttatagcgct ggtggggcta gtttcacgca aaaattcaat     420
aacggcacgc ttaatgtggg agagaatatc cgctttggag gcacaggtat taatgggggt     480
gatgtcggct atatcacagg aacttatgac gctcaaacga ttaattttaa ttctagccat     540
ttaacaaccg gaaactcata cgctgatggt ggtggggcca cgctcaattt taatgcggcc     600
aataatatca ctatcaatca agcgagtttt gacaatagcc atgcagggac gcaaaaatct     660
tacatgaatt ttaaaggctc taatatcaag gtcagtggct ctagttttac agatgatact     720
gatgggggct ttagtttcag cggtaatagt aataacagca ccatctcctt taatcaaacg     780
agcttcaatc aagggactta tcactttagt aatagcgcca ctttaagctt caatcatagc     840
gctttcaatc aagggactta taactttaat agcactcaat ctgcttttaa taacagcgct     900
ttcaatcaag ggacttatca tttcaatggc aacgccagct ttgataacga caccttcaat     960
caaggcactt atagctttaa taccagcaag gtgagtttct caggcatcaa cactttaaat    1020
```

tcaagttcgc cttttgctag ccttaaaggc agtgtgtctt ttggttctga tgcgattttt 1080
aacctcaatc aaacccttaa taatcaaacc tatgatattc tcactacaaa cggggcgatc 1140
cagtatgggg tttatcaaag ctatttgtgg gatctaatca actataaggg cgataaagcc 1200
attagccatg ttgaagtggg caataacact tatgatgtaa cctttgatat taacgggcaa 1260
gatgaaacct tacaagaaac ctttaacaaa caatccatta ttacccaatt tttaggagat 1320
gatttacaac aacaagccca aaaaacctac caacaagact tgagcaactc ccaaagcgct 1380
ttaaataacg ctgctagtga taataagatc gcaaatagcg atacagacta caccaagaat 1440
aaaaacgcca ctatcaaaaa agacgctcaa ggtttagaaa acaccaacca acaaatcgct 1500
caagatgaac aagcgttaca aggagattta gacaagctca aacaattagc caactcccca 1560
acaggcttta gtgaacaagc tttcaatcaa gctcaaaaac aagaacaaca agatgaacaa 1620
accttacaaa acgaagaaaa gacttttaat agcgagcaag agggattgaa acaagcgata 1680
caacaagcac aagcccaaca acaaaaacaa caacaaaaac aagaacaaca acaagcccaa 1740
caaacctatc aagaggatct cactcattcc caaagcgctt tgaatgatgt ggctagcgac 1800
aacacgatcg caagcaatga tacaaactac accaacaatc aaaacaccgc tatcaaagaa 1860
gacgctcaag gtttagaaaa caccaaccaa caaatcgctc aagatgaaca agcgttacaa 1920
ggagatttag acaagctcaa acaattagcc aactccccaa caggctttag tgaacaagct 1980
ttcaatcaag ctcaaaaaca agaacaacaa gatgaacaaa ccttacaaaa cgaagaaaag 2040
acttttaata gcgagcaaga gagattgaag caagcgatag ctaacgctaa gcctacaagc 2100
cccacaccaa gccatgcacc cactcctaca aaacacaccg cgccaaacac tcctcctaat 2160
aaagttccac ccacaccccc tactcaaaat ccacctgcag aaagcgtgtg gagtggggtt 2220
tattggcttc aaaacaaaac ctactcaaac aaaggcattt attatattga tcccaatctt 2280
tcaggacaga gcggtcaaag cggcaacacg ctcagcactt atacagctaa tttgtttgga 2340
agaagtttta gcgttaatat ccaaaatggc actttgatca tagggaataa tacagagagc 2400
gtgaatagta atgggttgat ttggataggg catggaggtt ttggctatat tacgggaact 2460
tttagtgcgg ctaacattta cttgaccaat aattttaaaa ccggtgaagg cgtttcaaat 2520
tcagatggtg ggggagcgaa cattaccttt aaagcaagcg ataatatcac tatggatggc 2580
ttgaattata atgacgctga aaccgttact aaaatgattc aaacaggggc tagccagcat 2640
tcctatgcca cttttgacgc tctaaataat atcagcgtga ctaattccag ttttagcgat 2700
atgacttggg gaaaattcag ttttagcgct aagaatattt cgttttctaa cgcttcgttc 2760
agcggcttta caaaccctgg aggatcaagc gttattagcg ctaacgctac taattcttta 2820
agctttatca attctcgttt gaatggggga gcggtttata atttgcaggc taatagcctt 2880
attttcaata acacgcaagc ggtttttaat gtcttgtatt ctagggggac aagcaatttt 2940
aacgccacca cacagctttt aggcaacacg aattttacgc tcagttctca aagtttgttg 3000
aattttaatg gcgatacaac cttgcaaaac aacgccaata tcacgcttgg caataaaagt 3060
caagccgctt ttaaaaattc tttaacgctt gataataatt ctaatttgag tttagacaat 3120
caaagcgttt tgaatgcgaa taacacaagc gcttttaaca atcaagcgag tctcaatatt 3180
tataacggga gtcaagcgac ctttaatagc ctctttttta atggcgggac actcagtctt 3240
aacgctagta gcaagctcaa cgcttctaac gctagttttt caaacaacac cactatcaat 3300
ttagacgata gcgttttatc ggctagtaac acaagctctt taaacgctaa tatcaatttt 3360
caaggcgcaa gccaggctga ttttggaggc aacacgatta ttgatacagc gagctttaat 3420
tttgacagcg caagttcatt gaattttaac aaccttacgg ctaatggagc gttaaatttt 3480
aatggttata cgccctcttt gactaaggct ttaatgagcg ttagcgggca gtttgtttta 3540
gggaataatg gggatattaa tttatctgac atcaatattt ttgataacat cacaaaatct 3600
gtaacctaca acatcctaaa cgctcaaaaa gggattactg gcatcagtgg ggctaatggc 3660
tatgaaaaaa tccttttta tggcatgaaa atccaaaacg ctacctatag cgacaacaat 3720
aacatccaaa cttggtcgtt tataaaccct ctcaattctt ctcaaatcat tcaagagagc 3780
attaaaaatg gggatttaac catagaagtt ttaaataacc ccaactcggc ttccaacact 3840
attttcaata tcgctcctga gctttataat taccaagctt ctaagcaaaa tcctaccggc 3900
tatagctatg attatagcga caatcaagca ggcacttatt acttgacaag caacattaaa 3960
ggtcttttca cccctaaagg ctctcaaact cctcaagccc caggcactta tagcccgttt 4020
aaccagcctt tgagtagttt gaatatctac aataagggtt tttctagcga gaatttaaaa 4080
acgcttttag ggatcctttc tcaaaattcc gctaccttaa aagaaatgat tgaatccaac 4140
caactagaca atatcactaa cattaatgaa gtgttgcaac tcttagacaa gattaaaatc 4200
acccaagtgc aaaagcaagc actcctagaa acgatcaacc atttgactga caacatcaat 4260
caaaccttta ataatgggaa tctaattata ggcgctactc aagataatgt tacaaactct 4320
actagctcta tatggtttgg gggcaatggc tatagcagtc cttgcacgct agatagcgcc 4380
acttgttctt cttttagaaa cacttactta gggcaattat taggctcaac ttccccctat 4440
ttaggctaca ttaacgctga ttttaaagct aaaagcattt atattaccgg aacaattgga 4500
agtggtaacg cctttgaaag cggagggagc gcggatgtaa cctttcaaag cgctaataac 4560
ttagtgttga ataaagccaa catagaagct caagctacag acaatatctt taatcttttg 4620
ggccaaaaag ggattgagaa aatctttaat caagggaatt tagcgaatgt tctcagtcaa 4680
gtggctatgg aaaaaatcaa gcaagccggc ggtttaggaa actttataga aaacgctcta 4740
agcccttga gtaaggaatt gcccgctagc ttgcaaaatg aaaccttagg ccaacttata 4800
ggtcaaaata acttagatga tttattgaat aatagcgggg tcatgaatgc aatccaaaat 4860
attatcagta aaaaactaag catttttggt aattttgtta ccccatccat catagaaaac 4920
taccttgcta agcagtcttt aaaaagcatg ctagacgata aagggctttt gaattttatc 4980
ggtgggtata tgaacgcttc tgaattaagt tctattttaa gcgtggtttt aaaagatatt 5040
actaatcccc ctacaagctt gcaaaaagac atcggtgtgg tagcgaacga cttgttgaac 5100

gagtttttag gacaagatgt tatcaaaaag ctagaaagtc aaggcttagt gagtaatatc 5160
attaataata tcatttctca aggcgggtta agcggcgttt ataatcaagg tttagggagc 5220
gtgttgccgc cctctttaca aaacgcgctc aaagaaaacg atttaggcac tcttttatcg 5280
cctagaggct tgcatgattt ttggcaaaaa gggtatttta acttttaag caatggctat 5340
gtttttgtca ataacagctc ttttagcaac gctacaggag gcagtttgaa ttttgtcgcc 5400
aacaagtcta ttatttttaa tggcgataat acgattgact ttagcaagta tcagggcgca 5460
ttgatttttg cttctaatga tgtttctaat atcaatatca ccaccctaaa cgctactaat 5520
ggcttaagcc ttaatgcggg tttgaataac gtgagcgttc aaaaagggga aatttgtgtc 5580
aatttagcca attgccccac aaccaaaaac agctcttcta caaactctag cgtaaccccc 5640
actaatgaat ctttaagcgt gcgcgctaac aacttcactt tcttaggcgc aatcgcttct 5700
aatggggcta ttgatttgtc tcaagtgaaa aataatagcg ttatagacac gctcaatctt 5760
aatgaaaatg cggccttgca agccaataat ttaacgatca ctaacgcttt taacaacgcc 5820
tctaactcta cagctaacat taatggtaat ttcaccttaa accaacaagc gaccttaagc 5880
actaacgcta gtggcttgaa tgtcatgggg aattttaata gctatggcga tttggtgttt 5940
aacctcagcc attcagttag ccatgccatt atcaacgctc aaggcagtgc gacaatcatg 6000
gctaataaca ataacccctt aatccaattc aacacttctt caaaagaagt tggcacttac 6060
acgcttattg atagcgctaa agccatttat tacgggtata acaaccaaat cacaggaggc 6120
agtagcctag ataattacct taagctttac actcttattg atattaatgg caagcacatg 6180
gtgatgactg acaacggctt aacctataac gggcaagccg tgagtgttaa agatggcggt 6240
ttagttgtgg gctttaaaga ctctcaaaat caatatattt acacttccat tctttataat 6300
aaagtgaaaa tcgctgtttc taatgatcct atcaataacc tacaagcccc cactttaaaa 6360
caatacatcg ctcaaattca gggcactcaa ggcgtggata gcattgatca agctggaggc 6420
agccaagcga ttaattggct caataaaatc tttgaaacta agggaagtcc tttattcgct 6480
ccctattatt tagaaagcca ttccacaaaa gatttaacca cgatcgctgg agatattgct 6540
aacactttag aagtcatcgc taaccctaat tttaaaaatg acgccaccaa tattttacag 6600
atcaacacct acacgcagca aatgagccgt ttagccaagc tctctgacac ttcaactttt 6660
gctagcgctg attttcacga gcgattagaa gcccttaaaa acaagcgatt cgctgatgcg 6720
atccctaacg ctatggatgt gattttaaaa tactctcaaa gaaacagagt caaaaataat 6780
gtatgggcga caggagttgg aggggctagt ttcattaatg gaggcactgg gactttatat 6840
ggtatcaatg tagggtatga ccgatttatt aagggcgtga ttgtgggggg ttatgccgct 6900
tatgggtata gcgggtttca tgcaaacatc actcaatcag gctctagcaa tgtcaatatg 6960
ggtgtttata gccgagcgtt tatcaaaaga agcgaattaa cgatgagctt gaatgagact 7020
tggggataca ataagacttt catcaactct tatgaccccc tactctcaat catcaatcag 7080
tcttacaaat acgacacctg gacgactgac gctaaaatca attatggcta tgatttcatg 7140
tttaaagata aaagcgttat ttttaaacct caaatagget tagcctatta ttacattggt 7200
ttgtctggtt taaggggcat tatggatgat cctatttaca atcagttcag agccaatgct 7260
gatcctaata aaaaatccgt tctaacgatt aattttgctc tagaaagtcg gcactacttc 7320
aataaaaact cttattattt tgtgattgcg gatgtgggca gagatttatt tattaattct 7380
atgggggata aaatggtgcg ttttattggt aataacaccc taagctatag agatggcggc 7440
agatacaaca cttttgctag cattatcaca ggcggggaga taaggttatt caaaaccttt 7500
tatgtgaatg cgggcattgg ggctaggttt gggcttgatt ataaagatat taatatcacc 7560
ggaaatattg gtatgcgcta tgctttt 7587

Seq ID 85
atgaatactt ataaaaacag cttgaatcac tttttaaatt tagtggattg tttagaaaaa 60
atccccaatg tgggtaaaaa gtccgccttt aaaatggcgt atcatttggg tttagaaaac 120
ccctatctgg cgctaaaaat cacgcacgct ttagagaacg ccctagaaaa ccttaaaaca 180
tgttcatctt gtaacgcgct cagcgagagt gaggtttgtg agatttgctc tgatgaaagc 240
cgacaaaatt ctcagctttg catggtttta cacccaagag atgtgtttat tttagaagat 300
ttaaaggatt ttttagggcg ctattatgtg ttaaactcca tagaagaagt ggattttaac 360
gccctagaaa aacgcctgat tgaagaaaac attaaagaaa tcatttttgc tttccctccc 420
actttagcta atgattctct aatgctttat attgaagaca aattacagca tttccacctc 480
actttcacta aaatcgctca aggcgtgcct actggagtga attttgaaaa cattgactca 540
gtttcgctct caagggcgtt taattcaagg atcaaagca 579

Seq ID 86
ttgtttaaaa gaatggtttt aatcgctctt ttaggggtgt tttcaagcgt ttcattaagc 60
gctaagagtc ttttaagaga tgatgggatt ttagtctctg atttaaaggg catgaaatca 120
gaactatctg atgctcctgc ttgggttttt gaagacgcta aagcccccta cgaagaaatg 180
ggcgtggcgt atatccctgt taataataaa tatttaggga ttgagcaagc gaccttaaac 240
gctaaattga gtctgatcgt ggtttttcat gaaatcatga tgaagtataa aaaacgcttc 300
atggagcaat tccatgagtc cgagcagacg actacgaata tcagttacgc tatctataat 360
tatctagcga ctaagatcca ggtatccaac acctacacga atttaaaatc ggaggtggcg 420
gtggtgaaaa tcaagctagt gggttgtcag attgagcaaa tcaaaaggta tttaaaagcg 480
agcgttgaaa accttaacga taatgaaatc gcttacatcg ctaaggtcgc tcaaaaagaa 540
tttggtagcg tttgtgcgtt aagg 564

Seq ID 87

ttgaaacatt taaccccact cactcacacc atctttaaag ccttatggct aggcacagcc 60
ttaagtgcat ctttaagttt agccgcaaca gaaagcccca ctaaaacaga gcctaagccc 120
gctaaagggg ttaaaaacaa gcccaaatcg cccgttacta aagtcatgat gaccaattgc 180
gacaatatta aagattttaa cgctaagcaa aaagaagtct taaaagccgc ttatcaattc 240
ggctctaaag aaaatttagg ctatgaaatg gcaggcattg catggaaaga gtcatgcgca 300
ggggtttata aaatcaattt ttcggatccg agcgcgggcg tgtatcattc ttatatccca 360
agcgttctaa aaagctatgg gcataatgat agccccttct tgcgtaatgt gatgggggaa 420
ttgctcatta aagacgatgc gtttgcttct gaagtggctt taaaagagtt gctctattgg 480
aaaacacgct accatgacaa tttaaaagac atgattaaat cttacaacaa gggcagtcgt 540
tgggaaagga gcgaaaaatc taacgctgat gctgaaaaat attacgaaga gatacaagac 600
agaatcaggc gtttgaaaga atctaaaatc tttgattcgc agtctagtaa tgaccaagaa 660
ttgcaaaaaa gcgctaatag caacctggat ttagacccta tcggcaacgc catgccccaa 720
gccttaattg ccaaagaaac taaaatagaa gaaacccaag cagaaaaatc ccaagaaatg 780
aaagagacaa ctagcgagca aacaaaaagt aagccagaaa aagcaaaaga taaacccatg 840
tatttggcgc aaatcaacag cactgatttc acacccgtta aaaaaagccc caaaaaaccg 900
gctaaagtga gccaaaaaca ctcctttaag aataacatta aaaataatgt aaaaaacaac 960
gccaaaaccg cttccaaaaa acaagaaatg tgcaaaaatt gctctccagg gcaaaggaat 1020
gcgattttag ctaaccacat cactctcatg caagagctt 1059

Seq ID 88
atgattgaat ggatgcaaaa tcatagaaaa tatttagtgg ttacaatatg gataagcacg 60
atcgctttta ttgccgctgg gatgataggc tgggggcaat acagcttttc tttagatagc 120
gatagcgctg ccaaagtggg acagattaag atttctcaag aagaattagc ccaagaatac 180
cgccgcctta aagacgcata tgctgagtct atccctgatt ttaaagaact caccaaagat 240
caaatcaaag ccatgcattt agaaaaaagc gctttagatt cgctcatcaa tcaagcctta 300
ttgagaaatc tcgctttaga tttagggctt ggcgctacaa agcaagaagt ggcgaaagag 360
atcagaaaaa cgagcgtttt ccaaaaagat ggcgtttttg atgaagaatt gtataaaaat 420
atcttaaagc aaagccatta ccgccccaaa cattttgaag aaagcgttga aaggctttta 480
atccttcaaa aaatcagcac tctattcccc aaaaccacta ccccttggga gcaatccagc 540
ctatcgcttt gggcaaaatt gcaagacaaa ttagacattc ttatcctaaa ccctagtgat 600
gttaaaatct ctcttaatga agaagagatg aaaaaatatt acgagtccca taaaaaggat 660
tttaaaaagc ccacgagctt taaaacacgc tctttatatt ttgacgctag tttggaaaaa 720
cctgatttga aggagttgga ggaatactac ataaaaaca aggtgtctta tttggacaaa 780
gaggggaaat tgcaggattt taaaagcgtt caagagcaag tcaagcatga tttaagcatg 840
caaaaagcga atgaaaaagc cttaaggagc tatatcgctc taaaaaaagc gaacgcgcaa 900
aactacacca cacaagattt tgaagagaac aactcccccc atactgctga aatcacgcaa 960
aaactcaccg ctctcaaacc ccttgaaatc ctaaagccag agccttttaa agatggtttt 1020
attgtggtgc aactcatctc tcaaattaaa gacgaattgc aaaattttaa tgaagctaaa 1080
agcgctctta aaacccgcct aactcaagaa aaaaccctta tggcgttgca aactttagcc 1140
aaagaaaagc ttaaggattt taagggcaaa agcgtgggct atgtaagccc taattttgga 1200
ggcactatta gtgagcttaa ccaagaagaa agtgctaagt ttatcaacgc tctttttaac 1260
cgccaggaaa aaaaggggtt tatcgctatt aataataaag tggtgctcta tcaaatcaca 1320
gaacaaaatt tcaaccactc atttagtgca gaagaaagcc agtatatgca gcgtttagtc 1380
aataacacta aaacggattt ttttgataaa gcgttgatag aagaattgaa aaaacgctat 1440
aagatagtca aatacattca a 1461

Seq ID 89
gtgtcccctc taaagacgat acggatctat tcttaccacg attctattaa ggactctatt 60
aaggcggtgg tgaatatctc cactgaaaag aagattaaaa acaattttat aggtggcggt 120
gtgtttaatg acccctttt ccaacaattt tttggggatt tgggtggcat gattcctaaa 180
gaaagaatgg aaagggcttt aggcagcggc gtaatcattt ctaaagacgg ctatattgta 240
actaataacc atgtgattga tggcgcggat aagattaaag ttaccattcc agggagcaat 300
aaagaatatt ccgccactct agtaggcacc gattctgaaa gcgatttagc ggtgattcgc 360
atcactaaag acaatctgcc cacgatcaaa ttctctgatt ctaatgatat ttcagtgggc 420
gatttggttt ttgcgattgg taacccttt ggcgtgggcg aaagcgttac gcaaggcatt 480
gtttcagcgc tcaataaaag cgggattggg atcaacagct atgagaattt cattcaaaca 540
gacgcttcca tcaatcctgg aaattccggc ggcgctttaa ttgatagccg tggagggtta 600
gtggggatta ataccgctat tatctctaaa actgggggca accacggcat tggctttgcc 660
atcccttcta acatggttaa agatactgta acccaactca tcaaaaccgg taagattgaa 720
agaggttact tgggcgtggg cttgcaagat ttgagtggcg atttgcaaaa ttcttatgac 780
aacaaagaag gggcggtagt cattagcgta gaaaaagact ctccggctaa aaaagcaggg 840
attttggtgt gggatttgat caccgaagtc aatgggaaaa aggttaaaaa cacgaatgag 900
ttaagaaatc taatcggctc catgctaccc aatcaaagag taaccttaaa agtcattaga 960
gacaaaaaag aacgcgcttt caccctcact ctagctgaaa ggaaaaaccc taacaaaaaa 1020
gaaaccattt ctgctcaaaa cggcgcgcaa ggccaattga acgggcttca agtagaagat 1080
ttaactcaag aaaccaaaag gtctatgcgt ttgagcgatg atgttcaagg ggttttagtc 1140
tctcaagtga atgaaaattc cccagcagag caagccggat ttaggcaagg taacattatc 1200
acaaaaattg aagaggttga agttaaaagc gttgcggatt ttaaccatgc tttagaaaag 1260

tataaaggca aacccaaacg attcttagtt ttagacttga atcaaggtta taggatcatt 1320
ttggtgaaa 1329

Seq ID 90
atgagtaaga gtttatacca aactttaaat gtgagcgaaa acgccagcca agatgaaatc 60
aaaaaatcct accgccgttt agcccgacaa taccacccgg atttgaataa aaccaaagaa 120
gccgaagaga aattcaaaga aatcaacgcc gcttatgaaa ttttgagcga tgaagaaaaa 180
cgccgccaat acgatcagtt tggcgataac atgtttggcg ggcagaattt cagcgatttt 240
gccagaagcc gtggtcctag tgaagattta gacgatattt taagctctat ttttgggaaa 300
ggaggctttt cgcaaagatt ttctcaaaac tcgcaaggct tttctggctt taatttttcc 360
aatttcgccc ctgaaaattt agacataacc gccgctttaa atgtctctgt tttagacacc 420
cttttaggca ataaaaaaca agtgagcatc aataatgaga cttttagcct taaaatccct 480
attggcgtgg aagagggcga aaagattagg gttcgcaaca aggggaaaac ggggcgaacg 540
actaggggcg atttgctctt agagatccat attgaagaag atgaaatgta taggcgcgag 600
aaagatgata ttacccaaat ctttgattta cccttaaaaa cggctctttt tggagggaaa 660
attgaaatcg ctacttggca taaaacctta accctaacca ttccccctaa caccaaagcg 720
atgcaaaaat tccgcattaa agaaaaaggg atcaaaaaca gaaaaacttc gcatgtgggg 780
gatttgtatt tgcaggctcg tttgattttg cctaaaactg aaacgctttc taatgagttg 840
aaagcgttat tagaaaaaga attg 864

Seq ID 91
atgaaacaaa caaccattaa ccactctgtg gaattagtag ggataggctt gcacaagggc 60
gttcctgtga agcttgtttt agagccttta ggggaaaatc aaggcattgt tttttaccgc 120
tctgatttgg gcgtgaatct ccccttaaaa cctgaaaaca tcgtggatac caaaatggca 180
accgtgttgg gtaaggataa tgctaggatt tctacgattg agcatttgct ttcagctgtc 240
catgcgtatg gcattgacaa tcttaagatc tctgtggata acgaagaaat ccctatcatg 300
gatgggagtg ctttgactta ttgcatgctt ttagatgaag cagggattaa agaactagac 360
gctcctaaaa aggtgatgga aatcaagcaa gccgttgaga ttagagagag cgataagttt 420
gttaaaattg agccagacag ccagctttct ttgaatttca cgattgattt taaccatccg 480
gttatcgcta agcaagccca tcattttgtc tttagtaaaa ccgcttacaa agagcaagtc 540
gctaaagctc gcacctttgg gtttttgcaa gaagtgaatt acttgcgatc cattggtttg 600
gcgaaaggag ggagtttgaa taattgcatc gtgctggatg aaaacagcat tttgaataaa 660
gagggcttga ggtgcgaaaa ggagtttgtg tgccataaga ttttagacgc tatgggggat 720
ctaatggttt taggcatgcc tgtgatgggc aaatacactt ctttttcagg gagtcataag 780
ctcaattcca tgttggttaa agccattttg gcggacgcta aaaattacga agttttgatc 840
gctgcagatc cggctaaaga atttgcgttg caaaaggctt tcgct 885

Seq ID 92
gtgcaaccga tgaaatctaa aaaactttat ttggctttaa tcataggggt tttattagcg 60
tttttaaccc tatcttcatg gctgggtaat agcggtttag tggggcgttt tggggtgtgg 120
tttgccgcac tcaataaaaa atattttggg catctttcat tcattaattt accctattta 180
gcatgggttt tattcctttt atacaagact aaaaaccctt ttacagaaat cgttttagaa 240
aaaactttag ggcatctatt aggcatttta tctttgctct ttttacaatc tagcctatta 300
aatcaagggg aaatcggcaa cagcgcgcgt ttgtttttac gccctttttat aggggatttt 360
gggctttatg cgctgataac gcttatggta gttatttctt atttgattct attcaaacta 420
ccccctaaaa gcgtttttta tccttatatg aacaaaacac aaaaccttt aaaagagatt 480
tacaaacaat gcttacaagc ctttagccct aattttagcc caaaaaaaga gggttttgaa 540
aacaccccat cagatattca aaaaaaagaa accaaaaacg acaaagaaaa agaaaaccgc 600
aaagaaaacc ctattaatga aaaccacaaa acccctaacg aagaaccgtt tttagcgatc 660
cctacccccc ataacacgac tttaaatgat tcagagccgc aagaaggctt agtccaaatt 720
tcctcccacc cccctaccca ttacaccatt taccctaaaa gaaaccgatt tgatgatttg 780
actaacccca ctaacccccc tttaaaagaa attaaacaag aaactaaaga aagagaaccc 840
acgcctacaa aagaaactct tacgcccacc acgcccaaac ctatcatgcc cacacttgca 900
cccataatag aaaatgacaa caaaacagaa aaccaaaaaa cccccaacca ccctaaaaaa 960
gaagaaaacc cacaagaaaa cacgcaagaa gaaatgatag aaggaaggat agaagaaatg 1020
ataaaggaaa atctaaaaaa agaagaaaaa gaagtgcaaa acgctccaaa ctttagccca 1080
gtaacccccа caagcgctaa aaaacccgtt atggttaaag aattgagcga aaataaagag 1140
atattagacg gattggatta tggcgaagtg caaaaaccca aagattatga gcttcccacc 1200
acgcaattat tgaatgcggt ttgtttgaaa gacacttctt tagacgaaaa cgagattgac 1260
caaaaaatcc aggatctatt gagcaaactg cgcaccttta aaattgatgg cgatattatc 1320
cgcacttatt caggccctat tgtaaccact tttgaattcc gcccagcccc taacgttaag 1380
gtgagtcgta ttttaggctt gagcgatgat ttagcgatga ctttatgcgc tgaatccatc 1440
cgcattcaag cccctattaa gggtaaagat gtcgttggca ttgaaatccc taacagccaa 1500
agccaaatta tttatttaag agaaattcta gagagcgaat tgtttcaaaa atccagctcg 1560
cccttaactc tagctttagg caaagacatt gtgggtaacc ctttcatcac ggatttaaaa 1620
aagctccccc atttgctcat cgctggcacg acaggaagcg gtaagagcgt gggcgtgaat 1680
gcgatgattt tatccttact ttataaaaac cctcccgatc aactcaaatt agtgatgatc 1740
gatcccaaaa tggtagaatt tagtatttat gcggatatcc ctcatttgct cacgcccatt 1800

atcaccgacc ctaaaaaagc tattggggct ttgcaaagcg tggctaaaga aatggaacgc 1860
cggtattctt taatgagcga atacaaggtt aaaaccattg attcttataa tgaacaagcc 1920
ccaagtaacg gcgttgaagc gttcccctat ttgattgtgg tgattgatga attagcggat 1980
ttaatgatga caggggggcaa agaagcggag tttcctatcg ctagaatcgc tcaaatgggg 2040
cgcgcgagcg gcttacacct cattgtagcg acccaacgcc caagcgtgga tgtcgtaacc 2100
ggcttgatta aaaccaactt gccttcaagg gtgagtttta gggtaggcac taagattgat 2160
tctaaagtga ttttagacac tgatggggcg caaagcttgt taggaagagg cgatatgctc 2220
tttacccccc caggagcgaa cgggttagtg cgcttgcatg ccccctttgc cactgaagat 2280
gaaatcaaaa aaatcgtgga ttttattaaa gcccaaaaag aagtacaata cgataaagat 2340
ttcttgctag aagaatcacg catgccttta gacaccccta attatcaagg cgatgacatt 2400
ttagaaaggg ctaaagcggt gattttagaa aaaaagatca cttctacgag ttttttacaa 2460
cgccaattaa aaatcggcta caaccaagcc gctaccatta ctgacgaatt agaagctcaa 2520
ggctttttat ccccaagaaa cgctaaaggc aacagagaga ttttgcaaaa cttt 2574

Seq ID 93
atgttagaaa atgtcaaaaa gtccttttt agggttttgt gcttgggtgc gttgtgttta 60
ggggggctaa tggcagagca agaccctaaa gagcttgtgg gtttgggggc aaagagctac 120
aaagagaaag atttcactca agcgaagaaa tattttgaga aagcgtgcga tttgaaagaa 180
aatagcgggt gttttaattt aggggtgctt tattatcaag ggcaaggggt ggaaaagaac 240
ttgaaaaaag ccgcctcctt ttacgctaaa gcttgcgatt tgaattacag caatgggtgt 300
catttgctag ggaatttata ttacagcggg caaggcgtgt cccaaaacac caataaagcc 360
ctacaatact actctaaagc gtgcgatttg aaatacgctg aagggtgcgc gagcttaggg 420
gggatttatc atgatggtaa agtggtaact agggatttta aaaaagcggt ggaatatttc 480
actaaagcgt gcgatttaaa cgatggcgat ggttgcacga tattagggag cttgtatgat 540
gcaggcagag gtacgcctaa agatttgaaa aaggcgctcg cttcgtatga taaagcttgc 600
gacttaaaag acagcccagg gtgctttaac gcagggaata tgtatcatca tggcgaaggt 660
gcaacgaaga attttaaaga ggctctcgct cgttattcta aagcatgcga attggaaaat 720
ggcggagggt gtttcaattt aggggctatg caatacaatg gcgaaggcgt aacaaggaat 780
gaaaagcaag ccatagaaaa ctttaaaaaa ggctgtaaat tgggcgctaa aggggcgtgc 840
gatattctca agcagcttaa gatcaaagtt 870

Seq ID 94
gtgaagttac ccaaagcctt aaacgaagcc accgcaggag cggccttaaa atatcacatt 60
aaaagagcgc ttgagagaag ccactcaata agcgatttta gtaagaattt agaactaagc 120
acacaaaaat cccactttag caacaacacg cttaaaatca ttgaagagct taacaacggc 180
gtcaaacaag cgagcgaaga aatcaaagaa aaagcgcgcg atttttctaa tcaaaaactc 240
actaacgagc aaatcaaaga tctattaaat aacgcagaaa tccctacaag cgggagagac 300
gctatcactt ttggagtgaa taacctaaac cctgagattg ttgaattcct gcacaaaaac 360
aacaagaaaa tgattataga aaaagcctct aacaaagaat tagaactttt aaaagacgct 420
aactttaaac accctgaaaa cataagggcg agtttagatc atgatgctat cgctcacata 480
ctcaaaaggc atggcgttaa ttctgttaat gttagaaatg gtgagatccc tattacgaac 540
gaagatattg ctaattatag atatatcgtt aataacgctg atgcaattct taggacttta 600
gacaacgaga ataaagaact tataagcgcg tttaaacaaa tcaacggcta tgcggtagtc 660
gtggagcaag cgatcaataa gaaaaatgaa ttagttttga aaacgatgta taagagtaaa 720
ggagattata aggataataa cgcttataag aagttttcaa gcacccatac actcaatgct 780
gatgcaaagg tgaaccatag gttgagttcc tatagcggtg ctacagagaa tactactcaa 840
aaagatttaa tagatcaaga gaatttatta aaaacaagcg aaaatttaaa cgaaagcaca 900
ccaaaaccta ccaacttaag cccgctagaa caagccaacg ctgaaaagtt agcgaagtta 960
gaaagcgaga agctagaaag cgaaaaagag tttttgaaag ctaaagagca agaagccaca 1020
cgcaaagccg cattaaaaaa gaaattagaa cacgagcgag gcaatgcggg caacattgaa 1080
agccagacta aaatagaagt aggagaggat atacccacac aaacacaagc gcaattaccc 1140
aaaagccgag tgaggctaaa cgaacgagag atttacgatc tagactatgc gatcgtcaaa 1200
gcgaaagatt taaaaccaag ctttaccaca ggcgggacgc aaaagagaac ggacatgaac 1260
gaagagcaga ttaaaagcat tgctgaaaat tttgatccta aaaagatatt tggtagcgga 1320
gggtttgaag atttaccgat cattctacat gacgggcaag tgatcgcagg aaaccacaga 1380
atccaaggca tgctaaactt cacgcctaaa agccgttttt cttacgagag agcgatcaag 1440
gaatactatc acatagactt aaaaccggac gagttgttag tgagagtgcc acacaagcgc 1500
ctaaacaaca ccgagatcaa caatttagcg gcttcatcca atcaaggacg cttcaatagc 1560
gaaagcgatc acgctatagc ggttttaagc cactatgaag ccaagttaaa agaattagac 1620
caaaaattag acgctgatag catctactca ttaaaaaaca ttgttgctaa aaatttgaat 1680
tttgataagg ctacgcatcc taatgtaacc gatagtaatt tagcgttgct gatgtttaac 1740
atgccacgaa ccaaaacgca agggatagaa ttactcaacc gctggaaaaa agaattttcc 1800
aacgacatta aaagctatga aaaagtaaaa aaaatgtttg tagataacgc gggcagtttt 1860
cacaatctca tccacgatct gaacttccct aaggtgagtt taaacgctta tttaagcgat 1920
attatggatc gcagttttgc gaatttaaag aattaccaaa gcacgagcga gagcctgaaa 1980
gatttgagcg aaaaattcta taaaacgagt tcgttagaga tgtttgaaaa gagcgatcaa 2040
agcacgagcg atattagcga gattttagga ggagcgatcg cacgatttgc acgatttgat 2100
gatccgagca aagcgttatt tgaagcctta agaagcgata acattaaaaa aggcttgaaa 2160

gattacaaga tcgcagatgt tactaaggac atgtttaacg ctgatagtaa agagtttaag 2220
gacattgata tttacgattt cacgcattac cttttaatgg taaatagaga gccgaatgaa 2280
aataacccta tcttaaagcg cttgatagaa gccgtgaaag acatgcaaaa agaaagcgag 2340
aaaggaataa aacaaaaact tgaaacgcct agcgaatggg gacacaatta tagcgagttt 2400
aaaggtgatg gtttaggagc gattaacaag ttattagaaa ctaaaaaagg ttttgtagcg 2460
ggagcgtttc ataaggaagg tttaggggat attgatttag tttatggaaa ctctaaatac 2520
ggactagaac atatatttaa tcgtagggaa agcgatgcga tagacaaagg catgagtaaa 2580
gaagaagcta aaaaatacgc attaaaaata attaacaata tccctaacat aataagcaat 2640
ggaaaactat caaaagataa tttagggcgt ttaagtattg agtttgaaaa tcaaagagtg 2700
ggtttgaatg atagttggaa aggtgagact ttaaataata ggtgggttat tacaagttat 2760
gaaatagata aatcaaggaa tgggctaatt gagtcgcctt tagcaccaaa ttacaagggg 2820
aaagatacta atcccctaaa ccttgatagc cctaatccta ccacaaaaaa t 2871

Seq ID 95
atgggatacg caagcaaatt agccttgaag atttgtttgg caagtttatg tttatttagc 60
gctcttggtg cagaacacct tgaacaaaaa aggaactata tttataaagg ggaggaagcc 120
tataataata aggaatatga gcgggcggct tctttttata agagcgcgat taaaaatggc 180
gagccgcttg cttatgttct tttagggatc atgtatgaaa atggtagggg tgtgcctaaa 240
gatgaaaaga aagcggctga atattttcaa aaagcggttg ataacgatat acctagaggg 300
tataacaatt taggcgtgat gtataaagag ggtagaggtg tgcctaaaga tgaaaagaaa 360
gccgtggagt attttagaat agctaccgag aagggctata ctaacgccta tataaactta 420
ggcatcatgt atatggaggg taggggagtt ccaagcaact atgtgaaagc gacagagtgc 480
tttagaaaag cgatgcataa gggtaatgta gaagcttata tccttttagg ggatatttat 540
tatagtggga atgatcaatt gggtattgag ccagacaaag ataaggcgat tgtctattat 600
aaaatggcgg ctgatatgag ctcttctaga gcttatgaag ggttagcaga gtcttatcag 660
tatgggttag gcgtggaaaa agataagaaa aaggctgaag aatacatgca aaaagcatgc 720
gattttgaca ttgataaaaa ttgtaagaaa aagaacactt caagccga 768

Seq ID 96
atgggcggaa tcttatcttc actcaacact tcttacaccg gccttcaagc ccatcagagc 60
atggtggatg ttaccgggaa taatatttct aacgctagcg atgaatttta tagccgccag 120
cgcgtgattg caaagcccca agcggcctat atgtatggca ctaaaaacgt gaatatgggc 180
gtggatgtgg aagccattga aagggtgcat gatgagtttg tttttgctcg ttacacgaaa 240
gctaattacg aaaacactta ttacgataca gaatttcgc atttaaaaga agcgagcgcg 300
tattttccgg acattgatga agcgagcctt tttacggatt tgcaagatta ttttaattca 360
tggaaagaat tgtctaaaaa cgccaaagac tccgctcaaa aacaggctct cgctcaaaaa 420
acagaagctt taacgcacaa cattaaagac accagagaga ggttaacgac cttacagcac 480
aaggcgagtg aagaattaaa aagcgtcatt aaagaagtca atagcttggg ttctcaaatc 540
gctgagatta acaaacgcat taaagaagtg gaaaacaaca agagtttaaa gcatgcgaac 600
gaattaaggg ataagcgaga tgaattggaa ttccatttgc gagagctttt agggggaat 660
gtttttaaaa gcagcattaa gactcattcg ctcaccgata aagactcagc ggattttgat 720
gagagctata accttaatat cgggcatggg ttcaatatca ttgatggctc tattttccat 780
cctttagtgg ttaaagaatc cgaaaataaa gggggtttga accaggttta ttttcaaagc 840
gatgatttta aggttactaa tattactgac aagctcaatc agggaagagt gggggcgtta 900
ttgaatgtgt ataatgacgg ctctaacggg actttaaagg gcaaattaca agattatatt 960
gatttgttgg attcttttgc taagggtttg atagaatcca ctaatgcgat ttacgctcaa 1020
agcgcgagtc attatattga gggcgagccg gtggagttta atagcgatga agcctttaaa 1080
gacactaact acaatatcaa aaacggctcg tttgacttaa tcgcttacaa caccgatggt 1140
aaagaaatcg ctagaaaaac cattgctatc acgcccatta caaccatgaa cgatattatc 1200
caagccatta acgctaacac tgatgacaat caggacaata acaccgaaaa cgattttgat 1260
gattatttca cagcgggctt taacaatgag actaaaaagt ttgttatcca gcctaaaaac 1320
gcttcgcaag ggttgtttgt ctctatgaaa gataacggca cgaattttat gggagcgtta 1380
aaactcaacc ctttttttca aggcgatgac gcttctaata tcagcttgaa taaggaatac 1440
aaaaaagagc ctaccactat ccgcccatgg cttgctccca ttaatgggaa ttttgatgtg 1500
gcgaacatga tgcagcaatt gcaatacgat agcgtggatt tttataacga taagtttgac 1560
attaaaccaa tgaaaatcag cgagttttat caatttttaa ccggtaaaat caacacggac 1620
gctgaaaaat ccgggcgtat tttggacact aaaaagagca tgttagaaac cattaaaaaa 1680
gagcaactct ctatttcgca agtgagcgtg gatgaagaaa tggtgaattt gatcaagttt 1740
caaagcggct atgcggctaa cgctaaagtc attaccgcta ttgatcggat gatagacact 1800
ttattgggga ttaaacaa 1818

Seq ID 97
atgaggtatt tatggctttt tttaatacac actatagggc tttttgcaac agataaaaca 60
ctagatatta ttaaaaccat tcaaaaactt cctaagattg aagtgcgcta ctctatagat 120
aacgatgcca attacgcttt aaaattgcat gaagtcttgg cgaatgattt aaagactagc 180
cagcattttg atgtttctca aaacaaggat caaggtgcta tcaattacgc agaactcaag 240
gataaaaaag tccatctcgt agcgcttgtg agcgtggcgg tagaaaacgg caataaaatt 300
tcacgattaa aactttatga tgtggataca ggaacgctca aaaagacttt tgactaccct 360

attgtaagtt tagatctata ccctttgca gcgcacaaca tggctattgt ggtgaatgac 420
tatttaaaag ccccttctat cgcttggatg aagcgcctta ttgtttttc taaatacatt 480
ggaccaggaa tcacaaatat cgcactagcg gattatacga tgcgttatca aaaagaaatc 540
atcaaaaaca ataggctcaa tatcttccct aaatgggcga acgctgagca aacggagttt 600
tattacacgc agtatggcga aagaacgccc atgattttaa aatacaacat tcaaaaagcc 660
actcatgaga atatcgctag ctctcaagga atggctgtgg tctctagcgt gagttctgat 720
ggctctaaaa ttttaatgtc tttagcccct gatggccaac cggatgtgta tttgtatgac 780
acgcataaaa aaactaaaac taaaataacg cgctatccgg ggatagatgt ctcaggagtg 840
tttttagaag atgacaagtc tatggctttt gtttcggata gatccggtta tcctaacatc 900
tacatgaaga aattggggtt aaaagagagc gcggagcaac tcctttatga agggagaagc 960
aatgaatcca ttgacgctta taaagatagt attgtgtatg tgagccggga aaaccttaat 1020
gaatttggca aaacggtgtt taatttgaat ttgatcacct taaatagcaa atatatccgc 1080
aggcttaccg tgaatggctc taaccagatg cctcgttttt ctacggatgg gagaaatatc 1140
atgtatatca aaaagacacc ccaagaatac gccatggggc ttattttgct agattataat 1200
cagagttttt tattcccttt aaagaatgtg aaaatacaag cctttgattg g 1251

Seq ID 98
atgtttcaag cgttaagcga tgggtttaaa aacgcgctca ataaaatccg ctttcaagat 60
gatgaaaaag cgctagacag agcgttagat gaattgaaaa aaacgctctt aaaaaacgat 120
gtgcatcata aagtggctag agaattgctc aaaaaagtgg aaagtcaaac taaacttaat 180
ggcattggta agcagcaatt tttagacgct ttagaaaaga gtttgttaga aattttaagc 240
gctaaaggga gcagtggttt cactttcgct caaacgcccc caactgtggt tttaatggcc 300
ggtttgcaag ggagcggtaa gacaaccacc accgctaaac tcgctcatta tttaaaaacc 360
aaaaataaaa aagtgctttt atgcgcatgc gatttgcaac gcctagcggc agtggagcaa 420
ttaaaggttt tgggcgaaca ggtgggcgtg gaagtttttt atgaagaaaa taaaagcgtg 480
aaagaaatcg ctagcaacgc tttaaaaagg gctaaagaag cgcaatttga tgttttgctc 540
gtggatagcg cggggcgttt agccattgat aaagagctta tgcaagaatt aaaagaagtt 600
aaagaaatct taaaccccca tgaagtgctg tatgtcgcag acgcattgag cgggcaagat 660
ggcgtcaaaa gcgcgaacac ctttaatgaa gaaataggcg tgagtggggt ggtgttaagc 720
aaatttgata gcgattctaa agggggtatc gccttaggca tcacttacca attaggctta 780
cccttgcgtt ttattgggag cggggaaaaa atccctgatt tagacgtgtt tgtgcctgaa 840
agaattgtgg ggcgtttgat gggggctgga gatattgtct cgctcgctga aaaaaccgct 900
agcgttttaa accctaatga agccaaagat ttaagcaaaa aactcaaaaa agggcaattc 960
actttcaatg acttttaaa ccagattgaa aaagtgaaaa aattaggctc tatgagttct 1020
ctaatctcta tgattccagg tttagggaat atggcaagcg cgttaaaaga cacggattta 1080
gaaagctctt tagaagtgaa aaaaatcaag gctatggtca attccatgac caaaaaagag 1140
caagaaaacc ccgagatttt aaacggcagc cgaagaaaaa ggatcgcttt agggagcggt 1200
ttagaagtgt ctgaaatcaa tcgcatcatc aaacgctttg atcaagcgag caaaatggcg 1260
aaacgcttaa ccaataaaaa gggtattagc gatttgatga atctaatgag tcaggctaaa 1320
aatcaaacgc cccctaaaat gcgc 1344

Seq ID 99
atgataatga aacaagaacc caccacctac caaccagaag agatagaaaa aaagatttat 60
gaaatttgct ctcatagggg gtattttgaa attgatggca atgaagcgat ccaagaaaaa 120
aacaaacgat tttgcttgat gatgcccccc cctaatgtga ccggtgtgtt gcacataggg 180
catgccctga ctttaagctt gcaagatatt ttagcgcgtt acaaacgcat ggatgggtat 240
aagactttgt atcagcccgg gttggatcac gctggcattg caacgcaaaa tgtcgtggaa 300
aagcagcttt taagtcaagg gattaaaaaa gaagatttag ggcgtgaaga gttcattaaa 360
aaagtgtggg aatggaaaga aaagagcggg ggagcgattt tagagcaaat gaagcgttta 420
ggcgtgagcg cggcctttc taggactcgt ttcacgatgg ataagggctt gcaaagagcg 480
gtcaaattgg cgtttttgaa atggtatgaa aaaggtctca ttattcaaga taattacatg 540
gtgaattggt gcactaaaga tggggcgttg agcgatattg aagtggagta tgaagagcgt 600
aaggggcgt tgtattatat tagatattat ttagaaaatc aaaaagatta tttagtggtg 660
gctaccacac gccctgaaac cttgtttggc gatagcgcgc ttatggtcaa tcctaacgat 720
gagagataca agcatttggt ggggcaaaaa gcgatcttgc ctttaatcca tcgcacaatc 780
cctattatcg ctgatgaaca tgttgaaatg gagtttggca cagggtgtgt gaaagtaacc 840
cctgggcatg attttaacga ttatgaagtg ggcaaacgcc accatttgga aacgattaaa 900
atctttgatg aaaaggggat tttaaacgcg cattgcgggg agtttgaaaa tttagaacga 960
ttagaagcta gagataaggt cgtagaaaga ttaaaagaaa acgccctatt ggaaaaaata 1020
gaagaacaca cgcatcaagt ggggcattgc tatcgttgtc ataatgtggt agaaccttat 1080
gtgtctaagc aatggtttgt caagcctgaa atcgctcaaa gttctattga aaaaatccaa 1140
caaggtttgg cgcgattcta cccttctaat tggatcaata attacaacgc ttggatgagg 1200
gaattacgcc cttggtgtat cagcaggcaa ttgttttggg ggcatcaaat accggtattc 1260
acttgcgaga ataaccacca gttcgtaagc ttagacaccc ccttaagttg ccctacttgt 1320
aagagcgaaa cactagagca agataaggat gtgctagaca catggtttag ttcagggcta 1380
tgggcgtttt ccactctagg gtgggggcaa gaaaaaagcg gtttgtttaa tgaaagcgat 1440
ttgaaagatt tctaccctaa cacaacgctc attactgggt ttgacatcct ctttttttgg 1500
gtggctagga tgctttttg cagcgaatcg cttttaggcg aattgcccct taaagatatt 1560

tacttgcacg ccttagtgag agatgaaaag ggtgaaaaaa tgagcaaatc taagggtaat 1620
gtgatcgatc ctttagagat gatagaaaaa tacggcgcgg atagcttgcg tttcacttta 1680
gccaatttgt gcgctacggg tagggacatt aagctttcca ctacgcattt agaaaataac 1740
aagaatttcg ccaacaagct ttttaatgcg gcgagttact tgaagctcaa acaagaatct 1800
ttcaaagata aagagcgttt gaatgaatac caaacgcctt tggggcgtta tgcgaaatcg 1860
cgcttgaatt cagcgactaa agaggcgcgt aacgctttag ataattatcg ttttaatgac 1920
gccacgactt tgttataccg ctttttgtgg ggggaatttt gcgactggtt cattgaattt 1980
tctaaagtgg aaaatgaagc gatagacgaa ttagggagcg tgttaaaaga ggctttaaaa 2040
ctcttgcacc ctttcatgcc ctttatcagc gagtctttat accacaagct cagcaatacg 2100
gaactagaaa acactgaatc tatcatggtc atgccttacc ctaaagattt ggcgcaagat 2160
gaaaaattag agcatgaatt tgaagtgatt aaagattgca ttgtgtcttt aaggcgttta 2220
aaaatcatgc tagaaacccc accgattgtt ctaaaagaag cgagcgtggg attaagagaa 2280
gccatagaaa acacagagcg tttgcaaact tacgcccaaa aattagcgag gttggaaaaa 2340
gtcagcgtga ttagttctaa gcctttaaaa agcgtgagcg atgtggggga attttgccag 2400
acttatgcga atttagaaaa tcttgattta agcccgcttg ttgcgcgttt gaaaaagcag 2460
ttggaaaaat tggaaaaaga aaaattaaaa ctcaatttgc acaatgaaaa ttttgtcaaa 2520
aacgcgccta aaagcgtgct agaaaaagct aaagagagtt taaaaacgct tttagaaaaa 2580
gaaagtaaaa ttaagcaaga attggacttg ttagaacaac ca 2622

Seq ID 100
atgaaaaaaa ctttttgat cgctttagcg cttacggctt ctcttgtagg cgctgaaaat 60
accaaatggg attataagaa taaagaaaat ggcccacacc gctgggacaa attgcacaaa 120
gattttgaag tgtgcaaaag cggtaaaagc caatcgccca tcaacattga gcattactac 180
cacacgcaag ataaagccga tttgcaattc aaatacgccg cttctaaacc taaagcggtc 240
tttttcaccc accacacttt aaaggcttcg tttgagccga ctaaccacat caattataga 300
gggcatgact atgtgttgga taatgtgcat ttccacgccc ctatggagtt tttaatcaat 360
aataaaacca ggcctttgag cgcgcatttc gtgcataaag acgctaaagg gcgtttgcta 420
gtgttagcga ttggttttga agaagggaaa gaaaacccca accttgatcc tattttagaa 480
ggcattcaaa agaaacaaaa ttttaaagag gtggctttag acgctttctt gcctaaaagc 540
atcaattact accatttaac ggctctctca ccgctcctcc ttgcacagag ggggtggcat 600
ggtttg 606

Seq ID 101
atgtcaaaaa aaattcccct aaaaaaccgc ttgagagctg attttacaaa aaccccaaca 60
gatttagaag tccctaattt attattatta caacgagaca gctatgattc tttcttgtat 120
tctaaagagg gtaaagagag cgggattgaa aaggttttta aatccatttt ccctatccaa 180
gatgagcata accgcatcac tttagaatac gcgggttgcg aatttggcaa gtctaaatac 240
accgttagag aagcgatgga gaggggcatt acctactcta tccctctcaa aattaaggtg 300
cgcttgatct tgtgggaaaa agataccaag agtggcgaaa agaacggcat taaggatatt 360
aaagaacaaa gcattttcat tcgtgagatc cctttgatga cagaacgcac ttcatttatt 420
attaatgggg tggagcgcgt ggtggtcaat caactccaca gaagccccgg tgtgattttc 480
aaagaagaag agtctagcac ttctttaaac aagctcattt acacagggca aatcattcct 540
gataggggtt cgtggttgta ttttgaatac gattctaaag atgttttata cgctcgtatc 600
aataaacgcc gtaaagtgcc tgttaccatt ttattcaggg cgatggatta tcaaaaacaa 660
gacatcatca aaatgttcta cccgcttgtt aaagtgcgtt atgaaaacga taaatatttg 720
atcccgtttg cttcattaga cgccaatcaa agaatggaat ttgacttgaa agatcctcaa 780
ggcaaggtta ttcttttagc gggtaaaaag ctcacttcaa gaaagattaa agagcttaaa 840
gaaaaccatt tagaatgggt ggaataccct atggatattt tactcaatcg ccatttagct 900
gagcctgtta tggtagggaa agaagtctta ttggacatgc tcactcagct agataaaaac 960
aaattagaaa aaatccacga tttaggcgtg caagaatttg tgatcatcaa cgatctggcg 1020
ttagggcatg acgcttccat tatccaatct ttttcagccg attctgagtc tttgaaatta 1080
ctcaagcaaa ccgaaaaaat tgatgatgaa aacgctctag cggcgattcg tatccataag 1140
gttatgaaac caggcgatcc cgttacgact gaagtggcta agcagtttgt caaaaaactt 1200
ttctttgatc cagaacgcta tgatttgacc atggtgggcc gcatgaaaat gaatcacaag 1260
ttaggcttgc atgtgcctga ttacattacg actttaacgc atgaagatat tatcaccacc 1320
gttaaatacc tcatgaagat caaaaacaat caaggcaaga ttgatgacag ggaccacttg 1380
ggcaatcgta ggattagggc ggtaggggaa ttgttggcca atgaattgca ttcaggttta 1440
gtgaaaatgc aaaagaccat taaagacaag ctcactacca tgagcggggc ttttgattcg 1500
ctcatgcccc atgacttggt caattctaaa atgatcacaa gcaccatcat ggaatttttc 1560
atgggcggtc agctctcgca atttatggat caaacgaatc ccttgagtga ggttacgcac 1620
aagcgccgcc tttcagcgct cggcgaaggg gggttggtga aagacagagt ggggtttgaa 1680
gccagggatg tgcaccccac gcattatggc cgaatttgtc ccattgagac cccagaaggt 1740
caaaatatcg gtctgatcaa cacccttccc actttcacaa gagtgaatga tttaggcttt 1800
attgaagccc cttataaaaa ggttgtggat ggcaaggtcg tgggtgagac gatttatttg 1860
accgctattc aagaagacag ccacatcatc gctcccgcaa gcacccccat tgatgaagag 1920
gggaatattt tgggcgattt gattgaaacg cgcgtggaag gcgagatcgt tttaaacgaa 1980
aaaagcaaag taaccttaat ggatttaagc tctagcatgc tagtgggggt agccgcatcg 2040
ctcattcctt tcttagagca tgatgacgcc aaccgtgcct taatggggac taacatgcag 2100

cgccaagcgg tgcccttatt aagaagcgac gctcccattg taggcacggg gattgaaaaa 2160
attattgcta gggattcttg gggagcgatc aaagccaatc gcgcaggcgt tgtagaaaaa 2220
attgattcta aaaatattta tattttaggc gaaagcaaag aagaagccta tattgatgcg 2280
tattctttgc aaaaaaactt gcgcaccaac caaaacacca gtttcaatca agtccctatc 2340
gttaaagtgg gcgataaagt gggagccggg caaatcatcg ctgatggccc tagcatggat 2400
agaggcgagt tggcgttagg gaaaaatgtg cgcgtggcgt tcatgccttg gaatggctat 2460
aactttgaag acgcgatcgt ggtgagtgag tgcatcacta aagatgatat tttcacttcc 2520
acccacattt atgaaaaaga agtggatgct agggagctta agcatggtgt ggaagaattt 2580
accgctgata ttcctgatgt gaaagaagaa gcgctcgctc atcttgatga aagcgggatc 2640
gttaaagtcg gtacttatgt gagcgctggc atgattttgg tgggcaaaac ttctcctaaa 2700
ggcgagatta aaagcacgcc tgaagagcgg cttttaaggg ctatttttgg ggataaagcc 2760
gggcatgtgg tcaataagag tttgtattgc cctcccagtt tggaaggcac ggtgattgat 2820
gtgaaagtct tcactaaaaa aggctatgag aaagacgcgc gagttttgag cgcgtatgaa 2880
gaagaaaaag ccaagcttga tatggagcat tttgatcgct tgaccatgct caatagagaa 2940
gaattgttgc gcgttagctc gctcctttct caagcgattt tagaagagcc tttcagccat 3000
aacggcaagg attataaaga aggcgatcaa atccctaaag aagaaatcgc ttcaatcaac 3060
cgcttcactt tggctagttt ggtcaaaaag tattctaaag aagtgcaaaa ccactatgaa 3120
atcactaaaa acaatttctt agagcaaaag aaagttttgg gcgaagagca tgaagaaaag 3180
ctttctattt tagaaaaaga tgatattttg cctaatggcg tgatcaaaaa agtcaagctc 3240
tatatcgcta caaaacgaaa gcttaaagtg ggcgataaaa tggcaggaag gcatgggaat 3300
aaagggattg tgtctaatat cgtgccggtt gcggatatgc cttataccgc tgatggcgag 3360
cctgtagata ttgttttaaa ccctttaggc gtgccaagcc gcatgaatat cgggcagatt 3420
ttagaaatgc atttaggctt agtggggaaa gaatttggga agcaaatcgc tcgcatgcta 3480
gaggataaaa ccaaagattt tgccaaagaa ttgcgtgcta aaatgctaga aatcgctaac 3540
gctattaatg aaaaagaccc cttgacaatc catgcgcttg agaattgttc tgatgaagag 3600
cttttggaat acgcaaaaga ttggagcaag ggcgttaaga tggctatccc tgtgtttgaa 3660
ggcatctcgc aagaaaaatt ttataagcta tttgaattag ctaagatcgc tatggatggc 3720
aaaatggatc tgtatgacgg acgcacaggc gagaaaatga gggagcgcgt gaatgtgggc 3780
tacatgtata tgatcaaact ccaccattta gtggatgaaa aagtccatgc cagaagcaca 3840
ggcccttata gcttagtaac gcaccagccc gtgggggtta aagcgctctt tgggggtcaa 3900
aggtttgggg aaatggaagt gtgggccttg gaagcttatg gcgcagcgca cactctaaaa 3960
gaaatgctca ccattaaatc cgatgatatt agaggcagag agaacgctta tagggctatc 4020
gctaaaggtg agcaagtggg cgagagtgaa atccctgaga ctttctatgt tttgactaaa 4080
gaattgcaat cgctcgcttt ggatattaat atttttgggg acgatgtgga tgaggatgga 4140
gcacctaaac ccattgtcat taaagaagat gacaggccta aagactttag ctctttccag 4200
ctcacactag ctagccctga aaaaatccat tcttggagtt atggggaagt taaaaagcca 4260
gaaacgatca attatcgcac cctaaaacct gaacgagacg gcttgttttg catgaaaatc 4320
tttggcccca ctaaagatta tgaatgcttg tgcggcaaat acaaaaagcc tcgcttcaaa 4380
gacattggca catgcgaaaa atgcggcgtg gcgatcacgc actccaaagt caggcgtttt 4440
agaatggggc atattgaatt ggccactcct gtagcgcata tctggtatgt taattccttg 4500
cctagccgta tcggcacgct tttaggcgtt aagatgaaag acttagagcg cgtgttgtat 4560
tatgaagctt atatcgttaa agaaccaggc gaagccgctt atgacaatga aggcactaag 4620
cttgtgatga aatacgatat tttgaatgaa gagcagtatc aaaatatctc acgaagatac 4680
gaagacaggg gctttgtagc gcaaatgggc ggtgaagcga tcaaggattt gttagaagaa 4740
attgatttga tcaccttatt gcagagtttg aaagaagaag tgaaagacac caattctgat 4800
gcgaaaaaga aaaaactcat taagcgtttg aaagtggtag aaagcttttt aaattctggt 4860
aataggcctg aatggatgat gctcacggtt ttaccggtat tgccaccgga tttaaggcct 4920
ttagtcgcgc tagatggcgg gaagtttgca gtcagcgatg tgaatgaatt gtatcgtcgt 4980
gtcatcaatc gtaaccaacg cttgaaacgc ttaatggagc ttggagcgcc agaaatcatt 5040
gtgcgcaatg aaaaaaggat gttgcaagaa gccgtggatg tgcttttga taacggccgc 5100
agcactaatg cggttaaagg ggctaacaaa cgcccttaa aatcgctcag tgaaatcatt 5160
aaaggcaagc aggggcgttt caggcaaaac cttttaggta agcgcgtgga tttttcaggc 5220
agaagcgtga ttgtggttgg gcctaatctc aaaatggatg aatgcgggtt gcctaaaaac 5280
atggcgttag aactcttcaa accgcatttg ttatccaagc ttgaagagag aggctatgcc 5340
accacgctca aacaggctaa acgcatgatt gagcaaaaaa gcaatgaagt atgggagtgc 5400
ttgcaagaaa tcacagaggg gtatccggtg ctactcaacc gcgctcctac cttgcacaag 5460
caatccattc aagcgttcca tccaaagctg attgacggca aagcgatcca attgcacccg 5520
ttagtgtgtt cagcgttcaa cgccgatttt gacggggacc aaatggcggt gcatgtgcct 5580
ttaagccagg aagcgatcgc tgaatgcaag gtgctgatgc taagctctat gaatatcctt 5640
ttgcctgcta gcggtaaggc cgtagccatt cctagccaag atatggtttt agggctttat 5700
tatctttctt tagaaaagag cggggtcaag ggcgagcata agcttttttc tagcgtgaat 5760
gaaatcatca ccgccattga cacgaaagaa ttagacatcc acgcaaagat tagggtttta 5820
gatcaaggga atattatcgc tacgagtgca gggcgcatga tcattaagtc cattttgcct 5880
gattttatcc ctacggattt gtggaacaga cccatgaaga aaaaagatat tggcgtgctt 5940
gtggattatg tgcataaagt tggcggtatc ggtattactg caacctttt ggataattta 6000
aaaacgcttg gctttaggta tgcgactaag gctggtattt ctatctctat ggaggatatt 6060
atcacgccaa aagacaagca aaaaatggtg gaaaaagcca aagtagaggt taaaaaaatc 6120
cagcaacaat acgatcaagg gctgctcact gaccaagagc gttacaataa gatcattgac 6180

acttggactg aagtcaatga caaaatgagt aaagaaatga tgaccgctat cgcgcaagat 6240
aaagagggct ttaactctat ttatatgatg gcagatagcg gcgcaagggg tagcgcggcg 6300
caaatccgtc agctttcagc gatgaggggt cttatgacaa agccggacgg cagtatcatt 6360
gaaacgccca ttatttctaa ctttaaagag gggttgaatg tcttagaata cttcaattcc 6420
acgcatggcg ctagaaaggg cttagcggat acagcgctaa aaacagccaa tgcggggtat 6480
ttgaccagaa agctcattga tgtttcgcaa aatgtcaagg tggtgtctga tgattgcggc 6540
acgcatgaag ggattgaaat cacggatatt gcggtgggga gtgagctgat tgaaccttta 6600
gaagagcgta tttttgggcg cgttttatta gaagatgtga tcgatcccat tacgaatgaa 6660
atcttgcttt atgcggacac tttgattgat gaagagggtg ctaaaaaggt ggttgaagcc 6720
gggattaaat ccattacgat ccgcacccca gtaacttgta aagcgccaaa gggcgtgtgc 6780
gcgaaatgct atggcttgaa tttgggcgaa ggcaagatga gttatccggg tgaagcggtg 6840
ggcgtggtag ccgcgcaatc tattggggag cctggaacgc agctcacttt aaggactttc 6900
catgtgggcg ggacagcgag caggagtcag gatgagcgcg aaatcgtagc gagcaaagaa 6960
ggttttgtgc gtttttacaa ccttaggact tacacgaata aagagggtaa aaacattatc 7020
gctaaccgcc gtaacgcttc tattttagtg gtagagccta agattaaagc gccttttgat 7080
ggggaattac gcattgaaac ggtttatgaa gaagtcgttg tgagcgtgaa aaatggcgat 7140
caagaagcta aatttgtttt aaggagaagc gatattgtca agccaagcga attagccggc 7200
gttggcggta agattgaggg gaaagtgtat ttgccttatg ctagtgggca taaggtgcat 7260
aaggggggaa gtatcgctga tattatccaa gagggctgga atgtgcctaa tcgcatccct 7320
tatgcgagcg aattgctagt caaggataat gaccctattg cgcaagatgt gtatgccaaa 7380
gaaaaaggcg taatcaaata ctatgtttta gaggctaacc atttagagcg cacccatggg 7440
atcaaaaagg gcgatatggt gagtgaaaaa ggcttgtttg cggtgatagc tgatgataat 7500
ggtagggaag ccgctcgcca ttatatcgct aggggttctg agatcttgat tgatgataat 7560
agtgaagtga gcactaatag cgtgatttct aaacccacga ctaacacttt caaaacgatt 7620
gccacatggg atccttacaa caccctatc attgcggact ttaaaggtaa ggtgggtttt 7680
gtggatgtta tcgcaggggt tacggtcgct gaaaaagaag acgaaaatac cggtatcaca 7740
agcttagtgg tgaatgatta cattccaagc ggatacaaac caagcttgtt tttagagggg 7800
gctaatggcg aagagatgcg ttatttccta gagccaaaaa cctctatcgc cattagcgat 7860
ggctctagcg tggagcaagc tgaagtgtta gcgaaaatcc ctaaagcgac cgttaaatct 7920
agggatatta ccgggggtct cccaagggtt tcggaactct ttgaagcgag aaaacccaag 7980
cctaaagatg tggcgatcct ttctgaagtt gatgggattg tgagttttgg caaacccatt 8040
cgcaataaag aacacatcat cgtaacttct aaagatggcc gttccatgga ttattttgtg 8100
gataaaggca agcaaatttt agtgcatgcc gatgaatttg tgcatgcggg agaagcgatg 8160
acggacggag taatttcaag ccatgatatt ttaaggatca gtggcgaaaa agagctttat 8220
aaatacattg tgagcgaagt ccagcaagtg tatcgcaggc agggggtgag cattgcggac 8280
aagcacattg aaatcattgt ttctcaaatg ctaagacagg tgcgtatttt agacagcggg 8340
gatagcaagt ttattgaagg ggatttagtc agtaaaaaac ttttcaaaga agaaaacgct 8400
cgtgtgatcg ctttaaaagg cgagccagcg attgctgaac cggtgctttt agggatcact 8460
agagcggcta ttgggagcga tagcatcatc tcagcggcct ctttccaaga aacgactaaa 8520
gttttaacag aagccagtat cgctatgaaa aaagactttt tagaggattt gaaagagaat 8580
gtggtgttgg ggaggatgat ccctgtggga acaggcatgt ataagaataa aaaaatcgtg 8640
ttaagagcgc ttgaggataa ctctaaattt 8670

Seq ID 102
atggcaaaag aaaagtttaa cagaactaag ccgcatgtta atattggaac cattgggcat 60
gtagaccatg gtaaaacgac tttgagtgca gcgatttcag cggtgctttc tttgaaaggt 120
cttgcagaaa tgaaagacta tgataatatt gataacgccc ctgaagaaaa agaaagaggg 180
atcactatcg ctacttctca cattgaatat gagactgaaa acagacacta tgcgcatgtg 240
gattgcccag gacacgctga ctatgtaaaa aacatgatca ccggtgcggc gcaaatggac 300
ggagcgattt tggttgtttc tgcagctgat ggccctatgc ctcaaactag ggagcatatc 360
ttattgtctc gtcaagtagg cgtgcctcac atcgttgttt tcttaaacaa acaagacatg 420
gtagatgacc aagaattgtt agaacttgta gaaatggaag tgcgcgaatt gttgagcgcg 480
tatgaatttc ctggcgatga cactcctatc gtagcgggtt cagctttaag agctttagaa 540
gaagcaaagg ctggtaatgt gggtgaatgg ggtgaaaaag tgcttaaact tatggctgaa 600
gtggatgcct atatccctac tccagaaaga gacactgaaa aaactttctt gatgccggtt 660
gaagatgtgt tctctattgc gggtagaggg actgtggtta caggtaggat tgaaagaggc 720
gtggtgaaag taggcgatga agtggaaatc gttggtatca gacctacaca aaaaacgact 780
gtaaccggtg tagaaatgtt taggaaagag ttggaaaaag gtgaagccgg cgataatgtg 840
ggcgtgcttt tgagaggaac taaaaaagaa gaagtggaac gcggtatggt tctatgcaaa 900
ccaggttcta tcactccgca caagaaattt gagggagaaa tttatgtcct ttctaaagaa 960
gaaggcggga gacacactcc attcttcacc aattaccgcc cgcaattcta tgtgcgcaca 1020
actgatgtga ctggctctat cacccttcct gaaggcgtag aaatggttat gcctggcgat 1080
aatgtgaaaa tcactgtaga gttgattagc cctgttgcgt tagagttggg aactaaattt 1140
gcgattcgtg aaggcggtag gaccgttggt gctggtgttg tgagcaatat tattgaa 1197

Seq ID 103
gtgttaatcg ttcaaaaata cggcggcacg agcatgggca gcatagaaag gatccacaat 60
gtcgctcaaa gggttttaga aagcgttaca ttagggcatc aagtcgtggt ggtggtttca 120

gcgatgagcg gcgaaaccga caggctttta gaatttggca agaattttag ccataaccct 180
aacaagcgag agatggacag gattgtaagc gtgggggaat tggtttcaag tgcggctttg 240
agcatggcgt tagaaaggta tgggcataga gccatttcct tgagcgggaa agaagcgggc 300
attttaacca gctcgcattt tcaaaacgcc gtgatccaat ccattgacac caaacgcatc 360
acagagcttt tagaaaaaaa ctacattgtg gtgatcgctg ggtttcaagg cgctgatatt 420
caaggtgaaa caacgacttt agggcgtggg gggagcgatt tgagcgcggt tgctttggcc 480
ggggctttaa aagcgcattt gtgcgaaatc tatacggatg tggatggcgt ttataccacc 540
gatccgcgca ttgaagaaaa ggctcaaaaa atcgcgcaaa tcagctatga tgaaatgctt 600
gaactggctt ctatgggggc taaagtttta ttaaaccgct cggtggaatt agccaaaaag 660
ctcagcgtga agttagtgac tcgcaattcg tttaaccata gcgaaggcac gctcattgtg 720
gctgaaaaag actttaaagg agaacgcatg gaaaccccta tagtgagtgg gatcgcattg 780
gataaaaatc aggctcgtgt gagcatggag ggcgtggaag atcggccagg cattgccgct 840
gaaatctttg gcgctttagc ggagtatcgc attaacgtgg atatgatcgt ccaaacgatc 900
ggcagagacg gcaaaaccga tttggatttt acgatcgtta aaacccaaat agaagaaacc 960
aagcaagcct taaagccttt tttagcgcaa atggattcca ttgattatga tgaaaatatc 1020
gctaaagtct ccatagtggg cgtgggcatg aagtcgcatt ctggggtggc gagtatcgct 1080
tttaaagccc tagccaaaga caatatcaat atcatgatga tttctacaag cgagattaaa 1140
atttcggttt tgattgacat taaatacgct gaattagctg ttagaacttt gcatgcggtg 1200
tatcaattag atcaa 1215

Seq ID 104
atgaaaaaac acatcctttc attagcttta ggctcgcttt tagtttccac tttgagcgct 60
gaagacgacg gcttttacac aagcgtaggc tatcagatcg gtgaagccgc tcaaatggta 120
acaaacacca aaggcatcca acagctttca gacaattatg aaaatttgaa caacctttta 180
acgagataca gcaccctaaa cacccttatc aaattgtccg ctgatccgag cgcaattaat 240
gcggtgcggg aaaatctggg cgcgagcgcg aagaatttga tcggcgataa agccaactcc 300
cccgcctatc aagccgtgct tttagcgatc aacgcggcgg tagggttttg gaatgtcgtg 360
ggctatgtga cgcaatgtgg gggtaacgcc aatggtcaag aaagcacctc ttcaaccacc 420
atcttcaaca acgagccagg gtatcgatcc acttccatca cttgttcttt gaacgggcat 480
aagcctggat actatggccc tatgagcatt gagaatttta aaaagcttaa cgaagcctat 540
cagatcctcc aaacggcttt aaaaaacggc ttacccgcgc tcaaagaaaa caacgggaag 600
gtcagtgtaa cctataccta cacatgctca gggcaaggga ataataactg ctcgccaagt 660
gtcaacggaa ccaaaaccac aacccaaacc atagacggca aaagcgtaac caccacgatc 720
agttcaaaag tggttggtag catcgctagt ggcaacacat cacatgtcat caccaacaaa 780
ttagacggtg tgcctgatag cgctcaagcg ctcttagcgc aagcgagcac gctcatcaac 840
accatcaacg aagcatgccc gtatttccat gctactaata gtagtgaggc taacgcccca 900
aaattctcta ctactactgg gaaaatatgc ggcgcttttt cagaagaaat cagcgcgatc 960
caaaagatga tcacggacgc gcaagagcta gttaatcaaa cgagcgtcat taacagcaac 1020
gaacaatcaa ctccggtagg caataataat ggcaagcctt tcaacccttt cacggacgca 1080
agttttgcgc aaggcatgct cgctaacgct agcgcgcaag ctaaaatgct caatttagcc 1140
catcaggtgg ggcaagccat taacccagag aatcttagcg agaattttaa aaatttgtt 1200
acaggctttt tagccacatg caataacaaa tcaacagctg gcactggtgg cacacaaggt 1260
tcagctccag gcacagtgac cactcaaact ttcgcttctg gttgcgcgta tgtggagcaa 1320
accctaacga acttaggcaa cagcatcgct cactttggca ctcaagagca gcagatacag 1380
caagccgaaa acatcgctga cactctagtg aatttcaaat ctagatacag cgaattaggc 1440
aacacctata acagcatcac caccgcgctc tccaaagtcc ctaacgcgca aagcttgcaa 1500
aacgtggtga gcaaaaagaa taacccctat agccctcaag gcatagagac caattactac 1560
ctcaatcaaa attcttacaa ccaaatccaa accatcaacc aagaactagg gcgtaacccc 1620
tttaggaaag tgggcatcgt caattctcaa accaacaatg gtgccatgaa tgggatcggt 1680
attcaggtgg gctataagca attctttggc caaaaaagaa aatggggcgc taggtattac 1740
ggctttttg attacaacca tgcgttcatc aaatccagct ttttcaactc ggcttctgac 1800
gtgtggactt atggttttgg agcggacgcg ctttataact tcatcaacga taaagccacc 1860
aatttcttag gcaaaaacaa caagctttct ttggggcttt ttggcgggat tgcgttagcg 1920
ggcacttcat ggctcaattc tgagtacgtg aatttagcca ccgtgaataa cgtctataac 1980
gctaaaatga atgtggcgaa tttccaattc ttattcaata tgggagtgag gatgaattta 2040
gccagatcca agaaaaaagg cagcgatcat gcagctcagc atgggattga gttagggctt 2100
aaaatcccca ccatcaacac gaactattat tcctttatgg gggctgaact caaatacaga 2160
aggctctata gcgtgtattt gaactatgtg ttcgcttac 2199

Seq ID 105
ttggactctt ttcattcatt taatcagcat gcatttaatc ggcatgccaa aacttatcac 60
ctttttgctc atatccagca gcaaatcgct atctgtcttg ttcaattttt aaaacaaaaa 120
cattacgcta aagttttgga tcttggatca gggagtgggg ctgtttttaa cgctttagag 180
cggcaaaata ttttgattga agagtttatc gctttggata attccataaa catgctcaaa 240
ttacacccca cgcattctat taacattcaa aaaatctctt tagagcatgc ggattttgaa 300
gaacatgttt tttgcactta tgatctggtt gtgtcttctt cttctttaca atgggcaagg 360
gatttaaaaa gcgttttaga aaaaatcgct ctttctagta aggaggtggc tttagctatc 420
catacggatt ttagtttgca tgaagtgcat gagtttttag gcacgccttc gcctttaagg 480

gatcttaaaa cgctcaaatc cttgattaaa aacgctttta aacattttca aatagaatta 540
gaaaacaagc gcttcgctct ttatttcaac cgcaaacaag attgcttgaa ttaccttaaa 600
aaatgcggtc ttttaggggg ttcaacgctg agtttcaagc aaaaaaaaca ttttttttcaa 660
aacatggcgt ttgaaaaatt gagctatgaa gtgttactct tttctgggat caagcgttct 720

Seq ID 106
ttgagcggct ttaacccctt aaattctccc ttagtcgcaa gctcttctct tagcttgaaa 60
gaagcctatt atttagaaaa attatctctt aaaaaagggt ttaaaatcca ttacaagatg 120
accaaagata gcttaaacct tttagaaaaa agcgatttgt gcgttttgtt tgggggtttt 180
tcaaacgctt gtttgaatga aaacgaacga tggattttag aaagcattag ccactcaaaa 240
cgcccctacg ccttgttaag acccttacaa gatacaagag acttgcaaga aaattgcctt 300
tttgcgtctt atgaaatcca cacggaagcg gcgattttgg ccttgatttt aaggggcatt 360
ttggaacaaa cttcccaatt aaaagggcat gttttagaaa aaatagatgt ggggtattta 420
agctctgaag cgaacatgag cgaagaggaa ttgcaagagc ttatcgcgct tattgttaaa 480
gcaaaaaaaa gggcacttgt tttaaataga gaaatcacta agcatgctaa caacgctttt 540
ttatacaccc ttttaagcga gttgcaaaat tacctagaaa ttttacacat cccttgctat 600
gattcaagtg caacgaccgc ttttttatgat tttaaagatc aagaatggct gctagaaaca 660
gcctttaaag agggcatttt gccttttaaa tcgcaactcc aatcaaaaga tttagagctt 720
ttagagcgaa tcagtgaggc taacggctcg tttgtctatg tttcttacaa gagccttgaa 780
acccccaaat tatcttttc caagcaattt aagatcgcta ataagattga gcattctaaa 840
gcggggtttc aaatctccaa tcaaacgcta gaatgcgagt tagaagaaaa cccccatttg 900
aagggtttga ttgcgatttt agaaggggcg ttttttgacg cttacccctta tatccctatt 960
ttatcccact ctcaaggaat ttca 984

Seq ID 107
atgatcagtc tcatagaaaa agccccttac attccctacc ccctagctct ttatgaaaaa 60
ttagagcaac cacacacctt gctttttgaa agcgctgaga ttgagagcaa agcacacacc 120
aaatcccttt taatggctaa agcctgtttg aagctcattt gcaaccacaa catcgtaact 180
atcactagcc tgacgcctaa tggcggggca tttttgcaaa aattgagcgc gttttttaaa 240
acgcccatac aagacaatgc cctaatttta acctacacca aaaataaaaa aacgcaagat 300
gagtttttaa aactctttga gcctagccct tttgacgctt taaggggct ttttaaaagc 360
gttaaaacaa aacccaaaca ccccttacg cttttaagcg cgggtgtttt ttcttttgaa 420
atgctcaatt tttttgaaga tttgcctcac ttaaaagcga aagacaacac agtgcatgac 480
tttatttttt atctcgcgca aaatttgatc atcatagacc ataaagaaaa aagcgttgaa 540
atcttggggg cgtgttttga tgagcgcttt aaaacagaga tagcccaaga attacaagac 600
ttaaaagagt tggctaaaag catcaaaagc gactttgtcc ctaaaaaatc caagcaaagt 660
agagaagtta gcgctaattg tagcgatagc gagtttgaaa aaagagtgct atccttacaa 720
gaagaaatca aaaaaggcga gatttttcaa gcggtgttgt cgcgcagctt ttatatggag 780
tgcttggagg gtttgagcgc gtattaccat ttaaagctaa ctaatcctag cccctatatg 840
ttctatatca aagacagcga tttcattctt tttggggcaa gccctgagag cgctttaaag 900
tacaacgctt taaccaacac ggctgaaatt tatcccattg ctggcacccg tttaaggggt 960
aaggacaaac aggggaatat tgattacgat ttggatagta aaatggaatt tgatttgcaa 1020
cacgactata aagaaagggc tgaacacatc atgctagtgg atttagccag aaacgacatg 1080
gccagagttt caaaaaaacg ctattgcgac aagcttttaa aagtggataa gtattccaat 1140
gtcatgcatt tagtctcaag ggttgtgggg gaattgaaaa aagggtgcga tagtttgcat 1200
gcctacagga gctttatgaa cgccggcacg cttagcgggg cgcctaaaat ctctgcgatc 1260
aggctcattt accaattaga aaaccaaagg agaggctctt atgggggggag cgtggggtat 1320
ttaaatagcg agggttctat ggattcttgc atcaccatcc gttcatgttt tgtcaaaaac 1380
aatagggccg tgatccaagc aggagccggt attgtgctag acagcgtgcc acaaaacgaa 1440
gcgaatgaaa caagagccaa agcgcaagcc cttattgatg cgatcaggaa aacaagctta 1500

Seq ID 108
atgatagaaa agatcattga tttaagcgtt aaaaacaaac tccttaccac tttagtcact 60
ctactcattt ttttagcctc tttgtgggcg ataaaaagcg ttcgtttaga cgctttgccg 120
gatttaagcc ccgctcaagt ggtcgtgcaa atcacttacc ccaatcaaag ccctaaaatc 180
gtgcaagagc aggttactta cccgttagtt tctactttca tgagcatcgc taacattgac 240
acggttaggg ggatttctag ctatgagagc ggtttgattt acatcatttt taaagacggc 300
gtcaatctgt attgggctag ggatagggtt ttagagcaat taaaccgagt gagtaacctc 360
cctaaggacg ctaaagtaga aatagggagc gattccactt ctattggttg ggcgtatcaa 420
tacgctctat ctagcgatag caagaattta agcgatttga aagtcttgca agatttttat 480
taccgctacg ctctttttagg ggttgatggg gtgagtgagg ttgcaagcgt gggggggcttt 540
gtaaaagatt atgaagtaac gcttcaaaac gattctctga tccgctataa cttgagttta 600
gagcaagtcg ctaacgcgat taaaaattcc aataacgata ccggtggggg cgttatttta 660
gaaaacgggt ttgaaaaaat tataagatcg catggctata tccaatcttt gaaggattta 720
gaagaaattg tggttaaaaa agaaggggct atcccttaa aaatcaaaga tatagccagc 780
gttaggctaa cgcccaaacc acgccgaggg gcggccaacc ttaatggcga taaggaagtg 840
gtgggcggga ttgttatggt gcgctatcac gctgacactt ataaggtgct taaagccatt 900
aaagaaaaaa tcgccacctt acaagcgagt aaccctgatg tgaaaatcac cagcgtgtat 960

gacaggagcg aattgattga aaaaggcatt gacaatttaa tccacacgct catagaagaa 1020
agcgtcattg tgctagtcat tattgcgatt tttttactgc atttcaggag cgctttagtg 1080
gtgattatca ctttgccttt aagcgtgtgc atcagtttct tgctcatgcg ttatttcaat 1140
attgaagcga gcattatgag tttagggggc attgcgatcg ctatagggac gatggtggat 1200
gcggctattg tgatggtaga gaacgctcac aagcacttgc aacacattga tgtaaaggac 1260
aacgctcaaa gggttaatgg cattatagaa ggggttaagc atgtgggggg cgcgatattt 1320
tttgctttaa tgatcatcgt ggtttctttc ttgccaattt ttgcactcac cggccaagaa 1380
gaaaagcttt ttgccccttt agcttacacc aaaacctttg ccatgctagt aggagcgctg 1440
ctttctatca ccatggtccc tattttaatg gtatggctca ttaaagggcg gattttagaa 1500
gagtctaaaa acccgattaa cgcttttttc atgaaaattt atggcgtgag cttgaatgtt 1560
gtgcttaaat tcagatacgc ttttttaata gcaagcgtcc tgggtttagg gggcttgtat 1620
gtagcgtata aaaaactcaa ctgggaattt atcccccaaa tcaatgaagg ggtagtgatg 1680
tatatgcctg taaccattaa tggcgtgagc attgataccg ctttagaata tttgaaaaaa 1740
agcaatagcg ctatcaagcg attggatttt gtcaaacaag tttttggtaa agtggggcgc 1800
gctaacacca gcaccgatgc tgccggcttg agcatgatag aaacctacat tgaattaaag 1860
ccgcaaaacg aatggaaaga aaagctcagt tataaagaag ttagggataa attagaaaaa 1920
accctgcaat taaaaggctt gaccaattca tggacttacc ccattcgtgg gagaacggac 1980
atgctcttaa ccgggattag aacgccccta ggcatcaagc tctatggcaa tgacacggat 2040
aaattacaag aattagcgat ccttatggag caacagctca aaaccctaaa agagagtttg 2100
tccgtctttg ccgagcgatc caataacggc tactacatca cgctggattt gaacgatgaa 2160
aatctggctc gttatggcat caataaaaag gccgtgttag atgcgattaa attcgctttg 2220
ggaggagcca cgctcactac catgattaag ggtgtagaaa actatcccat ttctttacgc 2280
ttagaagaca cagaaagaaa caccattgaa aaattaaaaa acctctacat caaaaccgct 2340
tacaattaca tgcccttaag ggagttagcc cgcatctatt acgacaactc gccggcggtg 2400
ttaaagagcg aaaagggctt gaacgtgaat tttatttata ttgtgccgca aaatggtatc 2460
agctctgatg cttacagaca actggctcaa aaagcgctag aaaaaatcca attgcctaac 2520
gggtattatt atgaatttag cggcgaaagc cagtatttag aagaagcgtt taaaaccttg 2580
caatacatcg tgccggtgag cgtgtttatc atttttattt taattgtctt tgctttaaag 2640
aatctcacca attccttact atgcttttte actctgcctt ttgcgttttt ggggggggtta 2700
atttttatga atctcatggg atttaacatg agcgtggcgg cgttagtggg ctttttggcc 2760
cttttagggg tagcgagcga aacggctatt gtgatgatta tttatttaga ggatgcgttt 2820
caaaaattca tcaaaacccc tttaaaagag caaaacagca ccactttaaa agaggccatc 2880
atgcatgggg cggtgcttag ggtaaggccc aagcttatga cctttttttag cattttagct 2940
tcactcattc caatcatgta tagccatggc acaggttctg aaatcatgaa atccatcgcc 3000
gcgcccatgc tagggggcat gataagcagc gttgttttaa cgcttttttat tatccctacg 3060
gcgtattttg tgatcaagaa tgcgggaatt aaaagcaatc aaaca 3105

Seq ID 109

atgtctgtat cgcatgttgc tttaatctta aggaaattgt tttatcatag acaaggagtt 60
tttatgggcg gtttttcagt gggaatgttg aaagattatg tggacatatt tgtttttgcg 120
gtgcttggcg tggccagttt tttagctttg tggtttgcga ttgaaagggt tatttttttat 180
tctaaagtcg atttgaaagc ttatgacgat atagatgccc tgaatttgga tttaaccaag 240
aatctaacca ttctctatgt gatttttttct aacgcgcctt atgtgggctt attagggacg 300
gttttaggga ttatggtgat tttctatgac atgggcgtga gcggcgggat ggacgctaaa 360
acgatcatgg taggtttgtc tttggcttta aaagcgaccg ctctagggct tgctgtggcg 420
attcccactt tgatcgctta taatagcttg ttgagaaaat ccgatgtttt gagcgaaaaa 480
ttcaggatca tgaaaaaa 498

Seq ID 110

atgaaaattt ctccatctcc acgcaagctc agtaaagttt caacgagtgt tagcttttta 60
atctcttttg ccctatacgc tatagggttt ggctattttt tactgcgcga agacgcccca 120
gagcctttag cgcaagccgg gaccactaag gttaccatga gtttagccag catcaacact 180
aattccaata caaagactaa tgctgagtcg gctaaaccca aagaagagcc taaagaaaaa 240
cccaagaaag aagagccaaa aaaagaagaa cccaaaaagg aggttacaaa gcctaaacct 300
aagcctaaac ccaagccaaa gccaaaacca aaacctaagc ctgaacccaa acctgaacca 360
aaacccgagc ctaagcctga gcctaaagtt gaagaggtta aaaaagaaga gcctaaagaa 420
gagcccaaaa aagaagaagc taaagaggaa gctaaagaaa aaagcgctcc taaacaagta 480
acaactaagg atatagtcaa agaaaaagac aagcaagaag aatccaacaa aacctctgag 540
ggggccactt ctgaagctca agcttataac ccaggggtga gcaacgaatt tttaatgaag 600
atccaaaccg ctatttcttc taaaaaccgc taccctaaaa tggcgcagat taggggtatt 660
gagggcgaag tgttggtgag ctttacgatc aatgctgatg ggagcgttac ggacattaaa 720
gtggtcaaaa gcaacaccac agatatttta aaccatgcgg ctttagaagc cattaaaagc 780
gcggcacatc tattccctaa accagaagaa accgtgcatc taaaaatccc tatcgcttat 840
agcttgaaag aagac 855

Seq ID 111

atgaaaaaat ccctcttact ctctctttct ctcatcgctt ccttatcaag agctgaagat 60
gacggatttt atacgagtgt gggctatcag atcggtgaag cggtccaaca agtgaaaaac 120

acaggagcat tgcaaaatct tgcagacaga tacgataact taaacaacct tttaaaccaa 180
tacaattatt taaattcctt agtcaattta gccagcacgc cgagcgcgat caccggtgcg 240
attgataatt taagctcaag cgcgattaac ctcactagcg ccaccaccac ttcccccgcc 300
tatcaagctg tggctttagc gctcaatgcc gctgtgggca tgtggcaagt catagccctt 360
tttattggct gtggccctgg ccctaccaat aatcaaagct atcaatcgtt tggtaacaca 420
ccagccctta atgggaccac caccacttgc aatcaagcat atgggacagg ccctaatggc 480
atcctatcta ttgatgaata ccaaaaactc aaccaagctt atcagatcat ccaaaccgct 540
ttaaaccaaa atcaaggggg tgggatgcct gccttgaatg acaccaccaa aacaggggta 600
gtcaacatac aacaaaccaa ttataggacc accacacaaa acaatatcat agagcattat 660
tatacagaga atgggaaaga gatcccagtc tcttattcag gcggatcatc attctcgcct 720
acaatacaat tgacatacca taataacgct gaaaaccttt tgcaacaagc cgccactatc 780
atgcaagtcc ttattactca aaagccgcat gtgcaaacga gcaatggcgg taaagcgtgg 840
gggttgagtt ctacgcctgg gaatgtgatg gatatttttg gtccttcttt taacgctatt 900
aatgagatga ttaaaaacgc tcaaacagcc ctagcaaaaa cccaacagct taacgctaat 960
gaaaacgccc aaatcacgca acccaacaat ttcaacccct acacctctaa agacaaaggg 1020
ttcgctcaag aaatgctcaa tagagctgaa gctcaagcag agattttaaa tttagctaag 1080
caagtagcga acaatttcca cagcattcaa gggcctattc aaggggattt agaagaatgt 1140
aaagcaggat cggctggcgt gatcactaat aacacttggg gttcaggttg cgcgtttgtg 1200
aaagaaactt taaactcttt agagcaacac accgcttatt acggcaacca ggtcaatcag 1260
gatagggctt tggctcaaac cattttgaat tttaaagaag cccttaacac cctgaataaa 1320
gactcaaaag cgatcaatag cggtatctcc aacttgccta acgctaaatc tcttcaaaac 1380
atgacgcatg ccactcaaaa ccctaattcc ccagaaggtc tgctcactta ttctttggat 1440
tcaagcaaat acaaccagct ccaaaccatc gcgcaagaat tgggcaaaaa ccctttcagg 1500
cgctttggcg tgattgactt tcaaaacaac aacggcgcaa tgaacgggat cggcgtgcaa 1560
gtgggttata aacaattctt tggtaaaaaa aggaattggg ggttaaggta ttatggtttc 1620
tttgattata accatgctta tatcaaatct aatttttca actccgcttc tgatgtgtgg 1680
acttatgggg tgggtatgga cgctctctat aacttcatca acgataaaaa caccaacttt 1740
ttaggcaaga acaacaagct ttcagtaggg ctttttggag gctttgcgtt agccgggact 1800
tcgtggctta attcccaaca agtgaatttg accatgatga atggcattta taacgctaat 1860
gtcagcactt ctaacttcca atttttgttt gatttaggct tgagaatgaa cctcgctagg 1920
cctaagaaaa aagacagcga tcatgccgct cagcatggca ttgaactagg ttttaagatc 1980
cccacgatca acaccaacta ttattctttc atgggcgcta aactagaata cagaaggatg 2040
tatagccttt ttctcaatta tgtgtttgct tac 2073

Seq ID 112
atgttagcta aaatgtcgtt tatgcaaaat gttaaaaaca ttcaagaagt ggaagtgagc 60
cataaaaggg tgcttattag agtggatttt aatgtgcctt tagatgaaaa tttgaatatt 120
accgatgata cgcgcattag agagagcttg cccaccatcc aatattgtat tgacaacaag 180
gctaaagata ttatttttagt gagccacttg ggccgcccta aaggggttga agaaaaattg 240
agtttaaagc ccttttttgaa acgccttgaa agactcttaa accatgaagt ggtttttttct 300
caaaatattg tgcaactcaa gcaggcttta aacgaaaacg cgcccacaag gatttttctt 360
ttagaaaata tccgcttttt aagaggcgaa gaagaaaatg atgaaaatct ggctaaagat 420
ttagcgagct tgtgcgatgt gtttgtgaat gacgcttttg gcacgagcca cagaaagcat 480
gccagcactt atggcaccgc caaattcgcc cctattaaag tgagcgggtt tttactcaaa 540
aaagaaattg attcgtttta tcaagcgttt aaccaccctt tacgccctct attgttgatt 600
gtaggggggg ctaaggtcag ctccaaactc accctattaa aaaacatttt agatctcatt 660
gacaagctca tcattgccgg ggcgatgagc aacaccttct taaaagcttt aggctatgat 720
gtgcaagatt cttctgtaga agacgctcta atcaatgacg ccctagaatt attgcaaagc 780
gcgaaagaaa aaaaagtcaa agtctattta cccatagacg ctgtaaccac tgatgatatt 840
ctcaacccca aacacattaa aatttcaccc gtccaagaca ttgagcctaa gcacaagatc 900
gctgatatag ggcctgcgag cttgaaatta ttttctgaag tcatagagag tgcacccacc 960
attttatgga atggcccctt aggcgtgcat gaaaaacaag aattcgctag aggcacaacc 1020
tttttagccc acaaaatcgc tgacacttac gctttctcgc tcattggtgg gggcgatacc 1080
attgatgcga tcaatcgcgc gggcgaaaag gataacatga gctttatctc taccggtggg 1140
ggagcgagtt tggaattgtt agagggcaaa attttacctt gttttgaggt tttggacaaa 1200
cgccat 1206

Seq ID 113
gtggtgttat taacaatgac aaaacgactt tttaaagggt tgttagcggt ttctcttgct 60
gtgagtttgc atggtggtga agttaaggaa aaaaagccgg ttaagccggt taaagaagat 120
ccgcaagaat tagcggctaa aagggtggaa gcgttcagtc gtttctctaa tgtggtttca 180
gaaattgaaa aaaaatatgt ggataaaatc agcatttctg agatcatgac taaagcgatt 240
gaaggcttgc tctctaattt ggacgcgcat tcagcgtatt tgaatgaaaa gaagtttaag 300
gaatttcaag cccaaaccga gggcgaattt ggggggcttg ggatcacggt gggcatgcgc 360
gatggcgttt taaccgttat tgccccttta gaaggcactc cagcttacaa ggctggggtt 420
aagtcaggcg ataacatttt aaaaatcaat aacgaaagca cgctgagcat gagcattgat 480
gatgcgatca acctcatgcg cggcaagcca aaaaccccta ttcagatcac cgttgtaaga 540
aaaaacgagc caaaaccttt agtgtttaac atcattagag acatcattaa actcccctct 600

gtctatgtga aaaagattaa agaaacccct tatctgtatg tgagagtgag tggttttgac 660
aagaatgtta ccaaatcggt tttagaaggc ttaaaagcta accctaaggc taaggggatc 720
gtgttggatt taaggggcaa tcctggaggg ctattaaacc aagcggtggg cttgtctaac 780
ctcttcatta aagaggggct tttagtctct caaaaaggca aaaataaaga agaaaattta 840
gaatacaagg ctaacggcag agccccttat accaatttgc ctattgcggt gttagtcaat 900
ggcggttcag cgagcgcgag cgagatcgtc gcaggggcac tgcaagatca caaacgggcc 960
gtgattatcg gtgaaaaaac ctttggtaag ggaagcgtgc agatgctgct ccctgtcaat 1020
aaagacgaag ccattaaaat cacaaccgca cgctactatt tgccgagcgg gcgtaccatt 1080
caagctaagg ggatcacgcc tgatattgtg atttatccgg gtaaagtgcc agaaaatgaa 1140
aacaaattca gcttgaaaga agcggatcta aaacaccatt tagagcaaga gcttaaaaag 1200
attgatgata aaacccccaa ttccaaagag gcggataaag acaagaaaaa cgaagaggaa 1260
aaagagatta ctcctaaaat gatcaacgat gatattcagc taaaaaccgc tattgacagc 1320
ttgaaaacct ggtctatcgt tgatgagaaa atggatgaaa aagcgcctaa gaagaaa 1377

Seq ID 114
atgaacgaaa cgctttattg cagtttttgc aaaaaaccag aatcaagaga tcccaaaaaa 60
cgccgcatta tttttgcgag caatctcaat aaagatgtgt gcgtgtgcga atattgtata 120
gatgtgatgc atggggaatt gcacaaatac gacaattctt tattggcgct caaaagagac 180
cgattgagaa gaatggaatc tagcgcttat gaagaagagt ttttactctc ttacattcca 240
gcccctaaag agcttaaggc ggttttagac aattatgtga tagggcaaga gcaggctaaa 300
aaggtttttt ccgtagccgt gtataaccat tacaaacgct tatcttttaa agaaaaactc 360
aaaaaacaag acaaccaaga cagcaatgtg gagttagagc atttagaaga agtggagttg 420
agcaagtcta atattttact aatcggccct acaggatcag gcaaaacttt aatggcgcaa 480
actctggcca agcatttgga tattcctatc gccattagcg atgcgactag cttgactgaa 540
gcgggctatg tgggcgaaga cgtggaaaat attctcacaa gattgttgca agcgagcgac 600
tggaatgtcc aaaaagccca aaaaggcatt gtgtttattg atgagattga taaaatcagc 660
cgtttgtcag aaaaccgctc tatcactaga gatgtttctg gcgagggcgt tcagcaagcg 720
ttgttgaaaa tcgttgaagg ttctttagtg aatatccccc ccaaaggcgg cagaaagcac 780
cctgagggca atttcattca aattgacacg agcgatattt tattcatttg tgctggagcg 840
tttgatgggt tagctgaaat cattaaaaaa cgcaccacgc agaatgtgtt gggtttcact 900
caagaaaaga tgagcaaaaa agagcaagaa gcgatcttgc atttagtcca aacccatgac 960
ctggttactt atgggcttat ccctgagctt attggccgtt tgccggtttt aagcacgcta 1020
gatagcatca gtttagaagc gatggtggat attttacaaa aacctaaaaa cgctcttatc 1080
aagcaatacc agcagctttt caaaatggat gaggtggatt tgatctttga agaagaagcc 1140
attaaagaaa tcgctcaact cgcattagaa agaaaaaccg gggctagggg cttaagggcg 1200
atcattgaag atttttgttt ggatattatg tttgatttac ccaagcttaa aggatcggaa 1260
gtgcgtatca ctaaagattg tgttttaaaa caggctgaac ctttgatcat tgctaaaacg 1320
cattctaaaa ttcttcct 1338

Seq ID 115
atgcgagatt tcaataacgc tcaaatcaca cgcttaaaag tgcgtcaaaa cgctgttttt 60
gaaaaattgg atctggagtt taaagacggc ttgagcgcga ttagtggggc tagcggggtg 120
ggaaaaagcg ttcttattgc gagtctttta ggggcgtttg ggcttaaaga gagcaacgct 180
tcaaacattg aagtggaatt gattgcgcct tttttagaca ctgaagaata cggcattttt 240
agagaagatg aacatgaacc cttagtcatc agcgtgatta aaaaagaaaa aacgcgctat 300
tttttaaacc aaacaagcct gtctaaaaac acgctcaaag cgttattaaa aggtttgatt 360
aaacgcttgt ctaacgatag attcagccag aatgaactca acgatatttt aatgctctcc 420
ttactggatg gctatatcca aaacgaaaat aaggcgttta gccccctttt aggcgcgctt 480
gaagaaaaat tcacccgatt agagaagcta gaaaaagaaa ggcgattgtt agaggataaa 540
aagcgtttcc aaaaggattt agaagaacga ttgaattttg aaaaaatgaa attagagagg 600
ctggatttaa aagaagatga atacgaacgc cttttagagc aaaaaaaatt gctttctagt 660
aaggaaaaac tgaacgataa aatcgctctg gcgttagagg tgctagaaaa tacccataaa 720
atcacgcatg ctttagagag cgtgggccat agcgcggagt ttttaaaaag cgctttatta 780
gaagcgagcg ctctattgga aaaagagcag gctaaattag aagagtgcga gcgtttggac 840
attgaaaaag ttctagaaag gcttggcatg ctaagtggga tcattaagga ttacgggagt 900
attatgcatg ctaaagaacg attagggcat gttaaaaacg aattgcacaa cctaaaagaa 960
attgatagtc attgcgaaac ttaccacaaa gaaatagagc gattaaaaac cgaatgcttg 1020
aaattgtgcg aagaaataag cggctttaga aaagagtatt tagccggttt taacgctctt 1080
ttaagcgcta aagcgaaaga tttgctccta aaaagcccca gtttggtttt agaagacgcc 1140
cccatgagcg aaaaaggcgc tcaaaaactc gttttgaatt tgcaaaattc ccaattagaa 1200
accttaagct ctggagaata cagccgtttg agactggcgt tcatgctttt agaaatggaa 1260
tttttaaagg attttaaagg cgtgttggtg ttagatgaaa tggattccaa tttgagcggc 1320
gaagagagtt tggcggtctc taaagccctt gaaaccttaa gcagccattc gcaaatcttt 1380
gccatttcgc accaagtcca tatcccagcg ctcgctaaaa accatatttt agtcttcaaa 1440
gaaaaccaca aaagccttgc caaaaccctt aataacgaag aaagggtttt agaaatcgcg 1500
cgcatgatag gggggagcga gaatatagag agcgcgattt ctttcgctaa ggaaaaatta 1560
aaggcgcaag aa 1572

Seq ID 116

```
atgccagacg agctaagggc agaaaaaagc tttccgtcta aaccctatga ctctttaaaa     60
aacaagagtg agtttgacag ggtttatcaa aaggggttta aaaaacataa ccctttttt     120
tcgctctttg ttttggattt gtcacaagag ccgccaaaag aaaaagcggg ctttaaagat     180
ccgctctttt gtaggcttaa agacaaaaaa acgctttatt tattaggctt gagcgtgtcc     240
aaaaaagtcg gcaacgccgt gaaacgaaac cttatcaaac gccgtttgcg ttcgcttaca     300
ttaaagcatg ccgctctttg tcaagggctt gctttggtgt ttgtgcctag aagcgattgt     360
taccatttgg atttttgggc tttagaaaaa catttttag aaatgctaac ttccattaaa     420
aactatatga acaaagcctt aaaagacttg aaaaaaggaa taactcatac ctatgcgaaa     480
caa                                                                  483
```

Seq ID 117

```
atgttaaaac tcgctagcaa aacgatttgt ttgtccctaa tcgggtcatt caccgctgta     60
gaagcctttc aaaaacacca aaaagacggc ttttttatag aagccgggtt tgaaaccggg     120
ctattgcaag gcacacaaac taaagaacaa accatagcca caactcaaga aaaacctaaa     180
cctaaaccaa agcccaaacc cattacccct caaagcacct atgggaaata ctacatctcc     240
caaagcaccg ttttaaagaa tgcgactgag ttgtttgcag aggacaatat caccaactta     300
acctttttatt ctttaacccc tgtgtatgta accgcttaca accaagaaag cgctgaagaa     360
gcaggctatg gcgatagcag cttaattatg atacaaaact tcttgcctta taatttaaac     420
aatattgagc tgagttatac agacaatcaa ggcaatgtag tcagtttggg cgtgatagag     480
actatcccta aacaatctca aatcattctg cccgcaagct tgtttaacga tccgcagctt     540
aacgctgatg gcttccaaca gctccaaact gccaccacac gattttctga tgccagcacg     600
cagaatctgt ttgataagct cagtaaggtt acaaccaatc ttcaaatgac ttatatcaat     660
tacaaccaat tttctagcgg taatggcagt ggttctaaac ccccatgccc tccatacgaa     720
aaccaagaaa actgcacggc taaagtgccg cctttcacct ctcaagacgc caagaatttg     780
accaatttaa tgctgaatat gatggcggtg tttgattcta aatcttggga agatgccgtt     840
aaaaacgctc cctttcagtt tagcgacaac aacttgtcag cgccatgtta ttctaattat     900
tccacatgcg tgaatcctta caacgatggg cttgttgatc ctaaattgat cgctaaaaat     960
aaaggagatg aatacaatat agaaaacggg caaacaggct cagtgatatt aacgccgcaa    1020
gatgttatct atagctatag ggttacgaat aatctttatg tgaatctctt acccccaaga    1080
ggaggggatt tagggctagg gtctcaatat ggcggcccca atggtccagg cgatgatggc    1140
accaattttg gcgctttagg gatattgtct cctttcttag accctgaaat actgtttggc    1200
aaagaattga ataaagtcgc catcatgcaa ttaagagaca ttatccatga atacgggcac    1260
actttaggct atacgcataa tgggaacatg acttatcaaa gggtgcgcat gtgtgaagaa    1320
aacaatgggc cagaagagcg ctgtaagggc gggaaaatag agcaagtgga tgggcaagaa    1380
gtgcaagtat ttgacaacgg gcatgaagtg cgagacaccg atggctcttt ctatgatgtg    1440
tgttctcgtt ttggcggcca aaatcagccc gctttcccta gcagttaccc caattccatt    1500
tatactgatt gctctcaagt ccccgctggg cttataggcg ttactagcgc ggtttggcaa    1560
caactcattg atcaaaacgc cctaccggtg gattacacta atttgagcag ccaaaccaac    1620
tatttaaacg ctagtttgaa cacgcaagat tttgcgacca ctatgcttag cgcgatcagt    1680
caaagccttt catctactag atctagcgcc actacctatc gcacttcaaa aacctcacgg    1740
ccctttggag ccccccctatt aggcgttaat cttaaaatgg gctatcaaaa atactttaat    1800
gattacttag ggttgtcttc ttatggcatc atcaaataca actacgctca agccaataac    1860
gaaaaaatcc aacaattaag ctatggcgtg ggaatggatg tgttgtttga ttttatcacc    1920
aattacacta acgaaaagaa ccctaaaaac aatctaacca agaaagtttt cacttcctct    1980
cttggggtgt ttgggggggtt aaggggctta tacaatagct attatttgtt gaaccaatac    2040
aaagggagcg gtaatttaaa tgtgaccggt gggttgaatt accgctacaa gcattctaaa    2100
tattctgtag gcattagcgt tcctttagtc cagttgaaat ctagagtcgt ttctagcgat    2160
ggcgcaacta ccaattctat caccctgaat gaaggggcga gccattttaa agtgtttttt    2220
aattacgggt ggattttc                                                  2238
```

Seq ID 118

```
atgaaaaaga ttattcttgc atgccttatg gcttttgtgg gtgccaattt aagcgcagag     60
cctaagtggt atagcaaggc ctacaacaaa acaaacaccc aaaaaggcta tctttatggg     120
agtggttcag ccacttctaa agaggcttct aaacaaaaag cgttagcgga tttagtggcg     180
tctattagcg tggtggttaa ttcccaaatc catattcaaa aaagtcgtgt ggacaataag     240
ttaaaatcca gcgattcgca aacgattaac ttaaagaccg atgacttgga attgaataat     300
gtagaaattg tcaatcaaga agtgcaaaaa gggatctact acaccagagt aaggatcaat     360
caaaacttgt ttttgcaggg tttaagggat aagtataacg ctctttatgg gcagttttcc     420
accttaatgc ctaaggtttg taaaggggtt tttttacagc aatccaagag catgggggat     480
ttattggcta aagcgatgcc tatagaaagg attttaaaag cgtattctgt tccggtgggt     540
tcgttagaaa attatgaaaa aatctattat caaaacgctt tcaaacctaa agtgcaaatc     600
acttttgata acaacggcga tgcggaaatc aaaagcgctc tcataagcgc ttatgccaga     660
gtgctaaccc ctagtgatga agaaaaactc tatcaaatca aaaatgaagt tttcacagac     720
agtgctaatg gcatcacgcg cattagagtg gttgttagcg cgagcgattg tcaaggcacg     780
cctgtattga atagaagcct tgaagtggat gaaaagaata agaattttgc tatcacgcgc     840
ttacaatctt tgctttataa agaactgaaa gattatgcca ataaagaagg gcaaggcaat     900
acggggtta                                                            909
```

Seq ID 119

atgaaagaga ataaagcttt tacgcatttg cacttgcaca cagaatattc gcttttagac 60
ggggcgaaca agattaaaat tctagccaaa cgcgttaaag aattgggcat gaaaagcgtg 120
agcgtaactg atcatgggaa catgtttgga gcgattgatt tttatacgag catgaaaaaa 180
gaaggcatta agcctatcat cggcatggaa gcgtatatcc ataatgatga caacctttct 240
agcaaagaaa ccaagcagcg tttccattta tgcttgttcg ctaaaaacca agagggctat 300
gaaaatttga tgttcttaag ctctatggcg tatttagagg ggttttatta tttcccacgc 360
atcaataaaa agcttctaaa agagcattct aaaggcatta tcgcttctag cgcatgcttg 420
caaggggaag tcaattacca tttgaatacc aataatgaga gaaaccgcaa gtatggggct 480
aaaggctatg atgaagctaa aaaaatcgct tgcgaatacc aagagatttt tgaagacgat 540
ttttatttag agatcatgcg ccatggcatt ttagatcagc gattcattga tgagcaagtc 600
attaaaatgt ctttagaaac agggttaaaa atcattgcca ccaacgacac ccactacacc 660
atgcctaatg acgccaaggc tcaagaagtg gcgatgtgcg tagcgatggg taaaacccta 720
aacgataagg ggcgcttgaa acactccgtg catgagtttt acattaaatc ccccgaagaa 780
atggcaaagc tctttgcaga tattccagaa gctttagaaa acacccaaga aatcgctgat 840
aaatgcgttt tagagattga tttaaaagac gataaaaaga acccccccaac ccccccaagc 900
ttcaaattca ctaaagctta cgctcaaaat gaggggctga attttgaaga tgacgcttct 960
tattttgcct ataaggctag agaaggcttg aaagagcgct tagttttagt accaaaagaa 1020
aagcatgatc aatataaaga gcgcctagaa aaagaaattg aagtcattac gaacatgaaa 1080
ttcccagggt atatgctgat tgtgtgggat tttatccgtt atgctaagga aatgggcatt 1140
cctgtagggc ctggtagggg gagtgcggcc gggagcttgg tggcttttgc tttaaaaatc 1200
acggatattg acccttttgaa atacgatttg ctctttgaaa ggtttttaaa ccccgaaaga 1260
atcagcatgc ctgatattga tacggatttt tgccagcgcc ggcgtaagga aatcatagaa 1320
tacatgattg aaaaatacgg caaatacaat gtggcacaag tcatcacttt taataagatg 1380
ttggctaaag gcgtgatcag agatgtcgca agggttttgg acatgcccta taaagaagcc 1440
gatgattttg ccaaactcat acccaaccgc ttaggcatca cgcttaaggg ctatgaaaaa 1500
aatggcgagt ttatcgaggg agcgtgggaa ttagagccta aaatcaagga attagtagag 1560
agtaatgaat tagccaaaca agtgtgggag tattcgctca atttagagaa tttaaaccgc 1620
aacgcaggcg tgcatgccgc agccttagtg gtggatagcc aaaaagagtt gtggcacaaa 1680
acccctttgt ttgcctctga aaagaccggc ggtatcgtta cgcaatattc catgaagtat 1740
ttggagccgg tggatttgat caagtttgac tttttggggc ttaaaacctt gaccgtgatt 1800
gatgatgcgc ttaaaatcat taaaacacaa cacaaaatta gcgtggattt tttatcgttg 1860
gatatggacg atccgaaagt gtataaaacg atccaaagcg gggatacggt ggggatcttc 1920
cagattgaat ccgggatgtt tcaagggctt aacaagcgct taaggccttc aagctttgaa 1980
gacattatcg ccattatcgc gctaggcaga ccagggccta tggaatcagg catggtagat 2040
gattttgtga acagaaagca tggcgttgag cctatcgctt atgcgtttaa agaattagag 2100
ccgattttaa agcccactta cggcacgatc gtctatcaag agcaggtgat gcaaatcgtg 2160
caaactatcg gcggtttcag tttgggtgaa gcggatctca tccgccgcgc tatggggaaa 2220
aaagacgctc agatcatggc ggacaataag gctaagtttg tagaaggcgc taaaaattta 2280
gggcatgatg gccaaaaggc ggctaatttg tgggatttga tcgttaaatt tgccggctat 2340
ggtttcaaca aatcgcattc ggccgcttat gcgatgatca ctttccaaac ggcgtattta 2400
aagacttatt acaagcatga gttcatggca gcgatgctca ctagcgaatc caataagatt 2460
gaatccgtgg cgcgctatat tgatgaggtc agggctttag aaattgaagt gatgcctccg 2520
catatcaatt cttctatgca agatttcagc gtggcggagt ttaaaaatca aaagggcgag 2580
ttagaaaaga aaatcgtgtt tggtttggga gcgattaaag gagttggggg tgagccgatt 2640
aaaaacatca ttgaagaaag ggctaaaggg gattataaga gtttggaaga ttttatttca 2700
cgggtggatt tttctaaact cactaaaaaa tctttagagc cattagtgaa atcagggagc 2760
ttggataatt taggctacac tagaaaaacc atgctcgcta acttggatct gatctgtgat 2820
gccgggcgcg ctaaagacaa ggctaatgaa atgatgcaag ggggtaattc tctttttgga 2880
gccatggagg gcggaaccaa agagcaggtt gttttggaca tgattgattt gggcgaacat 2940
gacgctaaaa cgcttttaga atgcgaatac gaaactttag gcatccatgt ttcaggcaac 3000
cctttagacg agtttaaaga agaaattaag ggttttaaaa atttagtcaa aagcattgat 3060
attgaagagt tagaaatcgg ctcgcaagct tatttgctcg gtaaaatcat ggaagttaaa 3120
aagaaaattg gcaaacgaag cggtaagcct tatggcatag cggacatttt ggatcgatac 3180
ggcaagtttg aactcatgct ttttgaaaag caattaaacg ccttagaaga gttggacatt 3240
aataagcctt tagtgttcaa atgcaagatt gaagagcaag aagaagtggt gcgattgagg 3300
ctttttgaaa tcttggatct agagagcgct agagaggtta aaatccctaa agcccgttat 3360
aaagaccctg aaaagcaaaa agaagaggtg cgcgaaatcc cccccatgga aatgcttgcc 3420
tctagttctt gctctttagc gatcgtgtta gaaaacgatg tgaaaaaaga gtttttaaga 3480
caaatcaaag agagcgcttt aaaacaccag ggcaaacgcc ccttgtattt gatcatcaaa 3540
gataaggata agcaattcaa aatccaaagc gatttaatgg taaatgaaaa gattaaggac 3600
gattttaaag ggttagagtg gagggattta gct 3633

Seq ID 120

atgacgcttt tagtaggttt aggcaaccct actttgcgtt acgctcacac cagacacaac 60
gctggttttg atattttaga ttcactcgtt agcgaattgg atctttcttt cacttttttct 120
cccaaacaca acgcttttttt atgcgtttat aaggatttta tcttcctaaa gccacaaact 180

tacatgaatt taagcggcga gagcgtttta agcgctaaaa atttttacaa aaccaaagag 240
cttttaattg tccatgacga cttggattta cctttgggcg ttgtgaggtt taaaaatggt 300
gggggaatg gagggcataa tggcttaaaa tccattgatt tgttgtgttc taattcttat 360
tatcgcttga gggtggggat ttctaaagga ataggcgtaa ttgagcatgt gctttcaaaa 420
ttccacaaaa acgaagagcc tttaaaaaac gctgcgtttg aacatgccaa aaacgcctta 480
aaatttttta tagaaagcca tgattttaac gctatgcaaa atcgtttcac gcttaaaaaa 540
cctttaaaaa tagaaagt 558

Seq ID 121
atgaaaaaat ccctttgtct gtctttcttt ctgactttct ctaaccctct tcaagccctt 60
gtgatcgagc ttttagaaga aatcaaaact tcgccgcata aaggcacttt taaggctaaa 120
gtccttgatt ctaaaaaacc aagacaagtt ttaggcgttt ataatatctc cccacacaaa 180
aaactcacgc tcactatcac ccacatatcc actgcaatcg tctatcaacc ccttgatgaa 240
aaactttctt tagaaacaac cttaaaccct aaccgcccta ctatccctag aaacacccag 300
attgtttttt cttcaaaaga attgaaagag tcgcacccgc accaaatgcc ttctttaaac 360
gcgcccatgc aaaaaccaca aaacaaaccc cattcatcgc aacaaccttc tcaaaacttt 420
tcttacccag agcccaaact aggctctaaa aactctaaaa acagcctttt acagccttta 480
gcaattccta gcaaaataag tcccactaac gaaactcaaa cgccaacaaa cgacactaaa 540
ccccctttaa agcattcttc agaagatcaa gaaagcaacc tctttataac gccacccact 600
gaaaaaacgc tccctaacaa cacctctaac gctgatatta gtgaaaacaa tgaaagcaat 660
gagaataaag ataatgtgga aaaacaagcc attagagatg ctaatattaa agaatttgca 720
tgcgggaagt gggtctatga cgatgaaaat ttacaagcct accgcccaag cattttaaaa 780
cgcgttgatg aagacaaaca aactgcaaca gatattaccc cttgcgatta cagcaccgct 840
gaaaataaaa gcggtaaaat cattaccccc tatactaaaa tctccgttca taaaacagag 900
cctttagaag agccacaaac ttttgaagct aaaaataatt tcgccattct tcaagccaga 960
agctctacag aaaaatgcaa aagggctaga gcaagaaaag acggcacgac taggcaatgc 1020
tatctaatag aagagccttt aaaacaagca tgggagagtg agtatgaaat caccacgcaa 1080
ttagtgaaag ccatttatga gcgccccaaa caagacgatc aagtagagcc gacttttat 1140
gaaaccagcg aattggctta ttcttccaca cgaaaaagcg aaataacgca caatgaattg 1200
aatttgaatg aaaaattcat ggaatttgtg gaagtgtatg aggggcatta tttaaacgat 1260
ataattaaag agagcagtga atataaagaa tgggttaaaa accatgtgcg ctttaaagaa 1320
ggggtgtgca tggctttaga aatagaagaa cagccacgag ctaaaagcac gcctttgagt 1380
attgaaaact ctcgtgtggt atgtgtcaaa aaggggaatt atttattcaa cgaagtt 1437

Seq ID 122
atgaatgcat tcaagcgtat tattagtgtg ggggtaattg ctttaggttt gtttaacctt 60
ttagacgcca aacaccacaa agagaaaaaa gaaaaccaca aaatcactcg tgagcttaaa 120
gtgggcgcta accccgttcc gcatgcgcaa atcttgcaat cagtcgtgga cgatttgaaa 180
gagaaaggga tcaaattagt gatcgtatct tttacggatt atgtgttgcc taatttagcg 240
ctcaatgacg gctctttgga tgcgaattac ttccagcacc gcccttattt ggatcggttt 300
aatttggaca ggaaaatgca ccttgttggt ttggccaata tccatgtgga gcctttaaga 360
ttttattctc aaaaaatcac agatattaaa aatcttaaaa agggttcagt gattgctgtg 420
ccaaatgatc cggccaatca aggtagggcg ttgattttac tccataaaca aggccttatc 480
gccctcaaag acccaagcaa tctatacgct acggagtttg atattgtcaa aaatccttac 540
aatatcaaaa tcaagccttt agaagccgcg ttattgccta aggttttagg ggatgtggat 600
ggggctatca taacagggaa ttatgccttg caagcaaaac tcaccggagc tttattttca 660
gaagataagg actcgcctta tgccaatcta atagccgctc gtgaggataa cgcgcaagat 720
gaagccataa aaacattgat tgaagcctta caaagtgaaa agaccaggaa attcattttg 780
gatacctata agggggcgat tatcccggct ttt 813

Seq ID 123
atgaaaaatc ttcgctataa gcttttgctc tttgttttta tagggttttg ggggttacta 60
gccttaaatt tatttatttt aagcgttaaa aatcaagaat actatgaaaa attggctgaa 120
cgaaacatga ctaaaaagga atttctagtc cctacaaggg gaaatattac agacagaaat 180
gatgagtttt tggccactaa tgaattggtg tttggcgtgt ttttgcccag cggactgaaa 240
caaaaagatc ttttagaaaa aattgaaatc atccaaaagt ttttccctaa cttttctaaa 300
gaaacgcttt taaacaatta ccaaaaagaa aattcgcttt ataaccataa cctcattaaa 360
gtggttggct tcattcctta tgccaccatg caacctcttt atgccaaact catccaaact 420
caaggcattt ttgcgcttcc cttagacaag cgttactacc ctaataacgc tttagcttcg 480
catgttttag gctatgtggg ggtggcaagc ttgcaagatt taaaagacga tgaggagaat 540
caatacagcc agattgtagg caaaaccggc attgaaaaag aatacaacaa gcttttacaa 600
ggcaaggtgg gttataaaat catgcgtgtc aatgcgctca atcaagaatt agccacctta 660
gaagtagtgc tgccaagcac caacaaccac ttgcaattga gtttagacaa acgcttgcaa 720
aaagaagcgg acaagctctt tgaaaataaa agggggggcta ttttagtgat ggatgcagaa 780
aatggggaat tgctcgttgc aggaagttac cctgaataca atttgaacga ttttgtaggc 840
gggatcagtc aagacaaatg gcaaaaactt caagatgata tttataaccc cttattaaac 900
cgcttcgcta acgccttgta tccgccggga tctgtggtta aaatgggcgt gggcttgagc 960
tttttagaaa accttcatat cacagaaaac accaccatac ccaccccgcc ttttattgaa 1020

gtgggcaagc acaaattcag agactggaaa aaaacagggc atggcaattc taatttgtat 1080
aaagccatta gggagtccgt ggatgtgtat ttttataagt ttgggcttga aatctctata 1140
gaaaaactct ctaaaacctt aagggaagtg ggctttgggg aaaaaacggg cgttgatttg 1200
ccgaatgaat ttgtggggat tgtgccggat aatttgtgga aactcaaacg cttcaatcaa 1260
gactggcgcg ttggggacac gctcattacc gctattgggc aaggctcttt tttagccacg 1320
cccttgcagg ttctagccta cacgggactc attgctacgg gcaaactggc aacgcctcat 1380
ttcgctatca acaacaaaca accgcttaaa gatcccctaa atagctttca aaaaaagaag 1440
ctccaagcct tgagagtggg catgtatgaa gtgtgtaacc ataaagacgg caccgcttat 1500
cattccacaa ggggttctaa gattacttta gcgtgtaaaa ccggcaccgc acaagtcgtg 1560
gaaatcgctc aaaacatcgt caatcgcatg aaagaaaagg atatggaata tttccatcga 1620
tcccatgcgt ggattaccgc atttttgcct tatgaaaaac ccaaatacgc tatcactatt 1680
ttagtagaac atggggaagg ggggtcaaaa ctagggggcc tgttagtgaa gatgagtaat 1740
aaactctatg agcttggcta tctt 1764

Seq ID 124
atgttcagcg gtctaatcca tcaaatagct aaagtgaaaa gtttccacaa caatatttta 60
aacatagaga gtgatctcaa tcccaagctt ggcgatagca ttgcgattaa tggggcatgt 120
ttgaccgcca tagaaagttc aaaaacgcat tttagcgtgg aattgagcca aaaaacccaa 180
aacagcgtag cgttagaaaa ttacaaggat ttagtccata ttgagccagc cctaaaagct 240
gatgcgagtt tggatgggca ttttgtgcaa gggcatattg acgctatagg ggtcattgaa 300
aaaatcattc acaacgctaa tcaagtggat tttttcatca gcgcttctga agaaacgctt 360
ttattgtgcg ttgagcaagg ctctattgca gttgatgggg tgagtttgac tttaagcaag 420
gtagaagaaa aggggttttg gctaacgatt atcccttaca ctttagaaaa caccctttt 480
aaggcttata aactcaaacg gcgcgtgaat attgaaacgg acatgttagt ccgcagcgtt 540
gcgtctattt tgaaaaaaac aaaagggttt gaaaaaaatt tctcttggaa tgaggctgac 600
gctttgactt tagggtat 618

Seq ID 125
aaaaagagcg aacgctttaa aattgaactt aagccattta aaaaaaggcc aaatcgtggt 60
gcgcatagac gagcgttatt tcaggcctac cgaagtggat ttgcttttag gcgatcccac 120

Seq ID 126
tggttcgcca aaaaagattt tagcgcttgg agcgcaacaa aaagggcatt t 51

Seq ID 127
aacctgcaaa cccaccttaa aaggctcaaa agaagtgagt ttgtgggcca aaaaggaatt 60
agagggcatg gggaggtttt ctttaaaaga aattttaatg ctcagcctta ccttattggc 120
tttactgggt tggatttttg gcaaaccttt aggcttgcat gcgagtgcga cggctttgat 180
tgtcatggtt ttaatggcgt tttg 204

Seq ID 128
acacaagcca ttattttgaa aaaaaaccag gcttgggggа gagggtggat tatgcggggc 60
gttgcttcta taataaattc cagagag 87

Seq ID 129
gccatgtgga tattactaaa aacaagcaag actcgcaact caaaaaagat tgtttggaat 60
ttatccaaag gtttaatgtc ccaaagccca ttatcattac cgctctttat aaccttaggg 120
gcattaagcc cactaaaaaa gaag 144

Seq ID 130
aaaaagaaga aaagcaaaaa ttccaaaaat tcgccctggg cttggaaatg tctttcaatg 60
tgtggcgtt 69

Seq ID 131
aaaaagctta taaaaagcct agcattaaag aaagacaccg ccatcgttat gaaatcaacc 60
ccaaataccg ccaagagtgg gaaaataagg gct 93

Seq ID 132
aggggcgcta cacccccacg caaaaaaaca ttatttttga aaaaaccgag cgttttatca 60
cgcccaaact cc 72

Seq ID 133
tcggctcaac caccatcgct aaaacggagc ttaggggggt tgaaagccat ggca 54

Seq ID 134
aaacatgatc acggcttttg ggtgcggcat tcaagagagt tt 42

Seq ID 135

gccaaaaata cggctttaaa atcccttgct ttgggcatac gggcgatggc aatgtgcatg 60

Seq ID 136
cgctttgaaa gacaaaacct atctctacgc tatggatcta ttggattaca acaactattt 60
atccatagaa aaccccatta tcaaaacaag agcaatggga acttatgcgg atttgattat 120
catcacaggc tcattagagc aagtcaatgg gtattacaac attctaaaag cgctcaacaa 180
acgcaacgc 189

Seq ID 137
tcgtcagttt catcaaaaaa gccagccaaa aattccctaa ctcgcttttt atcatcacag 60
gggatcattt tgacaggagc tatgaatacg ctaaaaacga tttgtatatc attaaatccg 120
tgccgcttat tttatatgcc cctactt 147

Seq ID 138
aagtggaaca tttctacccc aaaaccccca cccaagaatg gcgcgatagg gtgggggatt 60
atttcacttt tgagcaagac tatcttaata attttgggaa tc 102

Seq ID 139
aaaacgcgat ggataccaac agagaagtgg cgcaattcca ctatggaggc ggcacgccga 60
cctttttttc gcccattcaa t 81

Seq ID 140
aaaaactttc gtgctcatga ctttttgag cgcagggatt gtcaatattt ttattccgtc 60
tggcggaggg caatgggcga ttcaagctcc tatcatgctt ccggctgggc aaagcttagg 120
ggtggatccg ggagtggttt ctatggctat cgcttgggga gatgcttgga cgaatatgat 180
acagcctttt tgggctttgc ccgctttagc cattgcgggt ttgggcgc 228

Seq ID 141
aaggcccggt taaaacgctt tcagattatt ccacttatat cagccgaaaa agcaatgtta 60
caggcgatgc gt 72

Seq ID 142
cgggcaccat ttagacggga gccttggagg ttgggggggt gctgtaattt a 51

Seq ID 143
tttacaaggc ataaacaaac aagccgctca aaaagaagca aaagccttag cgttaaaaat 60
ggggttaga 69

Seq ID 144
ttcttcagtt acattcaata tgaaaggcgc tctagtggct atcaccgagc ttggcccttc 60
tttagggagc gttttgac 78

Seq ID 145
agggatttac ttgcaatacc gcagcgtttt gcgcgaaaac aggcttttaa aaaaccatct 60
ctc 63

Seq ID 146
aaatcgccca aaaaggcaac aaaaaagagg ttt 33

Seq ID 147
gcgcttgagc agcgtgatga aagatttacc cgtgggggt 39

Seq ID 148
cccatatctt gcaaagcccc taaattcgtg gtgagtttgt gcaattctgg catgccgtta 60
gacttaggcc cttggaaagg caagaccgcc acaaagtccc tttctaattc tttatttta 120
aagcgttcta aaaactcgct ttgggtttta aaaacaatcg ctctagcctt aactttccta 180
tgctcatctt taatggctga gattttaatc acggccctcc ctaaattacc ctttaaaatt 240
ttaagccccc cattagcggc aaaaggatca ctaacagggc gtaaaatatc cgtattcagg 300
cta 303

Seq ID 149
aagagcatca catcacgcca agctataaaa ccgatattga gagcg 45

Seq ID 150
tttaaaaccc ttgttgagct ttttaaaagc caaataccag gtgcctttag aaaacattcg 60
catccaagac actcaaattt tagcgttttt aaaaaatccg gaaaaagtgg ggtt 114

Seq ID 151

aacgctatta tgaagccaaa gaaaccgcaa tatttaaaaa attccctaaa ttcatccaac 60
tttatgataa cgccacttct aaaatccaag cct 93

Seq ID 152
ataaaagccc taaaaccaag cttgtttgag cgtctaaatt ctctaaac 48

Seq ID 153
gcgatgctgt tttttagatt cgttacggtt tctcccacat acgcgcagcc ggctccccaa 60
gtgttagaag taaccgtgcc agatggcgtg ccacggagat tgccgtcgct acccttttca 120
tggcatactc ctaaagagtc tttcacgaac gctgcaggga ttctttcaaa gtccttcacc 180
actgct 186

Seq ID 154
gggctttttc aaaatctaac gccccactca aagacaccgc gctcacttcg ccgagcgaat 60
gccctaaagc aaaaacgggt tttaaccccc catttacttg cttgt 105

Seq ID 155
tttgttggac cccaagaggt gccaccgatc gcaacgccca agaaaaaccc aaaatgcaag 60
ttctcacgat tgaaaatagc cgggttaaac aacacatctg tgccagcccc a 111

Seq ID 156
ataagagcgt ttttcaaagg tgtaaatctt gccaatttca ttgactatgg gcgtgatagc 60
cgcatttttg ggagcgatga tttcataagc ggtgttagtg gtagtggtga atttgcatgc 120
aaaaaaacgc ccgtcttcgg ttatttcgcc attgacttga aaatcccctt cgctaatggc 180
tgtttggtgg ttttgagtat ccaacctttc aaaaggcctt cgcatcaaat agccgtccgt 240
aaaaccccctg tttttaagcg tgttcaattc gctggcataa aaactcggct t 291

Seq ID 157
aagttcttta gcaatcactt gagaagaaag gtcgttttta tagatataag tttgcatgtc 60
aatgcttttt tggctcattc taataagtcc cactctatgc aacagagcgt caaagccatc 120
ttc 123

Seq ID 158
tccgtagggg tgaaaaaatc gcctccaaac tccacttccg ca 42

Seq ID 159
accctaactt gcaaaaaagt cgcttctaaa agggctttga tttgcgcatt gatttcgctc 60
acgctcaata catccaccag ctccccctttt tatagcaaac gagtgagatc attgaaaagc 120
cctaaaaaca tgataaaaac caaaaacccc acccccgcta gccacaacgc attttgtatg 180
ggtgttggca aagtgata 198

Seq ID 160
gcgtcaatga gtttgtctaa tcctgtgccg ctaggcatcg ccgcggttac gcctacgatt 60
ttttcatctt ttttagctaa ttctaaaagg gtgttagaat acgcttcagt gggcgataag 120
attgcgcttt tggatttttt agacaagccg gtatccaaat caaaaggccc caccccatgc 180
catttttca 189

Seq ID 161
atctttttga gcaacacctc tctttgcatg gggcggacaa attgcaacac aaaaagcaat 60
gaaaacgcgc tcgcttcttt aaactcaacc tctaaaaaat ccatgcattc aaaacgggca 120
ttgttaaaat cttttaattt ttcttgcgct tttttgagca tgggcatgga attatcaatc 180
cctacaagct caatctcttg ttggatttgt cggttaagcg cgataaaaaa gttcccggta 240
gaacagccca aatca 255

Seq ID 162
agggattttc aagtccttaa acatcgcttg caccctttct ttttcatttt tacgcaacaa 60
gccatgatcc acaaaaacag cgatcaaatt atccttaatg gctctgtgca acagcgtagc 120
gaccaccgta gaatccacgc ccccactcac cgcgcacaaa accttagcgt tagcgatttt 180
ttctttcaat cgtgcgattt ctctttgagc gaaatgctgc atcccccaag ttttttcaca 240
gccgcaaac 249

Seq ID 163
attatccaca tgaggggcga ccactctcat cacatgccct ctttttttca gcgcttcaaa 60
aaaacgaaac gctgtcatag aagtgccatt actggtgtct ttaaaactat ccacgac 117

Seq ID 164
atcattatcc cggctgtgct cgccaatgac catgcccaca taaaccttcg tttgggggtt 60
gataaaaagc gtgcctcttt cttggatatt gaaaagggaa aaagcggtcg cttcgccatt 120

ttccatgctg at 132

Seq ID 165
aaaaaccgcc cttctaaaaa cccgctcgcg caaaacgccg tagtgagcgc gttagctccg 60
ggcaaaacat cgtat 75

Seq ID 166
aaaccctcta gcgtttggat ctataaacca ataataaggg gcaaaaatat tcaaaccata 60
ccttcc 66

Seq ID 167
tcgtcagttt catcaaaaaa gccagccaaa aattccctaa ctcgcttttt atcatcacag 60
gggatcattt tgacaggagc tatgaatacg ctaaaaacga tttgtatatc attaaatccg 120
tgccgcttat tttatatgcc cctactt 147

Seq ID 168
cgcgctcgct cgcgctctct tttaggattt tttcttttga aagcgagttg caaaacaccg 60
cataagagcc taaattttca tctttccaat tcaaaacagg gtaagtggcg cataaaatct 120
ttttggaaa 129

Seq ID 169
gtttcagaaa tcttatccac gctcgttagc ccatcaaaac tccctgagga accaaaggct 60
aaattgatgc gttgggggcc atcagcgcca tttttagggt caaattgcaa aagaggcggg 120
ttcatgcctg caagcgatcc gtcgttatta aaatgcaaac ggcctccttc aaacacatta 180
ggcctagccg ctgacccccc tactaattcc ccaggctcag gcacgatcac cctaaaattc 240
cattccgctc ccccactcct a 261

Seq ID 170
ctgcctaacc ttaacaaaat cagttcatca tctttcacta aatacacaag caaaacatca 60
ggcttaatgt ggcattccct aaaaggtttc cactttccct ttaaggca 108

Seq ID 171
tcaaggttta gggagcgtgt tgccgccctc tttacaaaac gcgctcaaag aaaacgattt 60
aggcactctt ttatcgcc 78

Seq ID 172
aatattcatt ggccacacgc accaaatcgc tcacttttaa atccaaaaat tgtcgctggt 60
aatccgtcaa gccttgaata tcgttttgca ctaaatagtc cgcaaaaagc cccgcaacat 120
cgc 123

Seq ID 173
cccatatctt gcaaagcccc taaattcgtg gtgagtttgt gcaattctgg catgccgtta 60
gacttaggcc cttggaaagg caagaccgcc acaaagtccc tttctaattc tttatttta 120
aagcgttcta aaaactcgct ttgggtttta aaaacaatcg ctctagcctt aactttccta 180
tgctcatctt taatggctga gattttaatc acggccctcc ctaaattacc ctttaaaatt 240
ttaagccccc cattagcggc aaaaggatca ctaacagggc gtaaaatatc cgtattcagg 300
cta 303

Seq ID 174
gaatctttag tcctaaaacc tattttaggc aaacggcgtt gtaagggttg ttgccctcct 60
tcaaagcctc ttttagcctt a 81

Seq ID 175
ggttcaaatg agcgatcgca taaggagcga ttaagtattc aaacccatag aattgcttca 60
agagattttg atatttgtcc tctt 84

Seq ID 176
ctagggggca ataaatcttt cacgctatac tcccaccaca catcacagcc ttttttctca 60
aaaagattgg ccacatgctc taaaacttcg ctttcaaaac aaggcttatt cgtgcgtttg 120
tctatgaaaa aggccagtgg cacgccccat tttctttgcc ggctcaagca ccaatcaggg 180
cggttttcta tcatggtttt taggcggttt ttcccgctgc ttggcacaaa ttccaccttt 240
tcaatcgcat ctaaagccac ttctcttaag gttttt 276

Seq ID 177
gcgttcgtgc ttaagccttg taaaaaagcc tgctcttgga gttttaagtt ttccttggct 60
aattccacgc tagaaagcaa gcttttgtat tctttcaaa 99

Seq ID 178

gagagcatct cttctctgat cctgtcaaaa ataatgatcg tatcattaat ggaataccca 60
atcaaggtga gcaaggccgc aatcacttcc aaattcatat caatcttaaa aacaatcacc 120
gagcttgcca ctaaaatcac atcatgcaca agcgcaatga cgctcgctaa agcaaaacgc 180
cattca 186

Seq ID 179
MVKNTGELKKLSDTYENLSNLLTNFNNLNQAVTNASSPSEINATIDNLKANTQGLIGEKTNSPAYQAVYLALNAAV
GLWNVIAYNVQCGPGKSGDQSVIFDGQPGHDSRSINCNLTGYNNGVSGPLSIDNFKTLNQAYQTIQQALKQDSGFP
VLDSKGKQVTIKITTQTNGANKSETTTTTTTTNDAQTLLQEASKMISVLTTNCPWVNTAHNSNGGAPWNLNTTGNV
CQVFATEFSAVTSMIKNAQEIVTQAQSLNNPQSNQNAPKDFNPYTSADRAFAQNMLNHAQAQAKMLELADQMKKDL
NTIPKQFITNYLAACRNGGGTLPDAGVTSNTWGAGCAYVEETITALNNSLAHFGTQADQIKQSELLARTILDFRGS
LKDLNNTYNSITTTASNTPNSPFLKNLISQSTNPNNPGGLQAVYQVNQSAYSQLLSATQELGHNPFRRVGLISSQT
NNGAMNGIGVQIGYKQFFGEKRRWGLRYYGFFDYNHAYIKSSFFNSASDVFTYGVGTDVLYNFINDKATKNNKISF
GVFGGIALAGTSWLNSQYVNLATFNNFYSAKMNVANFQFLFNLGLRMNLAKNKKKASDHVAQHGVELGVKIPTINT
NYYSLLGTQLQYRRLYSVYLNYVFAY

Seq ID 180
MAKEIKFSDSARNLLFEGVRQLHDAVKVTMGPRGRNVLIQKSYGAPSITKDGVSVAKEIELSCPVANMGAQLVKEV
ASKTADAAGDGTTTATVLAYSIFKEGLRNITAGANPIEVKRGMDKAAEAIINELKKASKKVGGKEEITQVATISAN
SDHNIGKLIADAMEKVGKDGVITVEEAKGIEDELDVVEGMQFDRGYLSPYFVTNAEKMTAQLDNAYILLTDKKISS
MKDILPLLEKTMKEGKPLLIIAEDIEGEALTTLVVNKLRGVLNIAAVKAPGFGDRRKEMLKDIAILTGGQVISEEL
GLSLENAEVEFLGKAGRIVIDKDNTTIVDGKGHSHDVKDRVAQIKTQIASTTSDYDKEKLQERLAKLSGGVAVIKV
GAASEVEMKEKKDRVDDALSATKAAVEEGIVIGGGAALIRAAQKVHLNLHDDEKVGYEIIMRAIKAPLAQIAINAG
YDGGVVVNEVEKHEGHFGFNASNGKYVDMFKEGIIDPLKVERIALQNAVSVSSLLLTTEATVHEIKEEKAAPAMPD
MGGMGGMGGMGGMM

Seq ID 181
MKIKNILLSGGSGKRLWPLSRSLYPKQFLKLFDHKSLFELSFKRNASLVDETLIVCNEKHYFLALEEIKNEIKNKS
VGFLLESLSKNTANAIALSALMSDKEDLLIVTPSDHLIKDLQAYENAIKKAIDLAQKGFLVTFGVSIDKPNTEFGY
IESPNGLDVKRFIEKPSLDKAIEFQKSGGFYFNSGMFVFQAGVFLDELKKHAPTILKGCERAFESLENAYFFEKKI
ARLSEKSMQDLEDMSIDIALMQQSHKIKMVELNAKWSDLGNFNALFEEAANEPKENVSLNQTPVFAKESENNLVFS
HKVSALLGVENLAVIDTKDALLIAHKDKAKDLKALVNEVETNNQELLQTHTKVYRPWGSYEVLHESGCYKVKILEV
KPNARLSLQKHFHRSEHWVVISGMASVELDHQLFELQANESTYIPKNTLHRLANYGKIPLIIIEVQVGEYVGEDDI
VRIDDDFNRQNQNA

Seq ID 182
MAEWKTDTEEVKEVVKKCREFKRSLQEEKCSPFIKDLDSYALKIIVERRKIEHQLQEAIEKLRRAKKKRSSFWGSF
VEGARDLLDMVREIIPPAKLGAEACDKVLNLMEDNIEKWEHNVRLLERMLEIYATQAKASAELVEGAWKSVKKSLD
FYTDKHQEFIKRLNYASEAIDNEYNIAPPEILNESDFESPTIVYNPKKSVYDEHLKDLREDFSFSLYADLKNRINA
SSKLDRTTTSKEQEFEKNLEDLMPGFRGGTDTLSGDELEHMASFRGQEFEKNLEDLMPSSLGVHSYDESLNLAKKN
CVKNCKKALGDFTEKIKESPNDLNAINEAFNHLETELERATENLSQKIAPILERYENDKRQKLGYGEFLEKEKEGF
MVDEQNPYPEEVRFNELRLAEFESVFSAIVPLEDLDKPACAHHALKALEATLKNRDLGFDATELEQIAKGFIPKGY
LWHFDANVLGNVALVREELLLGVKHTKGYLLWKQFLQTQN

Seq ID 183
MNTYAQESKLRLKTKIGADGRCVIEDNFFTPPFKLMAPFYPKDDLAEIMLLAVSPGMMRGDAQDVQLNIGPNCKLR
ITSQSFEKIHNTEDGFASRDMHIVVGENAFLDFAPFPLIPFENAHFKGNTTISLRSSSQLLYSEIIVAGRVARNEL
FKFNRLHTKISILQDEKPIYYDNTILDPKTTDLNNMCMFDGYTHYLNLVLVNCPIELSGVRECIEESEGVDGAVSE
TASSHLCVKALAKGSEPLLHLREKIARLVTQTTTQKV

Seq ID 184
MKKISRKEYVSMYGPTTGDKVRLGDTDLIAEVEHDYTIYGEELKFGGGKTLREGMSQSNNPSKEELDLIITNALIV
DYTGIYKADIGIKDGKIAGIGKGGNKDMQDGVKNNLSVGPATEALAGEGLIVTAGGIDTHIHFISPQQIPTAFASG
VTTMIGGGTGPADGTNATTITPGRRNLKWMLRAAEEYSMNLGFLAKGNASNDASLADQIEAGAIGFKIHEDWGTTP
SAINHALDVADKYDVQVAIHTDTLNEAGCVEDTMAAIAGRTMHTFHTEGAGGGHAPDIIKVAGEHNILPASTNPTI
PFTVNTEAEHMDMLMVCHHLDKSIKEDVQFADSRIRPQTIAAEDTLHDMGIFSITSSDSQAMGRVGEVITRTWQTA
DKNKKEFGRLKEEKGDNDNFRIKRYLSKYTINPAIAHGISEYVGSVEVGKVADLVLWSPAFFGVKPNMIIKGGFIA
LSQMGDANASIPTPQPVYYREMFAHHGKAKYDANITFVSQAAYDKGIKEELGLERQVLPVKNCRNITKKDMQFNDT
TAHIEVNPETYHVFVDGKEVTSKPANKVSLAQLFSIF

Seq ID 185
MSMEFDAVIIGGGVSGCATFYTLSEYSSLKRVAIVEKCSKLAQISSSAKANSQTIHDGSIETNYTPEKAKKVRLSA
YKTRQYALNKGLQNEVIFETQKMAIGVGDEECEFMKKRYESFKEIFVGLEEFDKQKIKELEPNVILGANGIDRHEN
IIGHGYRKDWSTMNFAKLSENFVEEALKLKPNNQVFLNFKVKKIEKRNDTYAVISEDAEEVYAKFVLVNAGSYALP
LAQSMGYGLDLGCLPVAGSFYFVPDLLRGKVYTVQNPKLPFAAVHGDPDAVIKGKTRIGPTALTMPKLERNKCWLK
GISLELLKMDLNKDVFKIAFDLMSDKEIRNYVFKNMVFELPIIGKRKFLKDAQKIIPSLSLEDLEYAHGFGEVRPQ
VLDRTKRKLELGEKKICTHKGITFNMTPSPGATSCLQNALVDSQEIAAYLGESFELERFYKDLSPEELEN

Seq ID 186
MRYFLVVFLFLFVGCTKKDFTLKDLSLPQEASSYLASSQNGSNNNQSIDPQALRENLKESYLKAWYSPWLDMKVKS
NKKEVFWILKEMNKSTGYGEDLKPNAKAFNDALIKSMDIEHYPSVKIRAVVARDSDVRAVPTNKPYYLSQKGYPFD
RYQNSLIFQGTPVLITHFNLDKTYAHIQSSFVYGWIKVSDLVYMHDKDIELLTHLKDYVMPIKDKIPLYTDYGDFY
TNARVGELFALIPQSQKTPQKPQKKELKAYGFLRDAKGYAALQSVILEEKDFFVFPKAFNSENMAYFIDTMLGQKY
GWGGLLGNRDCSAFTRDSFANFGILLPRNSYAQSRYANNYVDLSSMKAKEKEDYILKNATPFGTLIYLKGHIMLYL
GAHNHQAIVAHSIWSVQTQKHFKTLSHKIGGVVITSLWLAEEHNGAFSKKKLLIDRVLGMSDLKDFVNKTSSPLNA
N

Seq ID 187
MKKKANEEKAQKRAKTEAKAEATQENKTKENNKAKESKIKESKIKEAKAKEPIPVKKLSFNEALEELFANSLSDCV
SYESIIQISAKVPTLAQIKKIKELCQKYQKKLVSSSEYAKKLNAIDKIKKTEEKQKVLDEELEDGYDFLKEKDFLE
WSRSDSPVRMYLREMGDIKLLSKDEEIELSKQIRLGEDIILDAICSVPYLIDFIYAYKDALINRERRVKELFRSFD
DDDENSVSDSKKDEDNEEDEENEERKKVVSEKDKKRVEKVQESFKALDKAKKEWLKALEAPIDEREDELVRSLTLA
YKRQTLKDRLYDLEPTSKLINELVKTMETTLKSGDGFEKELKRLEYKLPLFNDTLIANHKKILANITNMTKEDIIA
QVPEATMVSVYMDLKKLFLTKEASEEGFDLAPNKLKEILEQIKRGKLISDRAKNKMAKSNLRLVVSIAKRFTSRGL
PFLDLIQEGNIGLMKAVDKFEHEKGFKFSTYATWWIKQAISRAIADQARTIRIPIHMIDTINRINKVMRKHIQENG
KEPDLEVVAEEVGLSLDKVKNVIKVTKEPISLETPVGNDDDGKFGDFVEDKNIVSSIDHIMREDLKAQIESVLDQL
NEREKAVIRMRFGLLDDESDRTLEEIGKELNVTRERVRQIESSAIKKLRSPQYGRILRNYLRI

Seq ID 188
MVQKIGILGAMREEITPILELFGVDFEEIPLGGNVFHKGVYHNKEIIVAYSKIGKVHSTLTTTSMILAFGVQKVLF
SGVAGSLVKDLKINDLLVAIQLVQHDVDLSAFDHPLGFIPESAIFIETSESLNALAKEVANEQHIVLKEGVIASGD
QFVHSKERKEFLVSEFKASAVEMEGASVAFVCQKFGVPCCVLRSISDNADEEANMSFDAFLEKSAQTSAKFLKSMV
DEL

Seq ID 189
MSFRINTNIAALTSHAVGVQNNRDLSSSLEKLSSGLRINKAADDSSGMAIADSLRSQSANLGQAIRNANDAIGMVQ
TADKAMDEQIKILDTIKTKAVQAAQDGQTLESRRALQSDIQRLLEELDNIANTTSFNGQQMLSGSFSNKEFQIGAY
SNATVKASIGSTSSDKIGHVRMETSSFSGAGMLASAAAQNLTEVGLNFKQVNGVNDYKIETVRISTSAGTGIGALS
EIINRFSNTLGVRASYNVMATGGTPVQSGTVRELTINGVEIGTVNDVHKNDADGRLTNAINSVKDRTGVEASLDIQ
GRINLHSIDGRAISVHAASASGQVFGGGNFAGISGTQHAVIGRLTLTRTDARDIIVSGVNFSHVGFHSAQGVAEYT
VNLRAVRGIFDANVASAAGANANGAQAETNSQGIGAGVTSLKGAMIVMDMADSARTQLDKIRSDMGSVQMELVTTI
NNISVTQVNVKAAESQIRDVDFAEESANFSKYNILAQSGSFAMAQANAVQQNVLRLLQ

Seq ID 190
MKKNILNLALVGALSTSFLMAKPAHNANNATHNTKKTTDSSAGVLATVDGRPITKSDFDMIKQRNPNFDFDKLKEK
EKEALIDQAIRTALVENEAKTEKLDSTPEFKAMMEAVKKQALVEFWAKKQAEEVKKVQIPEKEMQDFYNANKDQLF
VKQEAHARHILVKTEDEAKRIISEIDKQPKAKKEAKFIELANRDTIDPNSKNAQNGGDLGKFQKNQMAPDFSKAAF
ALTPGDYTKTPVKTEFGYHIIYLISKDSPVTYTYEQAKPTIKGMLQEKLFQERMNQRIEELRKHAKIVINK

Seq ID 191
VRYIKFFKELNNKNVNLVGGKNASIGEMFQELVPIGIKVPDGFAITSEAYWYLLEQGGAKQKIIELLENVDATEID
VLKIRSKQIRELIFGTPFPSDLRDEIFQAYEILSQQYHMKEADVAVRSSATAEDLPDASFAGQQDTYLNIKGKTEL
IHYIKSCLASLFTDRAISYRASRGFDHLKVALSVGVQKMVRADKGSAGVMFSIDTETGFKDAVFITSAWGLGENVV
GGTINPDEFYVFKPTLEQNKRPIIKRQLGNKTQKMVYAPRGSEHPTRNIKTTKKEWQSFSLSDEDVLILAKYAIEI
EKHYSKEAKQYRPMDIEWAKDGESGEIFIVQARPETVQSQKSKEESQVFEKFKFKNPNEKKEIILQGRAIGSKIGS
GKVRIINDLEHMNSFKEGEILVTDNTDPDWEPCMKKASAVITNRGGRTCHAAIVAREIGVPAIVGVSGATDSLYTG
MEITVSCAEGEEGYVYAGIYEHEIERVELSNMQETQTKIYINIGNPEKAFGFSQLPNHGVGLARMEMIILNQIKAH
PLALVDLHHKKSVKEKNEIENLMAGYANPKDFFVKKIAEGIGMISAAFYPKPVIVRTSDFKSNEYMRMLGGSSYEP
NEENPMLGYRGASRYYSESYNEAFSWECEALALVREEMGLTNMKVMIPFLRTIEEGKKVLEILRKNNLESGKNGLE
IYIMCELPVNVILADDFLSLFDGFSIGSNDLTQLTLGVDRDSELVSHVFDERNEAMLKMFKKAIEACKRHNKYCGI
CGQAPSDYPEVTEFLVKEGITSISLNPDSVIPTWNAVAKLEKELKEHGLTEH

Seq ID 192
MSAELIAVYKDEQIIDLESAKVLGLSDGIKALNGTEPIYFDDSPLALEVIRHSCAHLLAQSLKALYPDAKFFVGPV
VEEGFYYDFKTSSKISEEDLPKIEAKMKEFAKLKLAITKETLTREQALERFKGDELKHAVMSKIGGDAFGVYQQGE
FEDLCKGPHLPNTRFLNHFKLTKLAGAYLGGDENNEMLIRIYGIAFATKEGLKDYLFQIEEAKKRDHRKLGVELGL
FSFDDEIGAGLPLWLPKGARLRKRIEDLLSQALLLRGYEPVKGPEILKSDVWKISGHYDNYKENMYFTTIDEQEYG
IKPMNCVGHIKVYQSALHSYRDLPLRFYEYGVVHRHEKSGVLHGLLRVREFTQDDAHIFCSFEQIQSEVSAILDFT
HKIMQAFDFSYEMELSTRPAKSIGDDKVWEKATNALKEALKEHRIDYKIDEGGGAFYGPKIDIKITDALKRKWQCG
TIQVDMNLPERFKLAFTNEYNHAEQPVMIHRAILGSFERFIAILSEHFGGNFPFFVAPTQIALIPINEEHHVFALK
LKEALKKRDIFVEVLDKNDSLNKKVRLAEKQKIPMILVLGNEEVETEILSIRDREKQDQYKMPLKEFLNMVESKMQ
EVSF

Seq ID 193

VKRILFFLVATTFLLRAETDSATINTTVDPNVMFSESSTGNVKKDRKRVLKSMVNLEKERVKNFNRYSETKMSKGD
LSAFGAFFKGSLESCVDQKICYYEHKDGKVSFVVNDREKFYKHVLKDLGTELSLPLFNWLYKGSDFGALHEQFGDM
YDGYIKYLISMVRISQKEKARKVDAIVLKKMEEQAEKDTKAAFQKRSSGELESHTDSPEFISSSKRTQNASNSDLN
SMTNANALKETASKEPEASSKKEKKSKKKRRLSKKEKQQQALQQEFEKQISDSSKSEK

Seq ID 194
MKEKNFWPLGIMSVLILGLGIVVFLVVFALKNSPKNDLVYFKGHNEVDLNFNAMLKTYENFKSNYRFLVGLKPLIK
SPKTPILPYFSKGTHGDKKLQENLLNNALILEKSNTLYAQLQPLKPALDSPNIQVYLAFYPSPSQPRWLGTLDCKN
ACEPLKFDLLESDKMGRYKILFKFVFKNKEELILEQLAFFKQRI

Seq ID 195
MAYFLEQTDSEIFELIFEEYKRQNEHLEMIASENYTFASVMEAMGSVLTNKYAEGYPNKRYYGGCEVVDKIESLAI
ERAKKLFNCQFANVQAHSGSQANNAVYHALLKPYDKILGMDLSCGGHLTHGAKVSLTGKHYQSFSYGVNLDGYIDY
EEALKIAQSVKPEIIVCGFSAYPREIDFKKFREIADEVGALLLGDIAHVAGLVVTGEHAHPFPHCHVVSSTTHKTL
RGPRGGIILTNDEEIAAKIDKAIFPGTQGGPLMHVIAAKAVGFKENLKPEFKAYAQLVKSNMQVLAKALKEKNHKL
VSGGTSNHLLLMDFLDKPYSGKDADIALGNAGITVNKNTIPGETRSPFVTSGIRIGSAALSARGMGAKEFEIIGNK
ISDILNDINNVSLQLHVKEELKAMVNQFPVYHQPIF

Seq ID 196
MKITYCDALIIGGGLAGLRASIACKQKGLNTIVLSLVPVRRSHSAAAQGGMQASLANAKKSEGDNEDLHFLDTVKG
SDWGCDQQVARMFVTTAPKAIRELASWGVPWTRIKKGDRPAVVNGEHVTITERDDRHGYILSRDFGGTKKWRTCFT
ADATGHTMLYAVANEALHHKVDIQDRKDMLAFIHHDNKCYGAVVRDLITGEISAYVSKGTLLATGGYGRVYKHTTN
AVICDGAGAASALETGVAKLGNMEAVQFHPTALVPSGILMTEGCRGDGGVLRDKFGRRFMPAYEPEKKELASRDVV
SRRILEHIQKGYGAKSPYGDHVWLDIAILGRNHVEKNLRDVRDIAMTFAGIDPADSKEQTKDNMQGVPANEPEYGQ
AMAKQKGWIPIKPMQHYSMGGVRTNPKGETHLKGLFCAGEAACWDLHGFNRLGGNSVSEAVVAGMIIGDYFASHCL
EAQIEINTQKVEAFIKESQDYMHFLLHNEGKEDVYEIRERMKEVMDEKVGVFREGKRLEEALKELQELYARSKNIC
VKNKVLHNNPELEDAYRTKKMLKLALCITQGALLRTESRGAHTRIDYPKRDDEKWLNRTLASWPSAEQDMPTIEYE
ELDVMKMEISPDFRGYGKKGNFIPHPKKEERDAEILKTILELEKLGKDRIEVQHALMPFELQEKYKARNMRLEDEE
VRARGEHLYSFNVHELLDQHNANLKGEHHE

Seq ID 197
MKDSFLFTSESVTEGHPDKMADQISDAVLDYIIERDQKAKVACETLVSNGFCMITGELKTSVYAPMQEIAREVVKK
IGYTDALYGFDYRSAAVLNGVGEQSPDINQGVDREDGEIGAGDQGLMFGYACKETETLMPLPIHLAHQLTFALAQK
RKDNTLPFLRPDGKSQVSVRYENNKPVSIDTIVISTQHSPEVSQKHLKEAVIEEIVYKVLSKEYLHDNIKFFVNPT
GKFVIGGPQGDAGLTGRKIIVDTYGGSCPHGGGAFSGKDPSKVDRSAAYAARYVAKNLVASGVCDKATVQLAYAIG
VIEPVSIYVNTHNTSKYSSAELEKCVKSVFKLTPKGIIESLDLLRPIYSLTSAYGHFGRELEEFTWEKTNKAEEIK
AFFKR

Seq ID 198
MMKIVIDLMGADHGVLPVIEGVSRALENKSFSTVLVGDKDKATPFISKELASKVEMIHTQDYIKMEEAATEAIKRK
ESSIYLGMDILKNGADALISAGHSGATMGLATLRLGRIKGVERPAICTLMPSVGKRPSVLLDAGANTDCKPEYLID
FALMGYEYAKSVLHYDSPKVGLLSNGEEDIKGNMLVKETHKMLKAYDFFYGNVEGSDIFKGVVDVVVCDGFMGNVV
LKTTEGVASAIGSIFKDEIKSSFKSKMGALMLKNAFDILKQKTDYAEYGGAPLLGVNKSVIISHGKSNARAIECAI
YQAISAVESQVCLRITQAFESLKPSVSQSDQQDA

Seq ID 199
MEFYASLKSIAMHVPSERVKNAEFQQFLDTSDEWIEKRTGIKERRFANDEEKSSDLGVIAAKQAIERAHLTPKDID
LVVVATLSPDFLAMPSTACVLSAKLGIENKPAFDISAACTGFIYLLSVAKAYVESGMYENVLIVGAEKTSSVLDFK
DRGTCILFGDGAGACVIGRTKRLKESILDVQISANGNFSNYLYTPRTLKPTPFNAKEEASEPFLCMKGNEVFKLAV
KTLLKDVEMILEKNALKPEDVRLFIPHQANFRIIQAVREHLDFKDEQVVLTVHKYGNTSAASIPMAMGEAYEEGRL
KKGDLMLLDAFGGGLTWGSALVYFGGS

Seq ID 200
MSNQEYTFQTEINQLLDLMIHSLYSNKEIFLRELVSNASDALDKLNYLMLTDEKLKGLNTTPSIHLSFDSQKKTLT
IKDNGIGMDKNDLIEHLGTIAKSGTKNFLSALSGDKKKDSALIGQFGVGFYSAFMVASKIVVQTKKVNSDQAYAWV
SDGKGKFEISECVKDEQGTEITLFLKDEDSHFASRWEIDSVVKKYSEHIPFPIFLTYTDTKHEGEGDNQKEIKEEK
CEQINQASALWKMNKSELKDKDYKEFYQSFAHDNSEPLSYIHNKVEGSLEYTTLFYIPSTAPFDMFRVDYKSGVKL
YVKRVFITDDDKELLPSYLRFVKGVIDSEDLPLNVSREILQQNKILANIRSASVKKILSEIERLSKDEKNYHKFYE
PFGKVLKEGLYGDFENKEKLLELLRFYSKDKEKLISLKEYKENLKENQKSIYYLLGENLDLLKASPLLEKYAQKGY
DVLLLSDEIDAFVMPGVNEYDKTPFKDASHSESLKELGLEEIHDEVKDQFKDLMKAFEENLKDEIKGVELSSHLTS
AVALIGDEQNAMMANWMRQMGQSVPESKKTLELNPNHAILQKLLKCEDKEQLSAFIWLLYDGAKLLEKGALKDAKS
FNERLNSVLLKAL

Seq ID 201
MLGNVKKTLFGVLCLGTLCLRGLMAEPDAKELVNLGIESAKKQDFAQAKTHFEKACELKNGFGCVFLGAFYEEGKG
VGKDLKKAIQFYTKGCELNDGYGCNLLGNLYYNGQGVSKDAKKASQYYSKACDLNHAEGCMVLGSLHHYGVGTPKD
LRKALDLYEKACDLKDSPGCINAGYIYSVTKNFKEAIVRYSKACELKDGRGCYNLGVMQYNAQGTAKDEKQAVENF
KKGCKSSVKEACDALKELKIEL

Seq ID 202
MRKKGMFEKIQKEWLSNIQKDLLSGFVVGLSVIPETAGFAIMVGLDVGVAFYTTFYMAFVLSLFGARKAMISAAAG
SVALILVGVVKNYGLEYAGVATLMAGVLQILLGYLKIGNLLRFIPQSVMYGFVNALGILLLMEQFKFLQNQNLGVF
VLLAIGILIIYLFPLITKKIPSNLICILIVSAIALIFDMHAPNLGSIEQGVSGFHFIIIPKNLDFKIMIELLPYAL
SLALVGTIESLLTAKTLDVILKDGVSDKNKETKAQGLGNIISGLLGGMTGCALVGQSIINAKSGAKTRLSTFFAGF
SLMVLILVFNEYVVKIPIVAVVAVMVMISFTTFNFQSIINIKKIKLYDTLNMLLVVAVVLYTHNLAIGVVVGVLVN
ALWIKSKGIA

Seq ID 203
MKKTILLSLMVSSLLAENDGVFMSVGYQIGEAVQQVKNTGEIQKVSNAYENLNNLLTRYNELKQTASNTNSSTAQA
IDNLKESASRLKTTPNSANQAVSSALSSAVAMWQVIVSNLANNSLPTSEYNKINAISQSLQNTLENKNNDLKIEND
YDHLLTQASTIINTLQSQCPGIDGGNGKPWGINASGNACNIFGNTFNAITSMIDSAKKAAADARRTAPESPNQPSA
FNNADFNKNLNQVSSVINDTISYLKGDNLATIYNTLQKTPDSKGFQSLVSRSSYSYSLNETQYSEFQTTTKEFGHN
PFRSVGLINSQSNNGAMNGVGVQLGYKQFFGKNKFFGIRYYAFFDYNHAYIKSNFFNSASNVFTYGAGSDLLLNFI
NGGSDKNRKVSFGIFGGIALAGTTWLNSQFMNLKTTNSAYSAKINNTNFQFLFNTGLRLQGIHHGVELGVKIPTIN
TNYYSFMGAKLAYRRLYSVYFNYVLAY

Seq ID 204
MGVKFLKILVCGLFFWSLNAHLWGKQDNSFLGVAEKAYKSGNYSKATSYFKKACNDGVSEGCTQLGIIYENGQGTR
IDYKKALEYYKTACQADDREGCFGLGGLYDEGLGTTQNYQEAIDAYAKACVLKHPESCYNLGIIYDRKIKGNADQA
VTYYQKSCNFDMAKGCYVLGVAYEKGFLEVKQSNHKAVIYYLKACRLDDGQACRALGSLFENGDAGLDEDFEVAFD
YLQKACGLNNSGGCASLGSMYMLGRYVKKDPQKAFNFFKQACDMGSAVSCSRMGFMYSQGDAVPKDLRKALDNYER
GCDMGDEVGCFALAGMYYNMKDKENAIMIYDKGCKLGMKQACENLTKLRGY

Seq ID 205
MELETHLSKYFTLAFTHKSMSLEMREKLAINSNATLKEFLQTIKNHCPNIKECMVLSTCNRFEIYASLKHGANTNE
QKNALLKILAQNKKMSVSDLEKCVLMNTDESAVHHVFSVCSSLDSLVVGETQITGQMKNAYKFAFEEKFCSKDLTR
LLHFAFKCAAKVRNLTGISKQGVSISSVAVKEALNIFEKERIKDKKALVIGLGEMAQLVIKHLLNKQFEALILGRN
AAKFEDFIKELEEPKKVSFQNIENLNAYINEYELLFCATSSPHFIVQNRMLKETIFRRFWFDLAVPRNIEKPVLDN
IFLYSVDDLEPMVRENVENRQESRMRAYEIVGLATMEFYQWIQSLEVEPVIKDLRELARISAQKELQKALKKRYVP
KEYENNIEKILHNAFNTFLHNPTIALKKNAQKEESDVLVGAIKNLFNLDKSNANHAQNLNLYKCEYYEE

Seq ID 206
MFIVAVLMLAFLIFVHELGHFTIARICGVKVEVFSIGFGKKLCFFKLFGTQFALSLIPLGGYVKLKGMDKEENGMN
ETTDDSYAQKSPFQKLWILFGGAFFNFLFAILVYFFLALGGEKVLLPVIGDLDKNALEAGLLKGDKILSINHKKIA
SFREIRSVVARARGELVLEIERNHQVLEKRLTPKIVAVISDSNDPNEMIRYKAIGIKPDMQKMGVVSYSLFQAFEK
ALSRFKEGVVLIVDSLRRLIMGSSSVKELSGVVGIVGALSHANSLSMLLLFGAFLSINLGILNLLPIPALDGAQML
GVVFKNIFHITLPTPIQNALWLAGVGFLVFIMFLGLFNDLTRLL

Seq ID 207
MLLKNASFYDDEVLKRADIRLKDSLITEIKENLSPINNEEVIECRDLFVLPSFIDLSVTGLEGYENLKQKAFKGGV
GLLNVFNCDQSGIKNIMAIKNNQLADIATLKNKGGEILIAPSDAFLELISHYAKSYNLPLLISLENSFEALNSGEL
AYELGQNFVENAFENTRLVRFMEVSRALQIPVLLDKVNSITTLKLIKAFNDLGAKLQAQTPLSHLVLDESVYEDYE
PRFKIAPPLRDKESQNALKEALKNNEIAMLTSLHASKNSNAQLFEESAFGCESIEDAFSVAYTFLVQKKVISFQQL
IKVMAINQAKFLKLNAGEVKENQLANLMIVDLNAQTRVSNQNSPFYGLELYGEVQRMILKGQTTFIKENACKKS

Seq ID 208
LKIAIVRLSALGDIIVSAVFLAVIKECLPNAQIEWFVDERFSAILEHSPYIDKLHPIALKSALKTLNPLKIFKLFK
SLRAYEYDIIIDMQGLVKSALITQMLKAPKKVGFDYASAREGLSMFFYSQKVSIAYDEPVLKRNFTLLSHALNLPQ
KEISKEISESLSSRAKAFSYQPSPKIDALNLNKNKPKILFILETSKINKTYPIERFKELALILENFQICLLWHADE
YKATTLYHALKHQRDVLLLPKLTLNEVKALLFKMDLIIGGDTGITHLAWALQKPSITLYGNTPMERFKLESPINVS
LTGNSNANYHKKDFSIQNIEPKKIKECVLNILKEKE

Seq ID 209
MKKFKKKPKSIKRSHQNQKTILKRPLWLMPLLISGFASGVYANNLWDLLNPKVGGEYVHWVKGSQYCAWWEFAGCL
KNVWGANHKGYDAGNAANYLSSQNYQAISVGSGNETGTYSLSGFTNYVGGNLTINLGNSVVLDLSGSNSFTSYQGY
NQGKDDVTFTVGAINLNGTLEVGNRVGSGAGTHTGTATLNLNANKVNINSNINAYKTSQVNIGNANSVITIGSVSL
SGDVCSSLASVGIGANCSTSGPSYSFKGTTNATNTAFSNASGSFTFEENATFSGAKWNGGTYTFNKEFSATNNTAF
SSGSFNFKGVSSFNGTSFSNASYTFDNQATFQNSSFNGGTFTFNNQTNPTNNAQHPQIQNSSFSGNATTLKGFVNF
QQAFNNSNHQLTIQNASFNNATFNNTGKITIEKDASFNNTTFNTSVDTNNMSVTGGVTLSGKNDLKNGSTLDFGSS
KITLAQGTTFNLTSLGSEKSVTILNSSGGITYSNLLNHAINGLTSALKTNESLSNPQSFAQGLWDIITYNGVTGQL
LNENAATSKPTDSSPSKSSTNSTQVYQVGYKIGDTIYKLQETFSHNSIIIQALESGTYTPPPVINGSKFDLSASNY
INADMPWYDHKYYIPKSQNFTESGTYYLPSVQIWGSYTNSFKQTFSANGSNLVIGYNSTWTDHNVSSSGTVSFGDT
SGSALNGHCGPWPYYQCTGTTNGTYSAYHVYITANLRSGNRIGTGGAANLIFNGVDSINIANATITQHNAGIYSSS
MTFSTQSMDNSQNLNGLNSNGKLSVYGTTFTNEAKDGKFIFNAGQAVFENTNFNGGSYQFSGDSLNFSNNNQFNSG
SFEISAKNASFNNANFNNSASFNFNNSNATTSFVGDFTNANSNLQIAGNAVFGNSTNGSQNTANFNNTGSVNISGN
ATFDNVVFNGPTNTSVKGQVTLNNITLKNLNAPLSFGDGTITFNAHSVINIAESITNGNPITLVSSSKEIEYNNAF

SKNLWQLINYQGHGASSEKLVSSAGNGVYDVVYSFNNQTYNFQEVFSQNSISIRRLGVNMVFDYVDMEKSDHLYYQ
NALGFMTYMPNSYNNNLGNANNTIYYYDKSIDFYASGKTLFTKAEFSQTFTGQNSAIVFGAKSIWTSLSDAPQSNT
IIRFGDNKGAGSNDASGHCWNLQCIGFITGHYEAQKIYITGSIESGNRISSGGGASLNFNGLQGILLTNATLYNRA
AGTQSSSMNFISNSANIQAQNSYFIDDTAQNGGNPNFSFNALNLDFSNSSFRGYVGKTQSVFKFNAKNAISFTNST
NLSSGLYQMQAKSVLFDNSNLSVSVGTSSIKANAINLSQNASINASNHSTLELQGDLNVNDTSSLNLNQSTINVSN
NATINDYASLIASNGSHLNFNGAVNFNSANITTSLNNSSIVFKGAVSLGGQFNLSNNSSLDFQGSSAITSNTAFNF
YDNAFSQSPITFHQALDIKAPLSLGGNLLNPNNSSVLDLKNSQLVFGDQGSLNIANIDLLSDLNDNKNRVYNIIQA
DMNSNWYERISFFGMHINDGIYDAKNQTYSFTNPLNNALKITESFKDNQLSVTLSQIPGIKNTLYNIGSEIFNYQK
VYNNANGVYSYSDDAQGVFYLTSNVKGYYNPNQSYQASGSNNTTKNNNLTSESSIISQTYNAQGNPISALHIYNKG
YNFNNIKALGQMALKLYPEIKKVLGNDFSPSSLNALNSNALNQLTKLITPNDWKNINELIDNANNSVVQNFNNGTL
IVGATQIGQTDTNSAVVFGGLGYQTPCDYTDIVCQKFRGTYLGQLLESSSADLGYIDTTFNAKEIYLTGTLGSGNA
WGTGGSASVTFNSQTSLILNQANIVSSQTDGIFSMLGQEGINKVFNQAGLANILGEVAVQSINKAGGLGNLIVNTL
GSNSVIGGYLTPEQKNQTLSQLLGQNNFDNLMNDSGLNTAIKDLIRQKLGFWTGLVGGLAGLGGIDLQNPEKLIGS
MSINDLLSKKGLFNQITGFISANDIGQVISVMLQDIVKPSNALKNDVAALGKQMIGEFLGQDTLNSLESLLQNQQI
KSVLDKVLAAKGLGPIYEQGLGDLIPNLGKKGLFAPYGLSQVWQKGDFSFNAQGNVFVQNSTFSNANGGTLSFNAG
NSLIFAGNNHIAFTNHAGTLQLLSDQVSNINITTLNASNGLKINAANNNVSVSQGNLFVSASCAQQSDPTTANIAN
PCALSAQSTNGASSNNASNNAPIALSNNDESLMVAANDFNFSGNIYANGVVDFSKIKGSANIKNLYLYNNAQFQAN
NLTISNQAVLEKNASFVTNNLNIQGAFNNNATQKIEVLQNLVIASNASLSTGIYGLEVGGALNNSGAIHFNLENTQ
TPTPLIQAEGIINLNTTQTPFMNVNNSMANNTTYTLLKSSRYIDYNINPNSLQSYLNLYTLININGNHIEEKNGAL
TYLGQRVLLQDKGLLLSVALPNSNNASQNNILSLSVLYNQVKMSCGDKAMDFTPPTLQDYIVGIQGQSALNQIEAV
GGNAIKWLSTLMMETKENPFFAPIYLKNHSLNEILGVTKDLQNTASLISNPNFRDNATNLLELASYTQQTSRLTKL
SDFRSREGESDFSLLELKNKRFSDPNPEVFVKYSQLSKHPNNLWVQGVGGASFISGGNGTLYGLNAGYDRLVKNVI
LGGYVAYGYSDFNGNIMHSLGNNVDVGMYARAFLKRNEFTLSANETYGGNATSINSSNSLLSVLNQRYNYNTWTTS
VNGNYGYDFMFKQKSVVLKPQVGLSYHFIGLSGMKGNDAAYKQFLMHSNPSNESVLTLNMGLESRKYFGKNSYYFV
TARLGRDLLIKSKGSNTVRFVGENTLLYRKGEVFNTFASVITGGEMHLWRLVYVNAGVGLKMGLQYQDINITGNVG
MRVAF

Seq ID 210
MFEKITLAHKDLFSRFLSAQKIVLSDVSFTNCFLWQHARLIQVAVIRDCLVIQTTYENQKPFYFYPIGKNAFECVK
ELLKLEKNLRFHSLTLEQKDDLKDNFVGVFDFTYNRDRSDYVYSIEELIALKGKKYHKKKNHLNQFLTNHANFVYE
KISPQNKKEVLEASQAWFLESQTDDIGLINENKGIQSVLENYESLDVKGGLIRVNGEIASFSFGEVLNEESALIHI
EKARTDIAGAYQIINQQLLLNEFSHLTYANREEDLGLEGLRRSKMSYNPVFLIDKYEAVAKN

Seq ID 211
MRVTFGSKYNQMNNYQNALQNKINDANTQIASGLKIRYGYQNSDINNQNLKFQYEENTLDQGIDVAQNAYTSTLNT
DKALQEFSKTMEAFKTKLIQSANDVHSETSRAAIANDLERLKEHMINVANTSIGGEFLFGGSKVDRPPIDSNGKYH
GNGEDLNVLISSDNLVPYNISGQDLFLGTDKDKHKLITTNIKLFNQNKLHPDVMDALEHSSLPEEVFIKPSDTLRE
LIGDNDKDPTNDPKEFFYLQGVRPDGSSFKEKFALDKAYQNQESASKVSDLLDKIAHAYGNTSQNKVVDVSLNNWG
QIEIKNLTPGSENLDFHLISSDGDFDDLDALRSSGKRVTEYIKSAFVTDRSLSQVKAVPNMYNPKVLEVPSVFVTK
DNVLANKNTKLSEIFGDSVETLKINASRLDETSAIKIPNLPVYLDIPILLDVKNSTIKDLKDAIKKRFNNEVDVEI
ETNGRLRIIDNSSKESPISLALSALDAKGLEVAGIPTNNASEYQKTYFNKEGAKLESNVAQTAQNGAANGSTKLSE
AAKGSLENSVFNMKLNDVNGLFLEAQMNLDNNGAFLSLPNGIKIPLYDPTSADIQASKPNEVTYRQLMDAMSIALN
YSNTDPAIYQQISDNPTSKESKERFIGLLKQAKDNLSVNLNEEGKVIIQDNMHSNTKMQFMLFDKDANDFSQNALH
SDKPSLKLNANNALIIDKPSVNFFDQLENTITSVRKGIYRPDALGDTYSSDMRNLGIQNGITLIDHLSDHIEKMIA
KNGAHGKAFENIIRRNEVLKTQVQSIRGETTGTDMAETYNKFSNLTNNYNAVLASTNKINNLSLTKYL

Seq ID 212
MDRAKFIFVTGGVLSSLGKGISSSSIATLLQHCNYQVSILKIDPYINIDPGTMSPLEHGEVFVTSDGAETDLDIGH
YERFLNRNLTRLNNFTTGQIFSSVIENERKGEYLGKTIQIVPHVTDEIKRRIKSAAKGLDFLIVEVGGTVGDMEGM
FYLEAIRQLKLELGNEKVINVHVTLIPYIQTTNELKTKPTQHSVQELRRLGVTPQIILARSPKPLDKELKNKIALS
CDVEQDSVIVATDTKSIYACPILFLQEGILTPIARRFNLNKLHPKMAAWNTLVEKIIAPKHKVKIGFVGKYLSLKE
SYKSLIEALIHAGAHLDTQVNIEWLDSENFNEKTDLEGVDAILVPGGFGERGIEGKICAIQRARLEKLPFLGICLG
MQLAIVEFCRNVLGLKGANSTEFNQRCEYPVVYLIGDFMDQNHQKQVRTYNSPLGGTMRLGEYECEIMPNSLLEKA
YKKPSIKERHRHRYEINPKYRQEWENKGLKVVGFGSNHLIEAIELEDHPFFVGVQFHPEFTSRLQSPNPIILDFIK
SALSKS

Seq ID 213
LDLKVLLQRIVDFFIKLNKKQKIALIAAGVLITALLVFLLLYPFKEKDYTQGGYGVLFEGLDSSDNALILQHLQQN
QIPYKVSKDDTILIPKDKVYEERITLASQGIPKTSKVGFEIFDTKDFGATDFDQNIKLIRAIEGELSRTIESLNPI
LKANVHIAIPKDSVFVAKEVPPSASVMLKLKPDMKLSPTQILGIKNLIAAAVPKLTIENVKIVNENGESIGEGDIL
ENSKELALEQLHYKQNFENILENKIVNILAPIVGGKNKVVARVNAEFDFSQKKSTKETFDPNNVVRSEQNLEEKKE
GASKKQVGGVPGVVSNIGPVQGLKDNKEPEKYEKSQNTTNYEVGKTISEIKGEFGTLVRLNAAVVVDGKYKIALKD
GVNTLEYEPLSDESLQKINALVKQAIGYNQNRGDDVAVSNFEFNPMAPVIDNATLSEKIMHKTQKILGSFTPLIKY
ILVFIVLFIFYKKVIVPFSERMLEVVPDEDKEVKSMFEEMDEEEDELNKLGDLRKKVEDQLGLNASFSEEEVRYEI
ILEKIRGTLKERPDEIAMLFKLLIKDEISSDGAKG

Seq ID 214

MYVEKILQSLQKKYPYQKEFHQAVYEAITSLKPLLDSDKSYEKHAILERLIEPEREIFFRVCWLDDNNQIQVNRGC
RVEFNSAIGPYKGGLRFHPSVNESVIKFLGFEQVLKNSLTTLAMGGAKGGSDFDPKGKSEHEIMRFCQAFMNELYR
HIGATTDVPAGDIGVGEREIGYLFGQYKKLVNRFEGVLTGKGLTYGGSLCRKEATGYGCVYFAEEMLQERNSSLEG
KVCSVSGSGNVAIYTIEKLLQIGAKPVTASDSNGMIYDKDGIDLELLKEIKEVRRGRIKEYALEKKSAEYTPTENY
PKGGNAVWHVPCFAAFPSATENELSVLDAKTLLSNGCKCVAEGANMPSSNEAIGLFLQAKISYGIGKAANAGGVSV
SGLEMAQNASMHPWSFEVVDAKLHHIMKEIYKNVSQTAKEFKDPTNFVLGANIAGFRKVASAMIAQGV

Seq ID 215
MDDLQEIMEDFLIEAFEMNEQLDQDLVELEHNPEDLDLLNRIFRVAHTIKGSSSFLNLNILTHLTHNMEDVLNRAR
KGEIKITPDIMDVVLRSIDLMKTLLVTIRDTGSDTNNGKENEIEEAVKQLQAITSQNLESAKERTTEAPQKENKEE
TKEEAKEENKENKAKAPTAENTSSDNPLADEPDLDYANMSAEEVEAEIERLLNKRQEADKERRAQKKQEAKPKQEV
TPTKETPKAPKTETKAKAKADTEENKAPSIGVEQTVRVDVRRLDHLMNLIGELVLGKNRLIRIYSDVEERYDGEKF
LEELNQVVSSISAVTTDLQLAVMKTRMQPVGKVFNKFPRMVRDLSRELGKSIELIIEGEETELDKSIVEEIGDPLI
HIIRNSCDHGIEPLEERRKLNKPETGKVQLSAYNEGNHIVIKISDDGKGLDPVMLKEKAIEKGVISERDAEGMSDR
EAFNLIFKPGFSTAKVVSNVSGRGVGMDVVKTNIEKLNGIIEIDSEVGVGTTQKLKIPLTLAIIQALLVGVQEEYY
AIPLSSVLETVRISQDEIYTVDGKSVLRLRDEVLSLVRLSDIFKVDAILESNSDVYVVIIGLADQKIGVIVDYLIG
QEEVVIKSLGYYLKNTRGIAGATVRGDGKITLIVDVGAMMDMAKSIKVNITTLMNESENTKSKNSPSDYIVLAIDD
SSTDRAIIRKCLKPLGITLLEATNGLEGLEMLKNGDKIPDAILVDIEMPKMDGYTFASEVRKYNKFKNLPLIAVTS
RVTKTDRMRGVESGMTEYITKPYSGEYLTTVVKRSIKLEGDQS

Seq ID 216
VIELDINASDKSLSHRAVIFSLLAQKPCFVRNFLMGEDCLSSLEIAQNLGAKVENTAKNSFKITPPTTIKEPNKIL
NCNNSGTTMRLYSGLLSAQKGLFVLSGDNSLNARPMKRIIEPLKAFGAKILGREDNHFAPLVILGSPLKACHYESP
IASAQVKSAFILSALQAQGASTYKESELSRNHTEIMLKSLGADIHNQDGVLKISPLEKPLEAFDFTIANDPSSAFF
FALACAITPKSRLLLKNVLLNPTRIEAFEVLKKMGASIEYAIQSKDLEMIGDIYVEHAPLKAINIDQNIASLIDEI
PALSIAMLFAKGKSMVKNAKDLRAKESDRIKAVVSNFKALGIECEEFEDGFYVEGLEDISPLKQRFSRIKPPLIKS
FNDHRIAMSFAVLTLALPLEIDNLECANISFPQFKHLLNQFKKGSLNGN

Seq ID 217
LDILDLNKAQAVQQNEQEVEDKERESKEPVVLEDLSALAWLELEEFSRLSGLPKERILELVNLGKIKSKISSNKLL
IDASSGTNALIKKVENSLISMDMNGRSLEPVFVEKTINTILNLHDKVIGAKDETISAFKNENMFLKDALISMQEVY
EEDKKTIDLLRDELNQAREEIEFMKRKYRLMWGKVADMSSVNKK

Seq ID 218
MILVLDFGSQYTQLIARRLRERGIYTEIVPFFESIENIQKKAPKGLILSGGPASVYAKDAYKPSGKIFDLNVPILG
ICYGMQYLVDFFGGVVVGANEQEFGKAVLEITQNSVIFEGVKIKSLVWMSHMDKVIELPKGFTTLAKSPNSPHCAI
ENGKIFGLQFHPEVVQSEEGGKILENFALLVCGCEKTWGMQHFAQREIARLKEKIANAKVLCAVSGGVDSTVVATL
LHRAIKDNLIAVFVDHGLLRKNEKERVQAMFKDLKIPLNTIDAKEVFLSKLKGVSEPELKRKIIGETFIEVFEKEA
KKHHLKGKIEFLAQGTLYPDVIESVSVKGPSKVIKTHHNVGGLPEWMDFKLIEPLRELFKDEVRLLGKELGVSQDF
LMRHPFPGPGLAVRILGEISESKIKRLQEADFIFIEELKKANLYDKVWQAFCVLLNVNSVGVMGDNRTYENAICLR
AVNASDGMTASFSFLEHSFLEKVSNRITNEVSGINRVVYDITSKPPGTIEWE

Seq ID 219
MKVNKGFKFRLYPTKEQQDKLQHCFFVYNQAYNIGLNELQEQYETNKDSPPKERKYKKSSELDNAIKQCLRARDLP
FSAVIAQQARMNVERALKDAFKVKNRGFPKFKNSKSAKQSFSWNNQGFSIKESDDECFKTFTLMKMPLLMRMHRRL
PPNFKVKQISISCSHRKYFVSFSVEYEQDITPIKNTKNGVGLDLNILDTACSCEINNHDKLTDFKQYQTDMKELLG
IEIDEELDTKRLIPTYSKLYSLKKYSKKFKRLQRKQSRRC

Seq ID 220
MLESALKYCKEKAIDLLVGFVPKTYSMAQECNILGLYDDAFIITKQENLVGIISLQGLSYSNLMQKDLEGYFDARQ
NVLNTISKDIQLRIVAKRRKEFINQSPNIDNIYAKAIITQFESKGIYKTEYFLVFETITSNVKSFFEKKKLEMTTS
INEELEESSKEDKQENENSSNETHSNTSSKKDKKNKFKKKITFSTKSKRALLIQTIERVKNALKEFKPTLLNSKEV
LNFYAEYINGKYIAFNPKLKRLSDSYIASNVHFKKDYFVIEFQNQNTFCACVGIKAYESEEISSLPISTLLHTQIE
LDLIFHIRSLGQFESLNFLKTKKKLTLSKIVKADIDNYIELVQANRLSMQECALNLVIRAKSKAKLDKSLKEILSL
LNNAGLGSVTETIGLKPSYFSFFPNNANINPRMRHQTSQVIASLILFEKNNTGFRANSWGDMPLSVFKNLDHSPYL
FNFHNQEVKHKGVLAHNVARVVGHTMIIGATGAGKTTLISYLMMSALKYSNIDILALDRLNGLYSFTKYFDGIYNQ
GENFHINPFSLEDSATNRAFLLHFYAQMAKVDSYDDHKDKVEDRTALLNAIDTMYRNYNDEVKQAKFSNQELPLPF
DLKEFVNAIAKTNTDILDSSFEDYLKSSLFSSRMDSLDFKTRISTINTDSILHNDDDAGLLAYYVFHKMIDRALKI
NRGFLCFIDEFKSYAQNEMMNKKINEIITQARKANGVIVLALQDINQLSEVRNAQSFIKNMGQLILYPQRNIDTKD
LNDKFGIRLSDTEKHFLENTAVNEYKVLLKNMNDGSSNIIDVSLSSLGNYLQIFSSNSSMVEHIDNLIKHYPKTWR
EVFVSNKHENFDDKKHLEKVLK

Seq ID 221
MKNIRNIAVIAHVDHGKTTLVDGLLSQSGTFSEREKVDERVMDSNDLERERGITILSKNTAIYYKDTKINIIDTPG
HADFGGEVERVLKMVDGVLLLVDAQEGVMPQTKFVVKKALSFGICPIVVVNKIDKPAAEPDRVVDEVFDLFVAMGA
SDKQLDFPVVYAAARDGYAMKSLDDEKKNLEPLFETILEHVPSPSGSVDEPLQMQIFTLDYDNYVGKIGIARVFNG
SVKKNESVLLMKSDGSKENGRITKLIGFLGLARTEIENAYAGDIVAIAGFNAMDVGDSVVDPANPMPLDPMHLEEP
TMSVYFAVNDSPLAGLEGKHVTANKLKDRLLKEMQTNIAMKCEEMGEGKFKVSGRGELQITILAENLRREGFEFSI

SRPEVIIKEENGVKCEPFEHLVIDTPQDFSGAIIERLGKRKAEMKAMNPMSDGYTRLEFEIPARGLIGYRSEFLTD
TKGEGVMNHSFLEFRPFSGSVESRKNGALISMENGEATAFSLFNIQERGTLFINPQTKVYVGMVIGEHSRDNDLDV
NPIKSKHLTNMRASGSDDAIKLTPPRTMVLERALEWIEEDEILEVTPLNLRIRKKILDPNMRKRAKK

Seq ID 222
MKKIGLSLCLVLSLGFLKAHEVSAEEIADIFYKLNAKEPKMKINHTKGFCAKGVFLPNAQAKKDLDVPLLNEKEIP
ASVRYSLGGVAMDDKSKVRGMALKLENQNASWTMVMLNTEINFAKNPNEFAQFFEMRIPKNGKVDEARIKKLYEEV
PSYRNFAAYTKTIGISSSVANTPYYSVHAFRFKDKKGKLLPARWKFVPKEGIKYLNPQELKQKDSNYLLSAFQQHL
KTKPIEYQMYLVFANKNDATNDTTALWKGKHKELLVGTLKVEKYEGMGCNKDVYFPADLPKGVEAPTDPLFQIRNE
VYGITFSRRQ

Seq ID 223
MLRLLIGLLLMSFISLQSASWQEPLRVSIEFVDLPKKIIRFPAHDLQVGEFGFVVTKLSDYEIVNSEVVIIAVENG
VATAKFRAFESMKQRHLPTPRMVARKGDLVYFRQFNNQAFLIAPNDELYEQIRATNTDINFISSDLLVTFLNGFDP
KIANLRKACNVYSVGVIYIVTTNTLNILSCESFEILEKRELDTSGVTKTSTPFFSRVEGIDAGTLGKLFSGSQSKN
YFAYYDALVKKEKRKEVRIKKREEKIDSREIKREIKQEAIKEPKKANQGTQNAPTLEEKNYQKAERKLDAKEERRY
LRDERKKAKATKKAMEFEEREKEHDERDEQETEGRRKALEMDKGDKKEERVKPKENEREIKQEAIKEPSDGNNATQ
QGEKQNAPKENNAQKEENKPNSKEEKRRLKEEKKKAKAEQRAREFEQRAREHQERDEKELEERRKALEAGKK

Seq ID 224
MFKDFYRTTLSFLKPLLLLLVLLLPFSLCIADEYISISDDWDEIVRNHKTYYFENGLDHFNQGQYQQAFKDFRLAQ
EYSIGLGSVYLAKMYLEGKGVKVDYKKAQFYAENAIKGYGSGLLGGALILGRMQAEGLGMKKDLKQALKTYRHVVR
MFSNKSTNFANNFRLPNLAEFTSMLIGSRFIDLSGLSANPIKFGKKFGILVKKSTQIKDKTLLWEDIAEISSNITL
LKQQMGEILYRIGIAYKEGLGTRKKKDRAKKFLQKSAEFGYEKAMEAL

Seq ID 225
MTEDRLSAEDKKFLEVERALKEAALNPLRHATEELFGDFLKMENITEICYNGNKVVWVLKNNGEWQPFDVRDRKAF
SLSRLMHFARCCASFKKKTIDNYENPILSSNLANGERVQIVLSPVTVNDETISISIRIPSKTTYPHSFFEEQGFYN
LLDNKEQAISAIKDGIAIGKNVIVCGGTGSGKTTYIKSIMEFIPKEERIISIEDTEEIVFKHHKNYTQLFFGGNIT
SADCLKSCLRMRPDRIILGELRSSEAYDFYNVLCSGHKGTLTTLHAGSSEEAFIRLANMSSSNSAARNIKFESLIE
GFKDLIDMIVHINHHKQCDEFYIKHR

Seq ID 226
MNEENDKLETSKKAQQDSPQDLSNEEATEANHFENLLKESKESSDHHLDNPTETQTHFDGDKSEETQTQMDSEGNE
TSESSNGSLADKLFKKARKLVDNKKPFTQQKNLDEETQELNEEDDQENNEYQEETQTDLIDDETSKKTQQHSPQDL
SNEEATEANHFENLLKESKESSDHHLDNPTETQTNFDGDKSEETQTQMDSEGNETSESSNGSLADKLFKKARKLVD
NKKPFTQQKNLDEETQELNEEDDQENNEYQEETQTDLIDDETSKKTQQHSPQDLSNEEATEANHFENLLKESKESS
DHHLDNPTETQTNFDGDKSEEITDDSNDQEIIKGSKKKYIIGGIVVAVLIVIILFSRSIFHYFMPLEDKSSRFSKD
RNLYVNDEIQIRQEYNRLLKERNEKGNMIDKNLFFNDDPNRTLYNYLNIAEIEDKNPLRAFYECISNGGNYEECLK
LIKDKKLQDQMKKTLEAYNDCIKNAKTEEERIKCLDLIKDENLKKSLLNQQKVQVALDCLKNAKTDEERNECLKLI
NDPEIREKFRKELELQKELQEYKDCIKNAKTEAEKNKCLKGLSKEAIERLKQQALDCLKNAKTDEERNECLKNIPQ
DLQKELLADMSVKAYKDCVSKARNEKEKQECEKLLTPEARKKLEQQVLDCLKNAKTDEERKKCLKDLPKDLQSDIL
AKESLKAYKDCVSQAKTEAEKKECEKLLTPEAKKLLEEEAKESVKAYLDCVSQAKTEAEKKECEKLLTPEAKKKLE
EAKKSVKAYLDCVSRARNEKEKKECEKLLTPEAKKLLEQQALDCLKNAKTDKERKKCLKDLPKDLQKKVLAKESVK
AYLDCVSQAKTEAEKKECEKLLTPEARKLLEEAKKSVKAYLDCVSQAKTEAEKKECEKLLTPEARKLLEEXAKESV
KAYLDCVSQAKNEAEKKECEKLLTLESKKKLEEAKKSVKAYLDCVSQAKTEAEKKECEKLLTPEAKKLLEQQALDC
LKNAKTEADKKRCVKDLPKDLQKKVLAKESLKAYKDCVSKARNEKEKKECEKLLTPEAKKLLEEAKKSVKAYLDCV
SQAKTEAEKKECEKLLTPEARKLLEEAKESVKAYKDCVSKARNEKEKKECEKLLTPEAKKLLEQQVLDCLKNAKTE
ADKKRCVKDLPKDLQKKVLAKESVKAYLDCVSRARNEKEKKECEKLLTPEAKKLLEEAKESLKAYKDCLSQARNEE
ERRACEKLLTPEARKLLEQEVKKSIKAYLDCVSRARNEKEKKECEKLLTPEARKFLAKQVLNCLEKAGNEEERKAC
LKNLPKDLQENILAKESLKAYKDCLSQARNEEERRACEKLLTPEARKLLEQEVKKSVKAYLDCVSRARNEKEKKEC
EKLLTPEARKFLAKELQQKDKAIKDCLKNADPNDRAAIMKCLDGLSDEEKLKYLQEAREKAVADCLAMAKTDEEKR
KCQNLYSDLIQEIQNKRTQNKQNQLSKTERLHQASECLDNLDDPTDQEAIEQCLEGLSDSERALILGIKRQADEVD
LIYSDLRNRKTFDNMAAKGYPLLPMDFKNGGDIATINATNVDADKIASDNPIYASIEPDIAKQYETEKTIKDKNLE
AKLAKALGGNKKDDDKEKSKKSTAEAKAENNKIDKDVAETAKNISEIALKNKKEKSGEFVDENGNPIDDKKKAEKQ
DETSPVKQAFIGKSDPTFVLAQYTPIEITLTSKVDATLTGIVSGVVAKDVWNMNGTMILLDKGTKVYGNYQSVKGG
TPIMTRLMIVFTKAITPDGVIIPLANAQAAGMLGEAGVDGYVNNHFMKRIGFAVIASVVNSFLQTAPIIALDKLIG
LGKGRSERTPEFNYALGQAINGSMQSSAQMSNQILGQLMNIPPSFYKNEGDSIKILTMDDIDFSGVYDVKITNKSV
VDEIIKQSTKTLSREHEEITTSPKGGN
"X" can be any amino acid

Seq ID 227
VKCFLSIFSFLTFCGLSLNGTEVVITLEPALKAIQADAQAKQKTAQAELKAIEAQSSAKEKAIQAQIEGELRTQLA
TMSAMLKGANGVINGVNGMTGGFFAGSDILLGVMEGYSSALSALGGNVKMIVEKQKINTQTEIQNMQIALQKNNEI
IKLKMNQQNALLEALKNSFEPSVTLKTQMEMLSQALGSSSDNAQYIAYNTIGIKAFEETLKGFETWLKVAMQKATL
IDYNSLTGQALFQSAIYAPALSFFSSMGAPFGIIETFTLAPTKCPYLDGLKISACLMEQVIQNYRMIVALIQNKLS
DADFQNIAYLNGINGEIKTLKGSVDLNALIEVAILNAENHLNYIENLEKKADLWEEQLKLERETTARNIASSKVIV
K

Seq ID 228
MAGTQAIYESSSAGFLSEISSIISSTSGVAGPFAGIVAGAMSAAIIPIVVGFTNPQMTAIMTQYNQSIAEAVSMPM
KAANQQYNQLYQGFNDQSMAVGNNILNISKLTGEFNVQGNTQGAQISAVNSQIASILASNTTPKNPSAIEAYATNQ
IAVPSVPTTVEMMSGILGNITSAAPKYALALQEQLRSQASNSSMNDTADSLDSCTALGALVGSSKVFFSCMQISMT
PMSVSMPTVYAKYQALXTNALTSGTNPMTTPACPIGDKVLAVYCYAEKVAEILREYYIEFVKNNTNLLQNASQMIL
NQSGLATSTYDTQAISNISSLYNYNIVANKSFLKSHLTYLDYIKNKLKGQKDSYLTERVQTKIIVK
"X" can be any amino acid

Seq ID 229
MKTNFYKIKLLFAWCLIIGMFNAPLNADQNTDIKDISPEDMALNSVGLVSRDQLKIEIPKETLEQKVAVLNDYNDK
NVNIKFDNISLGSFQPNDNLGINAMWGIQNLLMSQMMGDYGPNNPFMYGYAPTYSDSSFLPPILGY

Seq ID 230
VFVASKQADEQKKLVIEQEVQKRQFKKIEELKADMQKGVNPFFKVLFDGGNRLFGFPETFIYSSIFILFVTIVLSV
ILFQAYEPVLIVAIVIVLVALGFKKDYRLYQRMERAMKFKKPFLFKGVKNKAFMSIFSMKPSKEMANDIHLNPNRE
DRLVSAANSYLANNYECFLDDGVILTNNYSLLGTIKLGGIDFLTTSKKDLIELHASIYSVFRNFVTPEFKFYFHTV
KKKIVIDETNRDYSLIFSNDFMRAYNEKQKRESFYDISFYLTIEQDLLDTLNEPVMNKKHFADNNFEEFQRIIRAK
LENFKDRIELIEELLSKYHPIRLKEYTKDGVIYSKQCEFYNFLVGMNEAPFICNRKDLYLKEKMHGGVKEVYFANK
HGKILNDDLSEKYFSAIEISEYAPKSQSDLFDKINALDSEFIFMHAYSPKNSQVLKDKLAFTSRRIIISGGSKEQG
MTLGCLSELVGNGDITLGSYGNSLVLFADSFEKMKQSVKECVSSLNAKGFLANAATFSMENYFFAKHCSFITLPFI
FDVTSNNFADFIAMRAMSFDGNQENNAWGNSVMTLKSEINSPFYLNFHMPTDFGSASAGHTLILGSTGSGKTVFMS
MTLNAMGQFVHNFPANVSKDKQKLTMVYMDKDYGAYGNIVAMGGEYVKIELGTDTGLNPFAWAACVQKTNATMEQK
QTAISVVKELVKNLATKSDEKDENGNSISFSLADSNTLAAAVTNLITGDMNLDYPITQLINAFGKDHNDPNGLVAR
LAPFCKSTNGEFQWLFDNKATDRLDFSKTIIGVDGSSFLDNNDVSPFICFYLFARIQEAMDGRRFVLDIDEAWKYL
GDPKVAYFVRDMLKTARKRNAIVRLATQSITDLLACPIADTIREQCPTKIFLRNDGGNLSDYQRLANVTEKEFEII
TKGLDRKILYKQDGSPSVIASFNLRGIPKEYLKILSTDTVFVKEIDKIIQNHSIIDKYQALRQMYQQIKEY

Seq ID 231
LINNNSNKKLRGFFVKVLLSLVVFSSYGLANDDKEAKKEVLEKEKNTPNGLVYTNLDFDSFKATIKNLKDKKVTFK
EVNPDIIKDEVFDFVIVNRVLKKIKDLKHYDPVIEKIFDEKGKEMGLNVELQINPEVKDFFTFKSISTTNKQRCFL
SLRGETREILCDDKLYNVLLAVFNSYDPNDLLKHISTVESLKKIFYTITCEAVYL

Seq ID 232
MTNETIDQTRTPDQTQSQTAFDPQQFINNLQVAFIKVDNVVASFDPDQKPIVDKNDRDNRQAFDGISQLREEYSNK
AIKNPTKKNQYFSDFIDKSNDLINKDNLIDVESSTKSFQKFGDQRYQIFTSWVSHQKDPSKINTRSIRNFMENIIQ
PPIPDDKEKAEFLKSAKQSFAGIIIGNQIRTDQKFMGVFDESLKERQEAEKNGGPTGGDWLDIFLSFIFNKKQSSD
VKEAINQEPVPHVQPDIATTTTDIQGLPPEARDLLDERGNFSKFTLGDMEMLDVEGVADIDPNYKFNQLLIHNNAL
SSVLMGSHNGIEPEKVSLLYAGNGGFGDKHDWNATVGYKDQQGNNVATLINVHMKNGSGLVIAGGEKGINNPSFYL
YKEDQLTGSQRALSQEEIRNKVDFMEFLAQNNTKLDNLSEKEKEKFQNEIEDFQKDSKAYLDALGNDRIAFVSKKD
TKHSALITEFNNGDLSYTLKDYGKKADKALDREKNVTLQGSLKHDGVMFVDYSNFKYTNASKNPNKGVGATNGVSH
LEAGFNKVAVFNLPDLNNLAITSFVRRNLENKLTAKGLSLQEANKLIKDFLSSNKELAGKALNFNKAVAEAKSTGN
YDEVKKAQKDLEKSLRKREHLEKEVEKKLESKSGNKNKMEAKAQANSQKDEIFALINKEANRDARAIAYTQNLKGI
KRELSDKLEKISKDLKDFSKSFDEFKNGKNKDFSKAEETLKALKGSVKDLGINPEWISKVENLNAALNEFKNGKNK
DFSKVTQAKSDLENSVKDVIINQKVTDKVDNLNQAVSVAKAMGDFSRVEQVLADLKNFSKEQLAQQAQKNEDFNTG
KNSELYQSVKNSVNKTLVGNGLSGIEATALAKNFSDIKKELNEKFKNFNNNNNGLKNSTEPIYAKVNKKKTGQVAS
PEEPIYTQVAKKVNAKIDRLNQIASGLGGVGQAAGFPLKRHDKVDDLSKVGLSASPEPIYATIDDLGGPFPLKRHD
KVDDLSKVGRSRNQELAQKIDNLNQAVSEAKAGFFGNLEQTIDKLKDSTKKNVMNLYVESAKKVPASLSAKLDNYA
INSHTRINSNIQNGAINEKATGMLTQKNPEWLKLVNDKIVAHNVGSVSLSEYDKIGFNQKNMKDYSDSFKFSTKLN
NAVKDIKSGFTHFLANAFSTGYYCLARENAEHGIKNVNTKGGFQKS

Seq ID 233
VAINTFLKHSFLVCLLAVNSYAFDWNIFKYNLGFNMFIMDHEGSTPYWVNTNTNLKTRLTPNFGIQFYTRGVEQSL
TVGAYFFQNFHNYSTNFPYRWGPTMYYKARGKRFTFYGGIFPRKNLLGRYGLNIFAPYYWFIDPNARGFLLQFQNH
YSPSKPYYGHAEFMLDWFGGNCYNTCKFGRNPYGNAMDRFQMNGSVAYNFFKDLLGIGGYFVLFHNEDKYLLNGAD
GMQFNEKKAIDNSAIYLLDRLYYNAYISTSLLDIAPFMEKLSAKFGMVSEASRLRNREKEVPFINSVGGQFDVEIQ
YKGFGIHNLFFFAKTPEMPFYNQYQYVEMYCTPSYCPTPIYRGVPFFQANMYNRFDFYYNWKNDFASVRINFVLNA
MRGGFDRSLPWSESYQVYMTVAFDPYNLINKIARKK

Seq ID 234
MMIFIDACFRKETPYTPIWMMRQAGRYLSEYQESRKKAGSFLELCKNSDLATEVTLQPVEILGVDAAILFSDILVV
PLEMGLNLEFIPKKGPHFLETITDLKSVESLKVGAYKQLNYVYDTISQTRQKLSREKALIGFCGSPWTLATYMIEG
EGSKSYAKSKKMLYSEPEVLKALLEKLSLELIEYLSLQIQAGVNAVMIFDSWASALEKEAYLKFSWDYLKKISKEL
KKRYAHIPVILFPKGIGAYLDSIDGEFDVFGVDWGTPLTAAKKILGGKYVLQGNLEPTRLYDKNALEEGVETILKV
MGNQGHIFNLGHGMLPDLPRENAKYLVQLVHAKTRR

Seq ID 235

MYKTAINRPITTLMFALAIVFFGTMGFKKLSVALFPKIDLPTVVVTTTYPGASAEIIESKVTDKIEEAVMGIDGIK
KVTSTSSKNVSIVVIEFELEKPNEEALNDVVNKISSVRFDDSNIKKPSINKFDTDSQAIISLFVSSSSVPATTLND
YAKNTIKPMLQKINGVGGVQLNGFRERQIRIYANPTLMNKYNLTYADLFSTLKAENVEIDGGRIVNSQREFSILIN
ANSYSVADVEKIQVGNHVRLGDIAKIEIGLEEDNTFASFKDKPGVILEIQKIAGANEIEIVDRVYEALKRIQAISP
NYEIRPFLDTTGYIRTSIEDVKFDLVLGAILAVLVVFAFLRNGTITLVSAISIPISIMGTFALIQWMGFSLNMLTM
VALTLAIGIIIDDAIVVIENIHKKLEMGMSKRKASYEGVREIGFALVAISAMLLSVFVPIGNMKGIIGRFFQSFGI
TVALAIALSYVVVVTIIPMVSSVVVNPRHSRFYVWSEPFFKALESRYTKLLQWVLNHKIIISIAVVLVFVGSLFVA
SKIGMEFMLKEDRGRFLVWLKAKPGVSIDYMTQKSKIFQKAIEKHAEVEFTTLQVGYGTTQNPFKAKIFVQLKPLK
ERKKEHQLGQFELMSVLRKELRSLPEAKGLDTINLSEVTLIGGGGDSSPFQTFVFSHSQEAVDKSVENLKKFLLES
PELKGKVESYHTSTSESQPQLQLKILRQNANKYGVSAQTIGSVVSSAFSGTSQASVFKEDGKEYDMIIRVPDDKRV
SVEDIKRLQVRNKYDKLMFLDALVEITETKSPSSISRYNRQRSVTVLAEPNRNAGVSLGEILTQVSKNTKEWLVEG
ANYRFTGEADNAKESNGEFLVALATAFVLIYMILAALYESILEPFIIMVTMPLSFSGAFFALGLVHQPLSMFSMIG
LILLIGMVGKNATLLIDVANEERKKGLNIQEAILFAGKTRLRPILMTTIAMVCGMLPLALASGDGAAMKSPIGIAM
SGGLMISMVLSLLIVPVFYRLLAPIDDKIKRFYQNQKTLE

Seq ID 236
MKKVLIINGAKAFGSSGGKLNETLTDHAKKTLESLGLEVDTTIVDKGYEHAQEVEKVFSADATIWQMPGWWMGEPW
IVKKYIDEVFSVGHGKLYASDGRSSQNPTKNYGKGGLMQGKKYMLSLTWNAPIEAFNDPSEFFEGVGVDVVYLHLH
KAFQFLGLSALPTFICNDVVKNPQVEQYLNSLTTHLRQAFGK

Seq ID 237
LVFVFLFKCVNEETSLNFTPLLERMACNLQARFYSVYKDNTTSFYLQASAETTLEFAQKLSEILPFSLDFSFLSLK
EITEPLDENLFQTASLSKPLFMNAKEHQDFLDKNSSLYADTLGLIKNTAFKGDIIHSPKELIDCLTQLKGMLKTQD
FIPIFTSREALSLSLKNPSPSVIFSDLSSVLSCTKLPLEDAKYLASLEKPSIKAPLKSVFKDTFKNDEIIAQLPYD
PILNLLCHILQDEGIEFVFMHESRSCEALLYYEALFKTPKRLITPTKKFVLENNFSTFPFKDELEFLSATPNSIVL
YLSFKRPTRLLLHANGSLKTLLSVSFDFNKMFNALKQDEKASRMLQNYATKFPDFYARIVELSKYDLGGANLLDFF
CILGFVLGYSEDFCTQSVIPLAKECLRPKGPRIDYKILKDNSLKMALNFSKIMHSAMSFRLAGVENEILSLGILDS
LAEFLGNFIWDNAQNFSVQEVTIAGDFFGEKVFLDLFVRYFPKTLALKTHAFLDYE

Seq ID 238
IKKLILSSLVFACINTSVEALENDGSKPNDLTSPKEASQESQKNEAPKNEVQRNEAQKETPQSNQTPKEMKVKSIS
YVGLSYMSDMLANEIVKIRVGDIVDSKKIDTAVLALFNQGYFKDVYATFEGGILEFHFDEKARIAGVEIKGYGTEK
EKDGLKSQMGIKKGDTFDEQKLEHAKTALKTALEGQGYYGSVVEVRTEKVSEGALLIVFDVNRGDSIYIKQSIYEG
SAKLKRRMIESLSANKQRDFMGWMWGLNDGKLRLDQLEYDSMRIQDVYMRRGYLDAHISSPFLKTDFSTHDAKLHY
KVKEGIQYRISDILIEIDNPVVPLKTLEKALKVKRKDVFNIEHLRADAQILKTEIADKGYAFAVVKPDLDKDEKNG
LVKVIYRIEVGDMVYINDVIISGNQRTSDRIIRRELLLGPKDKYNLTKLRNSENSLRRLGFFSKVKIEEKRVNSSL
MDLLVSVEEGRTGQLQFGLGYGSYGGLMLNGSVSERNLFGTGQSMSLYANIATGGGRSYPGMPKGAGRMFAGNLSL
TNPRIFDSWYSSTINLYADYRISYQYIQQGGGFGVNVGRMLGNRTHVSLGYNLNVTKLLGFSSPLYNRYYSSVNEV
VSPRQCSTPASVIINRLSGGKTPLQPESCSSPGAITTSPEIRGIWDRDYHTPITSSFTLDVSYDNTDDYYFPRNGV
IFSSYATMSGLPSSGTLNSWNGLGGNVRNTKVYGKFAAYHHLQKYLLIDLIARFKTQGGYIFRYNTDDYLPLNSTF
YMGGVTTVRGFRNGSVTPKDEFGLWLGGDGIFTASTELSYGVLKAAKMRLAWFFDFGFLTFKTPTRGSFFYNAPVT
TANFKDYGVIGAGFERATWRASTGLQIEWISPMGPLVLIFPIAFFNQWGDGNGKKCKGLCFNPNMDDYTQHFEFSM
GTRF

Seq ID 239
MRKIFSYVLKALLFIGIVYAEPESKVEALEGRKQESSLDKKIRQELKNKDLKNKELKNKKEEKKNTEEKKETKAKR
KPRAEVHHGDTKNPTQKITPPKIKENAKGVQNQGVQSNAPKLEEKDTTSQTLEKKGASPSSQFNSIFGNPNDAANN
TLEDKVVGGISLLVNGSPITLYQIQEEQEKSKVSKAQARDRLIAERIKNQEIERLKIHVDDDKLDQEMAMMAQQQG
MDLDHFKQMLMAEGHYKLYRDQLKEHLEMQELLRNILLTNVDTSSETKMREYYNKHKEQFSIPTEIETVRYTSTNQ
EDLERAMADPNLEIPGVSKANEKIEMKTLNPQIAQVFISHEQGSFTPVMNGGGGQFITFYIKEKKGKNEVSFSQAK
QFIAQKLVEESKDKILEEHFEKLRVKSRIVMIRE

Seq ID 240
MLSVIILAAGKGTRMRSSLPKTLHTICGEPMLFYILETAFSISDDVHLILHHQQERIKEAVLERFKGVIFHTQIVE
KYSGTGGAIMQKDKTPISTKHERVLILNADMPLITKDALAPLLESKNNAIGLLHLADPKGYGRVVLENHQVKKIVE
EKDANDEEKEIKSVNAGVYGFERDFLEKYLPKLHDQNAQKEYYLTDLIALGINENETIDAIFLKEECFLGVNSQTE
RAKAEEIMLERLRKNAMDLGVVMQLPNSIYLEKGVSFKGECVLEQGVRLIGNCLIENAHIKAYSVIEESQIVNSSV
GPFAHARPKSVICNSHVGNFVETKNAKLQGTKAGHLSYLGDCEIGKNTNVGAGVITCNYDGKKKHQTIIGENVFIG
SDSQLVAPINIGSNVLIGSGTTITKDIPSGSLSLSRAPQTNIENGYFKFFKKP

Seq ID 241
MKEITIALVGQPNVGKSSLINALSNAHLKVGNFAGVTVDKMEVGLIHKEHQITIIDLPGTYALNDFTTEEKVTKDF
LEKGQYDLILNVVDSTNLERNLALSAQLLDTNKKMLLALNMWDEAQKEGIKINTEKLSKELGVVCVPTSARSKEDR
LNTELLLDEIVRLYSQNTTNNENIKVPSQSFKESLKYSQSAQRIAQLVISENQQNASFEHTYKIDKILMHKRYGIF
IFLGFMFIIFSLSFLIGGGVQKALETGFKFLSDGIKENVANEDLASLVGDGIIGGVGATVSFLPLIVVLYFGISLL
ETTGYMSRVAFLLDGILHKFGLHGKSFIPLITGFGCSVPAYMATRTLQNYNERLITLFVIGFMSCSARLPIYVLFV
GSFFPSSSAGFVLFCIYILGAVVALVMAKLLKLSVFKGQTESFIMEMPKYRFPSWRMVYFSIYTKSLSYLKKAGTY
ILVGAILIWFMSQYPKSDAAMKAYKQESLLVNKDTTLSSEAKEEKLKELKTELDKKNLKNSIVGRGGAYLEKVFSP

MDFDWRLSVSLVTGFMAKEVVVSTLGVLFSLGDQNEKSDAFRGILRKEVSVPSGIAFIVFVMFYIPCFAATITFGR
EAGGIKFVAYLFIFTTVVAYAFSLIAFYATQILV

Seq ID 242
MANLLKNGKTLKQARDEILARTEKTGHYNGLKKLEFKERDPIGYEKMFSKLRGGIVHARETAKRIAASPIVEQEGE
LCFTLYNAVGDSVLTSTGIIIHVGTMGSAIKYMVENNWEDNPGINDKDIFTNNDCAIGNVHPCDIMTLVPIFHDEK
LIGWVGGVTHVIDTGSVTPGSMSTGQVQRFGDGYMITCRKTGANDESFKDWLHESQRSVRTPKYWILDERTRIAGC
HMIRDLVMEVIKEDGIDSYMRFIDEVIEEGRRGLISRIKSMTIPGKYRKVAFVDVPYAHKDIGVCSEFAKLDTIMH
SPVEITINKDATWKLDFDGASRWGWHSFNCNQVSFTSGIWVMMTQTLIPTSRINDGAYFATQFRLKKGTWMNPDDR
RTGHAYAWHFLVSGWSALWRGLSQAYYSRGYLEEVNSGNANTSNWLQGGGINQDGEIHAVNSFETSSCGTGACAIK
DGLNHAAAIWNPEGDMGDVEIWEMAEPLLYLGRNVKANTGGYGKYRGGNGFETLRMVWGAHDWTMFFMGNGYMNSD
WGMMGGYPAASGYRFEAHNTDLKNRIKNNASLPLGGDFNPTDRDYEKHISHASQVKRDKQCITTENCFDNYDLYLN
YIKGGPGFGDPIERDLNAILEDLNSKQLLPEYAYKVYGAVVSQNKDGVWVGDEAKTKARRKEILENRKARSIPVKQ
WMEQERNAILEKEASKQVKHMYATSFDLSPKFLNDFKTFWNLPKNWSVKEDELGVFTYGSKYRMDLSKLPDVRTVL
LVDEK

Seq ID 243
MQDNSVNETKNIVEVGIDSSIEESYLAYSMSVIIGRALPDARDGLKPVHRRILYAMHELGLTSKVAYKKSARIVGD
VIGKYHPHGDNAVYDALVRMAQDFSMRLELVDGQGNFGSIDGDNAAAMRYTEARMTKASEEILRDIDKDTIDFVPN
YDDTLKEPDILPSRLPNLLVNGANGIAVGMATSIPPHRMDEIIDALVHVLENPNAGLDEILEFVKGPDFPTGGIIY
GKAGIIEAYKTGRGRVKVRAKVHVEKTKNKEIIVLDEMPFQTNKAKLVEQISDLAREKQIEGISEVRDESDREGIR
VVIELKRDAMSEIVLNHLYKLTTMETTFSIILLAIYNKEPKIFTLLELLHLFLNHRKTIIIRRTIFELEKAKARAH
ILEGYLIALDNIDEIVRLIKTSQSPEAAKNALMERFTLSEIQSKAILEMRLQRLTGLERDKIKEEYQNLLELIDDL
NGILKSEDRLNGVVKTELLEVKEQFSSPRRTEIQESYENIDIEDLIANEPMVVSMSYKGYVKRVDLKAYEKQNRGG
KGKLSGSTYEDDFIENFFVANTHDILLFITNKGQLYHLKVYKIPEASRIAMGKAIVNLISLAPDEKIMATLSTKDF
SDERSLAFFTKNGVVKRTNLSEFESNRSCGIRAIVLDEGDELVSAKVVDKNAKHLLIASHLGIFIKFPLEEVREIG
RTTRGVIGIKLNENDFVVGAVVISDDGNKLLSVSENGLGKQTLAEAYRGQSRGGKGVIGMKLTQKTGNLVGVISVD
DENLDLMILTASAKMIRVSIKDIRETGRNASGVKLINTADKVMYVNSCPKEEEPENLETSSAQNLFE

Seq ID 244
MEFMKKFVALGLLSAVLSSSLLAEGDGVYIGTNYQLGQARLNSNIYNTGDCTGSVVGCPPGLTANKHNPGGTNINW
HAKYANGALNGLGLNVGYKKFFQFKSFDMTSKWFGFRVYGLFDYGHATLGKQVYAPNKIQLDMVSWGVGSDLLADI
IDNDNASFGIFGGVAIGGNTWKSSAANYWKEQIIEAKGPDVCTPTYCNPNAPYSTKTSTVAFQVWLNFGVRANIYK
HNGVEFGVRVPLLINKFLSAGPNATNLYYHLKRDYSLYLGYNYTF

Seq ID 245
MAILRANLSPKNKLNATLKGWLPILQSELEDLEEVLKQNALDNPLIKIENKRIKNFSDRFSAKKSSDHLENFATAS
KSLFETLEAQIIPPLFPTETSQKIAMDIISGLNNEGYFEENIEERARILGVESEVYEKVRKRFSYLNPAGIGAKDV
KESFLFQLESRELDDNELYEETRKIILNLEKHHEFSKDFYYEKALKILKSFKNPPAIEFLEKEIEVIPELFIVEVD
NGIIVRLNDESYPTISLEENRFKDSGYLKEKLKEAKDLIDALNLRKATIYKIGLMLLEYQYDFFKGKELRPLKLLD
LANEFNHSVSTISRAISNKYLACERGVFPIKHFFSIALDNSETSNAVIKDYLLELIKNEDKKEPLSDAKILELIEE
KFHLKMVRRTITKYRQLLNIASSSERKRLYLMRA

Seq ID 246
MQVLALKYRPKHFSELVGQESVAKTLSLALDNQRLANAYLFSGLRGSGKTSSSRIFARALMCEEGPKAVPCDTCIQ
CQSALNNHHIDIIEMDGASNRGIDDVRNLIEQTRYKPSFGRYKIFIIDEVHMFTTEAFNALLKTLEEPPSHVKFLL
ATTDALKLPATILSRTQHFRFKKIPENSVISHLKTILEKEQVSYETSALEKLAHSGQGSLRDTITLLEQAINYCDN
AITESKVAEMLGAIDRSVLEDFFQSLINQDEARLKERYAILENYETESVLEEMMLFLKAKLLSPDFYSILLIERFF
KIIMSSLSLLLKEGANASFVLLLLKMKFKEALKFKALDDAILLELEQTPFNQNPSISYNAPKQESKNIEKREKIEQIE
RIEGTEKREKLEKKENAETPQTPMLSAKDRIFHNLFKQVQTLVYERNYELGAVFEKNIRFIDFDSQTKTLTWESLA
TDKDKELLRERFKIVKSIVDGVFGKGESIKIALKNHSENKSTLEVVKELKFPYSKPKPTTETTAETKEKETKEKEI
QENDTKEIQEVQPKQAPTALQEFMANHSELIEEIKSEFEIKSVELL

Seq ID 247
MRIFLKLLILLFCLKGQVMAQNLPTIALLATGGTIAGSGASASLGSYKSGELGIKELLKAIPSLNRLARIQGEQIS
NIGSQDMNEEVWFKLAKRAQELLDDSRIQGVVITHGTDTLEESAYFLNLVLRSTKPVVLVGAMRNAASLSADGALN
LYNAVSVALNEKSANKGVLVVMDDNIFSAREVIKTHTTHTSTFKALNSGAIGSVYYGKTRYYMQPLRKHTTESEFS
LSQLKTPLPKVDIIYTHAGMTPDLFQASLNSHAKGVVIAGVGNGNVSAGFLKAMQEASQMGVVIVRSSRVNSGEIT
SGEIDDKAFITSDNLNPQKARVLLQLALTKTNNKEKIQEMFEEY

Seq ID 248

MDFKNKKWLFLAPLAGYTDLPFRSVVKKFGVDVTTSEMVSSHSLVYAFDKTSKMLEKSPLEDHFMAQISGSKESVV
KEAVEKINALEHVNGIDFNCGCPAPKVANHGNGSGLLKDLNHLVKLLKTIRENTSKKITSVKVRLGFEKKIPKEIA
HALNDAPVDYVVVHGRTRSDKYQKDKIDYESIALMKKILKKPVIANGEIDSVKKAFEVLQITQADGLMIGRAALRA
PWIFWQIRNNTTKLPAVVKKDLVLEHFDKMVEFYGDMGVIMFRKNLHAYAKGEMQASAFRNCVNTLTEIKSMRESI
EEFFNQEMLQSEVPLWVELNQKSV

Seq ID 249
MAIGSLSSLGLGSKVLNYDVIDKLKDADEKALIAPLDKKMEQNVEKQKALVEIKTLLSALKGPVKTLSDYSTYISR
KSNVTGDALSASVGVGVPIQDIKVDVQNLAQGDINELGAKFSSRDDIFSQVDTTLKFYTQNKDYAVNIKAGMTLGD
VAQSITDATNGEVMGIVMKTGGNDPYQLMVNTKNTGEDNRVYFGSHLQSTLTNKNALSLGVDGSGKSEVSLNLKGA
DGNMHEVPIMLELPESASIKQKNTAIQKAMEQALENDPNFKNLIANGDISIDTLHGGESLIINDRRGGNIEVKGSK
AKELGFLQTTTQESDLLKSSRTIKEGKLEGVVSLNGQKLDLSALTKESNTSEENTDAIIQAINAKEGLSAFKNAEG
KLVINSKTGMLTIKGEDALGKASLKDLGLNAGMVQSYEASQNTLFMSKNLQKASDSAFTYNGVSITRPTNEVNDVI
SGVNITLEQTTEPNKPAIISVSRDNQAIIDSLTEFVKAYNELIPKLDEDTRYDADTKIAGIFNGVGDIRAIRSSLN
NVFSYSVHTDNGVESLMKYGLSLDDKGVMSLDEAKLSSALNSNPKATQDFFYGSDSKDMGGREIHQEGIFSKFNQV
IANLIDGGNAKLKIYEDSLDRDAKSLTKDKENAQELLKTRYNIMADVLPLMIAKSLKPIKNSIPCK

Seq ID 250
MQIATAIWKTRIWQLQTHFDKKEAHLKHLEAQHKEFVRDEKRYLEKEKKELEKERQILEQEKENFKKQRAVCKESQ
AKALDAMLNYMAYTKDEIKSMILEQLEEELEAQKSALIRRYEKEAKEEGKKKSYAILAEATARFAGNYAAENLTTR
IALPCSDYIGRVIGKDGKNIEAFKKVSGVDIEFSEDSSELCLSSFNLYRREVASETLKILIEDGRIQPNRIEEVYH
RVARNLEKELLSEGESVVLELELGAMEDELKILIGKMRYRSSFGQNALQHSKEVALLAGLIAEQLGGDKKLARRAG
ILHDIGKALTQELGRDHVNLGVEVCKRHKEDPVVINAIYAHHGHEEILSVECASVCAADALSAGRPGARRKSDEEY
AKRMQALEEIALEFDGVEKAYAMESGRELRVIVKSNQVRDNQVPIIARKIAKKIEESAQYVGEVGVQVVRESRFKT
TATLKQ

Seq ID 251
MPMRLHTAFFGINSLLVASLLISGCSLFKKRNTNAQLIPPSANGLQAPIYPPTNFTPRKSIQPLPSPRLENNDQPV
ISSNPTNAIPNTPILTPNNVIELNAWAWAWLQNPPFHPLKPWL

Seq ID 252
MENNPNNNQASLERNELHNTIWKVANELRGSVDGWDFKQYVLGILFYRYISENMTHYINKEERKRDPSFDYAKLSD
EKAERGRKHLIEQKGFFIPPSALFCNALKNACHNEDLNVTLQNIFNEIEKSSLGTPSEENVKGLFADLDVNSNKLG
SSHQNRVEKLTKILEAIGGMQLGDYLKSGIDVFGDAYEYLMAMYASNAGKSGGEFFTPQEVSELLAKITLHGQESV
NKVYDPCCGSGSLLLQFSKVLGDKNVSKGYFGQEINLTTYNLCRINMFLHDINYSKFHIAHGDTLLDPKHEDDEPF
DAIVSNPPYSTKWVGDSNPILINDERFSPAGVLAPKNAADLAFTMHMLSYLSNSGTAAIVEFPGVLYRGNAEAKIR
EYLVKENVIDCVIALPDNLFFGTSIATCILVLKKNKQDDTTLFIDASKEFVKEGKKNKLKERNREKILQTYIERKE
IKHFCALANIEKIKENDYNLSVNRYVEQEDTKEAIDIKALNSEIAQIVEKQSALRNRLESIIKELEGGQNA

Seq ID 253

MLQTINLTQRYATKKLFENVNIKLDKNKRYGLIGANGAGKSTFLKILSKSIDCSSGEVIITSGMKMGVLGQDQYAF
EDLSLKDAVLIGNKRLYDAIKEKERLYTEGDLSDDKVNARLGELETICVEEDPMYECEVAIEKILEDLGIPSSKHN
DLMKTLPSSDKFKILLAQVLFPKPDILLLDEPTNNLDLNAIEWLENNLKRHEGTMVVISHDRHFLNAVCTHILDLD
FHSVREFSGNYDDWYIASTLIAKQQEAERNKKLKEKEELEKFIARFSANASKAKQATSRQKQLDKLDIQSLAVSSR
RDPSIIFKPKRTIGNEALECENISKSYDDQIVLNQVSLKVMPKDKIALIGPNGVGKSTLCKILVEELKPDKGVVKW
GATVSKGYFPQNVSEEISGEETLYQWLFNFNKKIESAEVRNALGRMLFNGEEQEKCVNALSGGEKHRMVLSKLMLE
GGNFLVLDEPTNHLDLEAIIALGEALFKFDGALICVSHDRELIDAYANRIIELVPSPKGASIIDFKGSYEEYLASK
K

Seq ID 254
MNKPFLILLIALIVFSGCNMRKYFKPAKHQIKGEAYFPNHLQESIVSSNRYGAILKNGAVIGDKGLTQLRIGKNFN
YESSFLNESQGFFILAQDCLNKIDKKTNKSKVAKTEETELKLKGVEAEVQDKVCHQVELISNNPNASQQSIVIPLE
TFALSASVKGNLLAVVLADNSANLYDITSQKLLFSEKGSPSTTINSLMAMPIFMDTVVVFPMLDGRLLVVDYVHGN
PTPIRNIVISSDKFFNNITYLIVDGNNMIASTGKRILSVVSGQEFNYDGDIVDLLYDKGTLYVLTLDGQILQMDKS
LRELNSVKLPSSLNTIVLNHNKLYSLEKRGYVIEVDLNDFDSYNVYKTPTIGSFKFFSSNRLDKGVFYDKNRVYYD
RYYLDYNDFKPKLYPVVEKSASKKSQKGEKGNAPIYLQERHKAKENKQPLEENKVKPRNSGFEEEEVKTRRPEPIR
DQNNATQQGETKNNESKNAPVLKENAAKKEVPKPNSKEEKRRLKEEKKKAKAEQRARAREFEQRAREHQERDEKELEE
RRKALEMNKK

Seq ID 255
MKRRDFIKTTTLGATGAVLGAQILQAEESKGSVAKYKIEAQYSIDFDSAEHTSLFIPMPSVVASNVHLQGNHASYK
SMLNFGVPYLQVDFLKSTQKKQVHLSYEIASYQLNERLFETSDFVAMGRYERDDASVANIANQLKGTTPKESVRNF
YAFIKHEMPKRQKALEGKENLPKRESLPWFATISKESMFVSLCHACGIKSAEVQGLKLGQNSVVKNAPRVEVYLKD
SFLAFDFQNNHKEVFIPLNRHKDMQLDSALLATFGDAFALVDGRDLGNYESKLFEKRVSYTIV

Seq ID 256
MVNKDVKQTTAFGAPVWDDNNVITAGPRGPVLLQSTWFLEKLAAFDRERIPERVVHAKGSGAYGTFTVTKDITKYT
KAKIFSKVGKKTECFFRFSTVAGERGSADAVRDPRGFAMKYYTEEGNWDLVGNNTPVFFIRDAIKFPDFIHTQKRD
PQTNLPNHDMVWDFWSNVPESLYQVTWVMSDRGIPKSFRHMDGFGSHTFSLINAKGERFWVKFHFHTMQGVKHLTN
EEAAEVRKYDPDSNQRDLFNAIARGDFPKWKLSIQVMPEEDAKKYRFHPFDVTKIWYLQDYPLMEVGIVELNKNPE
NYFAEVEQAAFSPANVVPGIGYSPDRMLQGRLFSYGDTHRYRLGVNYPQIPVNKPRCPFHSSSRDGYMQNGYYGSL

QNYTPSSLPGYKEDKSARDPKFNLAHIEKEFEVWNWDYRADDSDYYTQPGDYYRSLPADEKERLHDTIGESLAHVT
HKEIVDKQLEHFKKADPKYAEGVKKALEKHQKMMKDMHGKDMHHTKKKK

Seq ID 257
MFLRVYPKLRYALCFPLLAETCYSEERTLNKVTTQAKRIFTYNNEFKVTSKELDQRQSNEVKDLFRTNPDVNVGGG
SVMGQKIYVRGVEDRLLRVTVDGAAQNGNIYHHQGNTVIDPGMLKSVEVTKGAANASAGPGAIAGVIKMETKGAAD
FIPRGKNYAASGAVSFYTNFGDRETFRSAYQNAHFDIIAYYTHQNIFYYRSGATAMKNLFNPTQADKEPGTPSEQN
NALIKMNGYLSDRDTLTFSWNMTRDNATRPLRSNAIGLAYPCEAPFSPDSSQGCPNVLDSFTRYMYHSINSANNLS
LQYKREAGNSFGDPRLDFTLYTSIRNAQFDPLFDPNGVYAKFPTSLASAWEKENYPCVEGAYCTPSFSDVDKPSSQ
PRNLFLNNTGLNLKVAHVIDEATDSLFEYGFNYQNLSVFDARIPKSELYRPNQVYTDDKGQKQIACSLVNNNPNDP
TLCQRGKANGNIYGGYVQANYSPHKIITFGAGVRWDAYTLYDKDWNHRYTQGFSPSAALVLSPIEPLSLKITYSQV
TRGVMPGDGVYMRQNDLRYAKNIKPEVGSNAEFNIDYSSQYFSGRAAAFYQALDNFISQYAQNLIVTNLSQAIRIY
GYEVGGTFRYKGVSLNVGVSRTWPTTRGYLMADSYELAASTGNVFIIKLDYTIPKTGINLAWLSRFVTGLDYCGFD
IYLPDYGTAEKPKTPTDLAKCGSQLGLVHMHKPGYGVSNFYINWSPKTKSRWKGLLLSAVFNNVFNKFYVDQTSPY
VMSPDMPGTDAVKRAIAEPGFNARFEVAYKW

Seq ID 258
MEIQQTHRKINRPLVSLALVGALVSITPQQSHAAFFTTVIIPAIVGGIATGAAVGTVSGLLGWGLKQAEEANKTPD
KPDKVWRIQAGKGFNEFPNKEYDLYRSLLSSKIDGGWDWGNAATHYWVKGGQWNKLEVDMKDAVGTYNLSGLRNFT
GGDLDVNMQKATLRLGQFNGNSFTSYKDSADRTTRVDFNAKNILIDNFLEINNRVGSGAGRKASSTVLTLQASEGI
TSSKNAEISLYDGATLNLASNSVKLMGNVWMGRLQYVGAYLAPSYSTINTSKVTGEVNFNHLTVGDHNAAQAGIIA
SNKTHIGTLDLWQSAGLNIIAPPEGGYKDKPKDKPSNTTQNNANNNQQNSAQNNSNTQVINPPNSAQKTEIQPTQV
IDGPFAGGKDTVVNIDRINTNADGTIKVGGYKASLTTNAAHLHIGKGGINLSNQASGRTLLVENLTGNITVDGPLR
VNNQVGGYALAGSSANFEFKAGTDTKNGTATFNNDISLGRFVNLKVDAHTANFKGIDTGNGGFNTLDFSGVTGKVN
INKLITASTNVAVKNFNINELVVKTNGVSVGEYTHFSEDIGSQSRINTVRLETGTRSIFSGGVKFKSGEKLVIDEF
YYSPWNYFDARNIKNVEITRKFASSTPENPWGTSKLMFNNLTLGQNAVMDYSQFSNLTIQGDFINNQGTINYLVRG
GQVATLNVGNAAAMFFSNNVDSATGFYQPLMKINSAQDLIKNKEHVLLKAKIIGYGNVSLGTNSISNVNLIEQFKE
RLALYNNNNRMDICVVRNTDDIKACGTAIGNQSMVNNPDNYKYLIGKAWKNIGISKTANGSKISVYYLGNSTPTEK
GGNTTNLPTNTTSNVRSANNALAQNAPFAQPSATPNLVAINQHDFGTIESVFELANRSKDIDTLYANSGAQGRDLL
QTLLIDSHDAGYARQMIDNTSTGEITKQLNAATTTLNNIASLEHKTSSLQTLSLSNAMILNSRLVNLSRRHTNNID
SFAQRLQALKDQKFASLESAAEVLYQFAPKYEKPTNVWANAIGGTSLNNGGNASLYGTSAGVDAYLNGEVEAIVGG
FGSYGYSSFNNQANSLNSGANNTNFGVYSRIFANQHEFDFEAQGALGSDQSSLNFKSALLRDLNQSYNYLAYSAAT
RASYGYDFAFFRNALVLKPSVGVSYNHLGSTNFKSNSNQVALKNGSSSQHLFNASANVEARYYYGDTSYFYMNAGV
LQEFANFGSSNAVSLNTFKVNAAHNPLSTHARVMMGGELKLAKEVFLNLGFVYLHNLISNIGHFASNLGMRYSF

Seq ID 259
MPQIQSSHSNHFDFTIDTADRTKLLMSYLVVPTTANFNNVMHGGELLNLLDKVAYVCSTRYCAKGTVTLSVDGVTF
KYPIPVGNLLTFLASINYVGNTSCEVGIKVLSEDIKTREITHTNSCYFTMVAVENGKPTPMPKYEPKTEVEIRRYE
GALKRKEMRTRGYLKSGKHEGV

Seq ID 260
LNNLDIKTLGQVFTPKKIVDFMLTLKHNHGSVLEPSAGDGSFLKRLKKAVRIEIDPKICPKNALCMDFFDYPLENQ
FDTIIGNPPYVKHKDIAPSTKEKLHYSLFDERSNLYLFFIEKAIKHLKPKGELIFITPRDFLKSTSSVKLNEWIYK
EGTITHFFELGDQKVFPNAMPNCVIFRFCKGNFSRITNDGLQFLCKKGILYFLNQSYTQKLSEVFKVKVGAVSGCD
KIFKNEKYGNLEFVTSITKRTNALEKMVFVNEPNDYLLQHKDSLMQRKIKKFNENNWFEWGRMHHISPKKRIYVNA
KTHQKNPFFIHQCPNYDGSILALFPYNQNLDLQNLCDKLNAINWQELGFVCGGRFLFSQRSLENALLPKDFLNLG

Seq ID 261
MKQNLKPFKMIKENLMTQSQKVRFLAPLSLALSLSFNPVGAEEDGGFMTFGYELGQVVQQVKNPGKIKAEELAGLL
NSNTTNNTNTNIAGTGGNVAGTLGNLFMNQLGNLIDLYPILNTKNIHQCGTTNNGSSSATTAAATTNNGLCFQGNL
DLYNEMVGSIKTLSQNISKNIFQGNNNTTSQNLSNQLSELNTASVYLTYMNSFLNANNQAGGIFQNNTNQAYGNGV
TAQQIAYILKQASITMGPSGDSGAAAAFLDAALAQHVFNSANAGNDLSAKEFTSLVQNIVNNSQNALTLANNANIS
NSTGYQVSYGGHIDQARSTQLLNNTTNTLAKVTALNNELKANPWLGNFAAGNSSQVNAFNGFITKIGYKQFFGENK
NVGLRYYGFFSYNGAGVGNGPTYNQVNLLTYGVGTDVLYNVFSRSFGSRSLNAGFFGGIQLAGDTYISTLRNSPQL
ANRPTATKFQFLFDVGLRMNFGILKKDLKSHNQHSIEIGVQIPTIYNTYYKAGGAEVKYFRPYSVYWVYGYAF

Seq ID 262
MAFKKARLISKFISKGSFKLNKISKKIFTLNQILKCEKPLKRHKKALKPIKKLSNRNKSFLKASVLLIGALGGLSH
LRANECRYWSWSSWSYQDNIESGPNSPTHNSYCLFSSTQGSGTYYLNTLTTYSAGGASFTQKFNNGTLNVGENIRF
GGTGINGGDVGYITGTYDAQTINFNSSHLTTGNSYADGGATLNFNAANNITINQASFDNSHAGTQKSYMNFKGSN
IKVSGSSFTDDTDGGFSFSGNSNNSTISFNQTSFNQGTYHFSNSATLSFNHSAFNQGTYNFNSTQSAFNNSAFNQG
TYHFNGNASFDNDTFNQGTYSFNTSKVSFSGINTLNSSSPFASLKGSVSFGSDAIFNLNQTLNNQTYDILTTNGAI
QYGVYQSYLWDLINYKGDKAISHVEVGNNTYDVTFDINGQDETLQETFNKQSIITQFLGDDLQQQAQKTYQQDLSN
SQSALNNAASDNKIANSDTDYTKNKNATIKKDAQGLENTNQQIAQDEQALQGDLDKLKQLANSPTGFSEQAFNQAQ
KQEQQDEQTLQNEEKTFNSEQEGLKQAIQQAQAQQQKQQQKQEQQQAQQTYQEDLTHSQSALNDVASDNTIASNDT
NYTNNQNTAIKEDAQGLENTNQQIAQDEQALQGDLDKLKQLANSPTGFSEQAFNQAQKQEQQDEQTLQNEEKTFNS
EQERLKQAIANAKPTSPTPSHAPTPTKHTAPNTPPNKVPPTPPTQNPPAESVWSGVYWLQNKTYSNKGIYYIDPNL
SGQSGQSGNTLSTYTANLFGRSFSVNIQNGTLIIGNNTESVNSNGLIWIGHGGFGYITGTFSAANIYLTNNFKTGE

GVSNSDGGGANITFKASDNITMDGLNYNDAETVTKMIQTGASQHSYATFDALNNISVTNSSFSDMTWGKFSFSAKN
ISFSNASFSGFTNPGGSSVISANATNSLSFINSRLNGGAVYNLQANSLIFNNTQAVFNVLYSRGTSNFNATTQLLG
NTNFTLSSQSLLNFNGDTTLQNNANITLGNKSQAAFKNSLTLDNNSNLSLDNQSVLNANNTSAFNNQASLNIYNGS
QATFNSLFFNGGTLSLNASSKLNASNASFSNNTTINLDDSVLSASNTSSLNANINFQGASQADFGGNTIIDTASFN
FDSASSLNFNNLTANGALNFNGYTPSLTKALMSVSGQFVLGNNGDINLSDINIFDNITKSVTYNILNAQKGITGIS
GANGYEKILFYGMKIQNATYSDNNNIQTWSFINPLNSSQIIQESIKNGDLTIEVLNNPNSASNTIFNIAPELYNYQ
ASKQNPTGYSYDYSDNQAGTYYLTSNIKGLFTPKGSQTPQAPGTYSPFNQPLSSLNIYNKGFSSENLKTLLGILSQ
NSATLKEMIESNQLDNITNINEVLQLLDKIKITQVQKQALLETINHLTDNINQTFNNGNLIIGATQDNVTNSTSSI
WFGGNGYSSPCTLDSATCSSFRNTYLGQLLGSTSPYLGYINADFKAKSIYITGTIGSGNAFESGGSADVTFQSANN
LVLNKANIEAQATDNIFNLLGQKGIEKIFNQGNLANVLSQVAMEKIKQAGGLGNFIENALSPLSKELPASLQNETL
GQLIGQNNLDDLLNNSGVMNAIQNIISKKLSIFGNFVTPSIIENYLAKQSLKSMLDDKGLLNFIGGYMNASELSSI
LSVVLKDITNPPTSLQKDIGVVANDLLNEFLGQDVIKKLESQGLVSNIINNIISQGGLSGVYNQGLGSVLPPSLQN
ALKENDLGTLLSPRGLHDFWQKGYFNFLSNGYVFVNNSSFSNATGGSLNFVANKSIIFNGDNTIDFSKYQGALIFA
SNDVSNINITTLNATNGLSLNAGLNNVSVQKGEICVNLANCPTTKNSSSTNSSVTPTNESLSVRANNFTFLGAIAS
NGAIDLSQVKNNSVIDTLNLNENAALQANNLTITNAFNNASNSTANINGNFTLNQQATLSTNASGLNVMGNFNSYG
DLVFNLSHSVSHAIINAQGSATIMANNNNPLIQFNTSSKEVGTYTYLIDSAKAIYYGYNNQITGGSSLDNYLKLYTL
IDINGKHMVMTDNGLTYNGQAVSVKDGGLVVGFKDSQNQYIYTSILYNKVKIAVSNDPINNLQAPTLKQYIAQIQG
TQGVDSIDQAGGSQAINWLNKIFETKGSPLFAPYYLESHSTKDLTTIAGDIANTLEVIANPNFKNDATNILQINTY
TQQMSRLAKLSDTSTFASADFHERLEALKNKRFADAIPNAMDVILKYSQRNRVKNNVWATGVGGASFINGGTGTLY
GINVGYDRFIKGVIVGGYAAYGYSGFHANITQSGSSNVNMGVYSRAFIKRSELTMSLNETWGYNKTFINSYDPLLS
IINQSYKYDTWTTDAKINYGYDFMFKDKSVIFKPQIGLAYYYIGLSGLRGIMDDPIYNQFRANADPNKKSVLTINF
ALESRHYFNKNSYYFVIADVGRDLFINSMGDKMVRFIGNNTLSYRDGGRYNTFASIITGGEIRLFKTFYVNAGIGA
RFGLDYKDINITGNIGMRYAF

Seq ID 263
MNTYKNSLNHFLNLVDCLEKIPNVGKKSAFKMAYHLGLENPYLALKITHALENALENLKTCSSCNALSESEVCEIC
SDESRQNSQLCMVLHPRDVFILEDLKDFLGRYYVLNSIEEVDFNALEKRLIEENIKEIIFAFPPTLANDSLMLYIE
DKLQHFHLTFTKIAQGVPTGVNFENIDSVSLSRAFNSRIKA

Seq ID 264
LFKRMVLIALLGVFSSVSLSAKSLLRDDGILVSDLKGMKSELSDAPAWVFEDAKAPYEEMGVAYIPVNNKYLGIEQ
ATLNAKLSLIVVFHEIMMKYKKRFMEQFHESEQTTTNISYAIYNYLATKIQVSNTYTNLKSEVAVVKIKLVGCQIE
QIKRYLKASVENLNDNEIAYIAKVAQKEFGSVCALR

Seq ID 265
LKHLTPLTHTIFKALWLGTALSASLSLAATESPTKTEPKPAKGVKNKPKSPVTKVMMTNCDNIKDFNAKQKEVLKA
AYQFGSKENLGYEMAGIAWKESCAGVYKINFSDPSAGVYHSYIPSVLKSYGHNDSPFLRNVMGELLIKDDAFASEV
ALKELLYWKTRYHDNLKDMIKSYNKGSRWERSEKSNADAEKYYEEIQDRIRRLKESKIFDSQSSNDQELQKSANSN
LDLDPIGNAMPQALIAKETKIEETQAEKSQEMKETTSEQTKSKPEKAKDKPMYLAQINSTDFTPVKKSPKKPAKVS
QKHSFKNNIKNNVKNNAKTASKKQEMCKNCSPGQRNAILANHITLMQEL

Seq ID 266
MIEWMQNHRKYLVVTIWISTIAFIAAGMIGWGQYSFSLDSDSAAKVGQIKISQEELAQEYRRLKDAYAESIPDFKE
LTKDQIKAMHLEKSALDSLINQALLRNLALDLGLGATKQEVAKEIRKTSVFQKDGVFDEELYKNILKQSHYRPKHF
EESVERLLILQKISTLFPKTTTPLEQSSLSLWAKLQDKLDILILNPSDVKISLNEEEMKKYYESHKKDFKKPTSFK
TRSLYFDASLEKPDLKELEEYYHKNKVSYLDKEGKLQDFKSVQEQVKHDLSMQKANEKALRSYIALKKANAQNYTT
QDFEENNSPYTAEITQKLTALKPLEILKPEPFKDGFIVVQLISQIKDELQNFNEAKSALKTRLTQEKTLMALQTLA
KEKLKDFKGKSVGYVSPNFGGTISELNQEESAKFINALFNRQEKKGFIAINNKVVLYQITEQNFNHSFSAEESQYM
QRLVNNTKTDFFDKALIEELKKRYKIVKYIQ

Seq ID 267
VSPLKTIRIYSYHDSIKDSIKAVVNISTEKKIKNNFIGGGVFNDPFFQQFFGDLGGMIPKERMERALGSGVIISKD
GYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRITKDNLPTIKFSDSNDISVGDLVFAIGNPFGV
GESVTQGIVSALNKSGIGINSYENFIQTDASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKD
TVTQLIKTGKIERGYLGVGLQDLSGDLQNSYDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNELRNL
IGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQGQLNGLQVEDLTQETKRSMRLSDDVQGVLV
SQVNENSPAEQAGFRQGNIITKIEEVEVKSVADFNHALEKYKGKPKRFLVLDLNQGYRIILVK

Seq ID 268
MSKSLYQTLNVSENASQDEIKKSYRRLARQYHPDLNKTKEAEEKFKEINAAYEILSDEEKRRQYDQFGDNMFGGQN
FSDFARSRGPSEDLDDILSSIFGKGGFSQRFSQNSQGFSGFNFSNFAPENLDITAALNVSVLDTLLGNKKQVSINN
ETFSLKIPIGVEEGEKIRVRNKGKTGRTTRGDLLLEIHIEEDEMYRREKDDITQIFDLPLKTALFGGKIEIATWHK
TLTLTIPPNTKAMQKFRIKEKGIKNRKTSHVGDLYLQARLILPKTETLSNELKALLEKEL

Seq ID 269
MKQTTINHSVELVGIGLHKGVPVKLVLEPLGENQGIVFYRSDLGVNLPLKPENIVDTKMATVLGKDNARISTIEHL
LSAVHAYGIDNLKISVDNEEIPIMDGSALTYCMLLDEAGIKELDAPKKVMEIKQAVEIRESDKFVKIEPDSQLSLN

FTIDFNHPVIAKQAHHFVFSKTAYKEQVAKARTFGFLQEVNYLRSIGLAKGGSLNNCIVLDENSILNKEGLRCEKE
FVCHKILDAMGDLMVLGMPVMGKYTSFSGSHKLNSMLVKAILADAKNYEVLIAADPAKEFALQKAFA

Seq ID 270
VQPMKSKKLYLALIIGVLLAFLTLSSWLGNSGLVGRFGVWFAALNKKYFGHLSFINLPYLAWVLFLLYKTKNPFTE
IVLEKTLGHLLGILSLLFLQSSLLNQGEIGNSARLFLRPFIGDFGLYALITLMVVISYLILFKLPPKSVFYPYMNK
TQNLLKEIYKQCLQAFSPNFSPKKEGFENTPSDIQKKETKNDKEKENRKENPINENHKTPNEEPFLAIPTPYNTTL
NDSEPQEGLVQISSHPPTHYTIYPKRNRFDDLTNPTNPPLKEIKQETKEREPTPTKETLTPTTPKPIMPTLAPIIE
NDNKTENQKTPNHPKKEENPQENTQEEMIEGRIEEMIKENLKKEEKEVQNAPNFSPVTPTSAKKPVMVKELSENKE
ILDGLDYGEVQKPKDYELPTTQLLNAVCLKDTSLDENEIDQKIQDLLSKLRTFKIDGDIIRTYSGPIVTTFEFRPA
PNVKVSRILGLSDDLAMTLCAESIRIQAPIKGKDVVGIEIPNSQSQIIYLREILESELFQKSSSPLTLALGKDIVG
NPFITDLKKLPHLLIAGTTGSGKSVGVNAMILSLLYKNPPDQLKLVMIDPKMVEFSIYADIPHLLTPIITDPKKAI
GALQSVAKEMERRYSLMSEYKVKTIDSYNEQAPSNGVEAFPYLIVVIDELADLMMTGGKEAEFPIARIAQMGRASG
LHLIVATQRPSVDVVTGLIKTNLPSRVSFRVGTKIDSKVILDTDGAQSLLGRGDMLFTPPGANGLVRLHAPFATED
EIKKIVDFIKAQKEVQYDKDFLLEESRMPLDTPNYQGDDILERAKAVILEKKITSTSFLQRQLKIGYNQAATITDE
LEAQGFLSPRNAKGNREILQNF

Seq ID 271
MLENVKKSFFRVLCLGALCLGGLMAEQDPKELVGLGAKSYKEKDFTQAKKYFEKACDLKENSGCFNLGVLYYQGQG
VEKNLKKAASFYAKACDLNYSNGCHLLGNLYYSGQGVSQNTNKALQYYSKACDLKYAEGCASLGGIYHDGKVVTRD
FKKAVEYFTKACDLNDGDGCTILGSLYDAGRGTPKDLKKALASYDKACDLKDSPGCFNAGNMYHHGEGATKNFKEA
LARYSKACELENGGGCFNLGAMQYNGEGVTRNEKQAIENFKKGCKLGAKGACDILKQLKIKV

Seq ID 272
VKLPKALNEATAGAALKYHIKRALERSHSISDFSKNLELSTQKSHFSNNTLKIIEELNNGVKQASEEIKEKARDFS
NQKLTNEQIKDLLNNAEIPTSGRDAITFGVNNLNPEIVEFLHKNNKKMIIEKASNKELELLKDANFKHPENIRASL
DHDAIAHILKRHGVNSVNVRNGEIPITNEDIANYRYIVNNADAILRTLDNENKELISAFKQINGYAVVVEQAINKK
NELVLKTMYKSKGDYKDNNAYKKFSSTHTLNADAKVNHRLSSYSGATENTTQKDLIDQENLLKTSENLNESTPKPT
NLSPLEQANAEKLAKLESEKLESEKEFLKAKEQEATRKAALKKKLEHERGNAGNIESQTKIEVGEDIPTQTQAQLP
KSRVRLNEREIYDLDYAIVKAKDLKPSFTTGGTQKRTDMNEEQIKSIAENFDPKKIFGSGGFEDLPIILHDGQVIA
GNHRIQGMLNFTPKSRFSYERAIKEYYHIDLKPDELLVRVPHKRLNNTEINNLAASSNQGRFNSESDHAIAVLSHY
EAKLKELDQKLDADSIYSLKNIVAKNLNFDKATHPNVTDSNLALLMFNMPRTKTQGIELLNRWKKEFSNDIKSYEK
VKKMFVDNAGSFHNLIHDLNFPKVSLNAYLSDIMDRSFANLKNYQSTSESLKDLSEKFYKTSSLEMFEKSDQSTSD
ISEILGGAIARFARFDDPSKALFEALRSDNIKKGLKDYKIADVTKDMFNADSKEFKDIDIYDFTHYLLMVNREPNE
NNPILKRLIEAVKDMQKESEKGIKQKLETPSEWGHNYSEFKGDGLGAINKLLETKKGFVAGAFHKEGLGDIDLVYG
NSKYGLEHIFNRRESDAIDKGMSKEEAKKYALKIINNIPNIISNGKLSKDNLGRLSIEFENQRVGLNDSWKGETLN
NRWVITSYEIDKSRNGLIESPLAPNYKGKDTNPLNLDSPNPTTKN

Seq ID 273
MGYASKLALKICLASLCLFSALGAEHLEQKRNYIYKGEEAYNNKEYERAASFYKSAIKNGEPLAYVLLGIMYENGR
GVPKDEKKAAEYFQKAVDNDIPRGYNNLGVMYKEGRGVPKDEKKAVEYFRIATEKGYTNAYINLGIMYMEGRGVPS
NYVKATECFRKAMHKGNVEAYILLGDIYYSGNDQLGIEPDKDKAIVYYKMAADMSSSRAYEGLAESYQYGLGVEKD
KKKAEEYMQKACDFDIDKNCKKKNTSSR

Seq ID 274
MGGILSSLNTSYTGLQAHQSMVDVTGNNISNASDEFYSRQRVIAKPQAAYMYGTKNVNMGVDVEAIERVHDEFVFA
RYTKANYENTYYDTEFSHLKEASAYFPDIDEASLFTDLQDYFNSWKELSKNAKDSAQKQALAQKTEALTHNIKDTR
ERLTTLQHKASEELKSVIKEVNSLGSQIAEINKRIKEVENNKSLKHANELRDKRDELEFHLRELLGGNVFKSSIKT
HSLTDKDSADFDESYNLNIGHGFNIIDGSIFHPLVVKESENKGGLNQVYFQSDDFKVTNITDKLNQGRVGALLNVY
NDGSNGTLKGKLQDYIDLLDSFAKGLIESTNAIYAQSASHYIEGEPVEFNSDEAFKDTNYNIKNGSFDLIAYNTDG
KEIARKTIAITPITTMNDIIQAINANTDDNQDNNTENDFDDYFTAGFNNETKKFVIQPKNASQGLFVSMKDNGTNF
MGALKLNPFFQGDDASNISLNKEYKKEPTTIRPWLAPINGNFDVANMMQQLQYDSVDFYNDKFDIKPMKISEFYQF
LTGKINTDAEKSGRILDTKKSMLETIKKEQLSISQVSVDEEMVNLIKFQSGYAANAKVITAIDRMIDTLLGIKQ

Seq ID 275
MRYLWLFLIHTIGLFATDKTLDIIKTIQKLPKIEVRYSIDNDANYALKLHEVLANDLKTSQHFDVSQNKDQGAINY
AELKDKKVHLVALVSVAVENGNKISRLKLYDVDTGTLKKTFDYPIVSLDLYPFAAHNMAIVVNDYLKAPSIAWMKR
LIVFSKYIGPGITNIALADYTMRYQKEIIKNNRLNIFPKWANAEQTEFYYTQYGERTPMILKYNIQKATHENIASS
QGMAVVSSVSSDGSKILMSLAPDGQPDVYLYDTHKKTKTKITRYPGIDVSGVFLEDDKSMAFVSDRSGYPNIYMKK
LGLKESAEQLLYEGRSNESIDAYKDSIVYVSRENLNEFGKTVFNLNLITLNSKYIRRLTVNGSNQMPRFSTDGRNI
MYIKKTPQEYAMGLILLDYNQSFLFPLKNVKIQAFDW

Seq ID 276
MFQALSDGFKNALNKIRFQDDEKALDRALDELKKTLLKNDVHHKVARELLKKVESQTKLNGIGKQQFLDALEKSLL
EILSAKGSSGFTFAQTPPTVVLMAGLQGSGKTTTTAKLAHYLKTKNKKVLLCACDLQRLAAVEQLKVLGEQVGVEV
FYEENKSVKEIASNALKRAKEAQFDVLLVDSAGRLAIDKELMQELKEVKEILNPHEVLYVADALSGQDGVKSANTF
NEEIGVSGVVLSKFDSDSKGGIALGITYQLGLPLRFIGSGEKIPDLDVFVPERIVGRLMGAGDIVSLAEKTASVLN

PNEAKDLSKKLKKGQFTFNDFLNQIEKVKKLGSMSSLISMIPGLGNMASALKDTDLESSLEVKKIKAMVNSMTKKE
QENPEILNGSRRKRIALGSGLEVSEINRIIKRFDQASKMAKRLTNKKGISDLMNLMSQAKNQTPPKMR

Seq ID 277
MIMKQEPTTYQPEEIEKKIYEICSHRGYFEIDGNEAIQEKNKRFCLMMPPPNVTGVLHIGHALTLSLQDILARYKR
MDGYKTLYQPGLDHAGIATQNVVEKQLLSQGIKKEDLGREEFIKKVWEWKEKSGGAILEQMKRLGVSAAFSRTRFT
MDKGLQRAVKLAFLKWYEKGLIIQDNYMVNWCTKDGALSDIEVEYEERKGALYYIRYYLENQKDYLVVATTRPETL
FGDSALMVNPNDERYKHLVGQKAILPLIHRTIPIIADEHVEMEFGTGCVKVTPGHDFNDYEVGKRHHLETIKIFDE
KGILNAHCGEFENLERLEARDKVVERLKENALLEKIEEHTHQVGHCYRCHNVVEPYVSKQWFVKPEIAQSSIEKIQ
QGLARFYPSNWINNYNAWMRELRPWCISRQLFWGHQIPVFTCENNHQFVSLDTPLSCPTCKSETLEQDKDVLDTWF
SSGLWAFSTLGWGQEKSGLFNESDLKDFYPNTTLITGFDILFFWVARMLFCSESLLGELPFKDIYLHALVRDEKGE
KMSKSKGNVIDPLEMIEKYGADSLRFTLANLCATGRDIKLSTTHLENNKNFANKLFNAASYLKLKQESFKDKERLN
EYQTPLGRYAKSRLNSATKEARNALDNYRFNDATTLLYRFLWGEFCDWFIEFSKVENEAIDELGSVLKEALKLLHP
FMPFISESLYHKLSNTELENTESIMVMPYPKDLAQDEKLEHEFEVIKDCIVSLRRLKIMLETPPIVLKEASVGLRE
AIENTERLQTYAQKLARLEKVSVISSKPLKSVSDVGEFCQTYANLENLDLSPLVARLKKQLEKLEKEKLKLNLHNE
NFVKNAPKSVLEKAKESLKTLLEKESKIKQELDLLEQP

Seq ID 278
MKKTFLIALALTASLVGAENTKWDYKNKENGPHRWDKLHKDFEVCKSGKSQSPINIEHYYHTQDKADLQFKYAASK
PKAVFFTHHTLKASFEPTNHINYRGHDYVLDNVHFHAPMEFLINNKTRPLSAHFVHKDAKGRLLVLAIGFEEGKEN
PNLDPILEGIQKKQNFKEVALDAFLPKSINYYHLTALSPLLLAQRGWHGL

Seq ID 279
MSKKIPLKNRLRADFTKTPTDLEVPNLLLLQRDSYDSFLYSKEGKESGIEKVFKSIFPIQDEHNRITLEYAGCEFG
KSKYTVREAMERGITYSIPLKIKVRLILWEKDTKSGEKNGIKDIKEQSIFIREIPLMTERTSFIINGVERVVVNQL
HRSPGVIFKEEESSTSLNKLIYTGQIIPDRGSWLYFEYDSKDVLYARINKRRKVPVTILFRAMDYQKQDIIKMFYP
LVKVRYENDKYLIPFASLDANQRMEFDLKDPQGKVILLAGKKLTSRKIKELKENHLEWVEYPMDILLNRHLAEPVM
VGKEVLLDMLTQLDKNKLEKIHDLGVQEFVIINDLALGHDASIIQSFSADSESLKLLKQTEKIDDENALAAIRIHK
VMKPGDPVTTEVAKQFVKKLFFDPERYDLTMVGRMKMNHKLGLHVPDYITTLTHEDIITTVKYLMKIKNNQGKIDD
RDHLGNRRIRAVGELLANELHSGLVKMQKTIKDKLTTMSGAFDSLMPHDLVNSKMITSTIMEFFMGGQLSQFMDQT
NPLSEVTHKRRLSALGEGGLVKDRVGFEARDVHPTHYGRICPIETPEGQNIGLINTLSTFTRVNDLGFIEAPYKKV
VDGKVVGETIYLTAIQEDSHIIAPASTPIDEEGNILGDLIETRVEGEIVLNEKSKVTLMDLSSSMLVGVAASLIPF
LEHDDANRALMGTNMQRQAVPLLRSDAPIVGTGIEKIIARDSWGAIKANRAGVVEKIDSKNIYILGESKEEAYIDA
YSLQKNLRTNQNTSFNQVPIVKVGDKVGAGQIIADGPSMDRGELALGKNVRVAFMPWNGYNFEDAIVVSECITKDD
IFTSTHIYEKEVDARELKHGVEEFTADIPDVKEEALAHLDESGIVKVGTYVSAGMILVGKTSPKGEIKSTPEERLL
RAIFGDKAGHVVNKSLYCPPSLEGTVIDVKVFTKKGYEKDARVLSAYEEEKAKLDMEHFDRLTMLNREELLRVSSL
LSQAILEEPFSHNGKDYKEGDQIPKEEIASINRFTLASLVKKYSKEVQNHYEITKNNFLEQKKVLGEEHEEKLSIL
EKDDILPNGVIKKVKLYIATKRKLKVGDKMAGRHGNKGIVSNIVPVADMPYTADGEPVDIVLNPLGVPSRMNIGQI
LEMHLGLVGKEFGKQIARMLEDKTKDFAKELRAKMLEIANAINEKDPLTIHALENCSDEELLEYAKDWSKGVKMAI
PVFEGISQEKFYKLFELAKIAMDGKMDLYDGRTGEKMRERVNVGYMYMIKLHHLVDEKVHARSTGPYSLVTHQPVG
GKALFGGQRFGEMEVWALEAYGAAHTLKEMLTIKSDDIRGRENAYRAIAKGEQVGESEIPETFYVLTKELQSLALD
INIFGDDVDEDGAPKPIVIKEDDRPKDFSSFQLTLASPEKIHSWSYGEVKKPETINYRTLKPERDGLFCMKIFGPT
KDYECLCGKYKKPRFKDIGTCEKCGVAITHSKVRRFRMGHIELATPVAHIWYVNSLPSRIGTLLGVKMKDLERVLY
YEAYIVKEPGEAAYDNEGTKLVMKYDILNEEQYQNISRRYEDRGFVAQMGGEAIKDLLEEIDLITLLQSLKEEVKD
TNSDAKKKKLIKRLKVVESFLNSGNRPEWMMLTVLPVLPPDLRPLVALDGGKFAVSDVNELYRRVINRNQRLKRLM
ELGAPEIIVRNEKRMLQEAVDVLFDNGRSTNAVKGANKRPLKSLSEIIKGKQGRFRQNLLGKRVDFSGRSVIVVGP
NLKMDECGLPKNMALELFKPHLLSKLEERGYATTLKQAKRMIEQKSNEVWECLQEITEGYPVLLNRAPTLHKQSIQ
AFHPKLIDGKAIQLHPLVCSAFNADFDGDQMAVHVPLSQEAIAECKVLMLSSMNILLPASGKAVAIPSQDMVLGLY
YLSLEKSGVKGEHKLFSSVNEIITAIDTKELDIHAKIRVLDQGNIIATSAGRMIIKSILPDFIPTDLWNRPMKKKD
IGVLVDYVHKVGGIGITATFLDNLKTLGFRYATKAGISISMEDIITPKDKQKMVEKAKVEVKKIQQQYDQGLLTDQ
ERYNKIIDTWTEVNDKMSKEMMTAIAQDKEGFNSIYMMADSGARGSAAQIRQLSAMRGLMTKPDGSIIETPIISNF
KEGLNVLEYFNSTHGARKGLADTALKTANAGYLTRKLIDVSQNVKVVSDDCGTHEGIEITDIAVGSELIEPLEERI
FGRVLLEDVIDPITNEILLYADTLIDEEGAKKVVEAGIKSITIRTPVTCKAPKGVCAKCYGLNLGEGKMSYPGEAV
GVVAAQSIGEPGTQLTLRTFHVGGTASRSQDEREIVASKEGFVRFYNLRTYTNKEGKNIIANRRNASILVVEPKIK
APFDGELRIETVYEEVVVSVKNGDQEAKFVLRRSDIVKPSELAGVGGKIEGKVYLPYASGHKVHKGGSIADIIQEG
WNVPNRIPYASELLVKDNDPIAQDVYAKEKGVIKYYVLEANHLERTHGIKKGDMVSEKGLFAVIADDNGREAARHY
IARGSEILIDDNSEVSTNSVISKPTTNTFKTIATWDPYNTPIIADFKGKVGFVDVIAGVTVAEKEDENTGITSLVV
NDYIPSGYKPSLFLEGANGEEMRYFLEPKTSIAISDGSSVEQAEVLAKIPKATVKSRDITGGLPRVSELFEARKPK
PKDVAILSEVDGIVSFGKPIRNKEHIIVTSKDGRSMDYFVDKGKQILVHADEFVHAGEAMTDGVISSHDILRISGE
KELYKYIVSEVQQVYRRQGVSIADKHIEIIVSQMLRQVRILDSGDSKFIEGDLVSKKLFKEENARVIALKGEPAIA
EPVLLGITRAAIGSDSIISAASFQETTKVLTEASIAMKKDFLEDLKENVVLGRMIPVGTGMYKNKKIVLRALEDNS
KF

Seq ID 280
MAKEKFNRTKPHVNIGTIGHVDHGKTTLSAAISAVLSLKGLAEMKDYDNIDNAPEEKERGITIATSHIEYETENRH
YAHVDCPGHADYVKNMITGAAQMDGAILVVSAADGPMPQTREHILLSRQVGVPHIVVFLNKQDMVDDQELLELVEM
EVRELLSAYEFPGDDTPIVAGSALRALEEAKAGNVGEWGEKVLKLMAEVDAYIPTPERDTEKTFLMPVEDVFSIAG
RGTVVTGRIERGVVKVGDEVEIVGIRPTQKTTVTGVEMFRKELEKGEAGDNVGVLLRGTKKEEVERGMVLCKPGSI

TPHKKFEGEIYVLSKEEGGRHTPFFTNYRPQFYVRTTDVTGSITLPEGVEMVMPGDNVKITVELISPVALELGTKF
AIREGGRTVGAGVVSNIIE

Seq ID 281
VLIVQKYGGTSMGSIERIHNVAQRVLESVTLGHQVVVVVSAMSGETDRLLEFGKNFSHNPNKREMDRIVSVGELVS
SAALSMALERYGHRAISLSGKEAGILTSSHFQNAVIQSIDTKRITELLEKNYIVVIAGFQGADIQGETTTLGRGGS
DLSAVALAGALKAHLCEIYTDVDGVYTTDPRIEEKAQKIAQISYDEMLELASMGAKVLLNRSVELAKKLSVKLVTR
NSFNHSEGTLIVAEKDFKGERMETPIVSGIALDKNQARVSMEGVEDRPGIAAEIFGALAEYRINVDMIVQTIGRDG
KTDLDFTIVKTQIEETKQALKPFLAQMDSIDYDENIAKVSIVGVGMKSHSGVASIAFKALAKDNININIMMISTSEIK
ISVLIDIKYAELAVRTLHAVYQLDQ

Seq ID 282
MKKHILSLALGSLLVSTLSAEDDGFYTSVGYQIGEAAQMVTNTKGIQQLSDNYENLNNLLTRYSTLNTLIKLSADP
SAINAVRENLGASAKNLIGDKANSPAYQAVLLAINAAVGFWNVVGYVTQCGGNANGQESTSSTTIFNNEPGYRSTS
ITCSLNGHKPGYYGPMSIENFKKLNEAYQILQTALKNGLPALKENNGKVSVTYTYTCSGQGNNNCSPSVNGTKTTT
QTIDGKSVTTTISSKVVGSIASGNTSHVITNKLDGVPDSAQALLAQASTLINTINEACPYFHATNSSEANAPKFST
TTGKICGAFSEEISAIQKMITDAQELVNQTSVINSNEQSTPVGNNNGKPFNPFTDASFAQGMLANASAQAKMLNLA
HQVGQAINPENLSENFKNFVTGFLATCNNKSTAGTGGTQGSAPGTVTTQTFASGCAYVEQTLTNLGNSIAHFGTQE
QQIQQAENIADTLVNFKSRYSELGNTYNSITTALSKVPNAQSLQNVVSKKNNPYSPQGIETNYYLNQNSYNQIQTI
NQELGRNPFRKVGIVNSQTNNGAMNGIGIQVGYKQFFGQKRKWGARYYGFFDYNHAFIKSSFFNSASDVWTYGFGA
DALYNFINDKATNFLGKNNKLSLGLFGGIALAGTSWLNSEYVNLATVNNVYNAKMNVANFQFLFNMGVRMNLARSK
KKGSDHAAQHGIELGLKIPTINTNYYSFMGAELKYRRLYSVYLNYVFAY

Seq ID 283
LDSFHSFNQHAFNRHAKTYHLFAHIQQQIAICLVQFLKQKHYAKVLDLGSGSGAVFNALERQNILIEEFIALDNSI
NMLKLHPTHSINIQKISLEHADFEEHVFCTYDLVVSSSSLQWARDLKSVLEKIALSSKEVALAIHTDFSLHEVHEF
LGTPSPLRDLKTLKSLIKNAFKHFQIELENKRFALYFNRKQDCLNYLKKCGLLGGSTLSFKQKKHFFQNMAFEKLS
YEVLLFSGIKRS

Seq ID 284
LSGFNPLNSPLVASSSLSLKEAYYLEKLSLKKGFKIHYKMTKDSLNLLEKSDLCVLFGGFSNACLNENERWILESI
SHSKRPYALLRPLQDTRDLQENCLFASYEIHTEAAILALILRGILEQTSQLKGHVLEKIDVGYLSSEANMSEEELQ
ELIALIVKAKKRALVLNREITKHANNAFLYTLLSELQNYLEILHIPCYDSSATTAFYDFKDQEWLLETAFKEGILP
FKSQLQSKDLELLERISEANGSFVYVSYKSLETPKLSFSKQFKIANKIEHSKAGFQISNQTLECELEENPHLKGLI
AILEGAFFDAYPYIPILSHSQGIS

Seq ID 285
MISLIEKAPYIPYPLALYEKLEQPHTLLFESAEIESKAHTKSLLMAKACLKLICNHNIVTITSLTPNGGAFLQKLS
AFFKTPIQDNALILTYTKNKKTQDEFLKLFEPSPFDALRGLFKSVKTKPKHPFTLLSAGVFSFEMLNFFEDLPHLK
AKDNTVHDFIFYLAQNLIIIDHKEKSVEILGACFDERFKTEIAQELQDLKELAKSIKSDFVPKKSKQSREVSANCS
DSEFEKRVLSLQEEIKKGEIFQAVLSRSFYMECLEGLSAYYHLKLTNPSPYMFYIKDSDFILFGASPESALKYNAL
TNTAEIYPIAGTRLRGKDKQGNIDYDLDSKMEFDLQHDYKERAEHIMLVDLARNDMARVSKKRYCDKLLKVDKYSN
VMHLVSRVVGELKKGCDSLHAYRSFMNAGTLSGAPKISAIRLIYQLENQRRGSYGGSVGYLNSEGSMDSCITIRSC
FVKNNRAVIQAGAGIVLDSVPQNEANETRAKAQALIDAIRKTSL

Seq ID 286
MIEKIIDLSVKNKLLTTLVTLLIFLASLWAIKSVRLDALPDLSPAQVVVQITYPNQSPKIVQEQVTYPLVSTFMSI
ANIDTVRGISSYESGLIYIIFKDGVNLYWARDRVLEQLNRVSNLPKDAKVEIGSDSTSIGWAYQYALSSDSKNLSD
LKVLQDFYYRYALLGVDGVSEVASVGGFVKDYEVTLQNDSLIRYNLSLEQVANAIKNSNNDTGGGVILENGFEKII
RSHGYIQSLKDLEEIVVKKEGAIPLKIKDIASVRLTPKPRRGAANLNGDKEVVGGIVMVRYHADTYKVLKAIKEKI
ATLQASNPDVKITSVYDRSELIEKGIDNLIHTLIEESVIVLVIIAIFLLHFRSALVVIITLPLSVCISFLLMRYFN
IEASIMSLGGIAIAIGAMVDAAIVMVENAHKHLQHIDVKDNAQRVNGIIEGVKHVGGAIFFALMIIVVSFLPIFAL
TGQEEKLFAPLAYTKTFAMLVGALLSITMVPILMVWLIKGRILEESKNPINAFFMKIYGVSLNVVLKFRYAFLIAS
VLGLGGLYVAYKKLNWEFIPQINEGVVMYMPVTINGVSIDTALEYLKKSNSAIKRLDFVKQVFGKVGRANTSTDAA
GLSMIETYIELKPQNEWKEKLSYKEVRDKLEKTLQLKGLTNSWTYPIRGRTDMLLTGIRTPLGIKLYGNDTDKLQE
LAILMEQQLKTLKESLSVFAERSNNGYYITLDLNDENLARYGINKKAVLDAIKFALGGATLTTMIKGVENYPISLR
LEDTERNTIEKLKNLYIKTAYNYMPLRELARIYYDNSPAVLKSEKGLNVNFIYIVPQNGISSDAYRQLAQKALEKI
QLPNGYYYEFSGESQYLEEAFKTLQYIVPVSVFIIFILIVFALKNLTNSLLCFFTLPFAFLGGLIFMNLMGFNMSV
AALVGFLALLGVASETAIVMIIYLEDAFQKFIKTPLKEQNSTTLKEAIMHGAVLRVRPKLMTFFSILASLIPIMYS
HGTGSEIMKSIAAPMLGGMISSVVLTLFIIPTAYFVIKNAGIKSNQT

Seq ID 287
MSVSHVALILRKLFYHRQGVFMGGFSVGMLKDYVDIFVFAVLGVASFLALWFAIERVIFYSKVDLKAYDDIDALNL
DLTKNLTILYVIFSNAPYVGLLGTVLGIMVIFYDMGVSGGMDAKTIMVGLSLALKATALGLAVAIPTLIAYNSLLR
KSDVLSEKFRIMKK

Seq ID 288

MKISPSPRKLSKVSTSVSFLISFALYAIGFGYFLLREDAPEPLAQAGTTKVTMSLASINTNSNTKTNAESAKPKEE
PKEKPKKEEPKKEEPKKEVTKPKPKPKPKPKPKPKPEPKPEPKPEPKPEPKVEEVKKEEPKEEPKKEEAKEEAK
EKSAPKQVTTKDIVKEKDKQEESNKTSEGATSEAQAYNPGVSNEFLMKIQTAISSKNRYPKMAQIRGIEGEVLVSF
TINADGSVTDIKVVKSNTTDILNHAALEAIKSAAHLFPKPEETVHLKIPIAYSLKED

Seq ID 289
MKKSLLLLSLSLIASLSRAEDDGFYTSVGYQIGEAVQQVKNTGALQNLADRYDNLNNLLNQYNYLNSLVNLASTPSA
ITGAIDNLSSSAINLTSATTTSPAYQAVALALNAAVGMWQVIALFIGCGPGPTNNQSYQSFGNTPALNGTTTTCNQ
AYGTGPNGILSIDEYQKLNQAYQIIQTALNQNQGGGMPALNDTTKTGVVNIQQTNYRTTTQNNIIEHYYTENGKEI
PVSYSGGSSFSPTIQLTYHNNAENLLQQAATIMQVLITQKPHVQTSNGGKAWGLSSTPGNVMDIFGPSFNAINEMI
KNAQTALAKTQQLNANENAQITQPNNFNPYTSKDKGFAQEMLNRAEAQAEILNLAKQVANNFHSIQGPIQGDLEEC
KAGSAGVITNNTWGSGCAFVKETLNSLEQHTAYYGNQVNQDRALAQTILNFKEALNTLNKDSKAINSGISNLPNAK
SLQNMTHATQNPNSPEGLLTYSLDSSKYNQLQTIAQELGKNPFRRFGVIDFQNNNGAMNGIGVQVGYKQFFGKKRN
WGLRYYGFFDYNHAYIKSNFFNSASDVWTYGVGMDALYNFINDKNTNFLGKNNKLSVGLFGGFALAGTSWLNSQQV
NLTMMNGIYNANVSTSNFQFLFDLGLRMNLARPKKKDSDHAAQHGIELGFKIPTINTNYYSFMGAKLEYRRMYSLF
LNYVFAY

Seq ID 290
MLAKMSFMQNVKNIQEVEVSHKRVLIRVDFNVPLDENLNITDDTRIRESLPTIQYCIDNKAKDIILVSHLGRPKGV
EEKLSLKPFLKRLERLLNHEVVFSQNIVQLKQALNENAPTRIFLLENIRFLRGEEENDENLAKDLASLCDVFVNDA
FGTSHRKHASTYGTAKFAPIKVSGFLLKKEIDSFYQAFNHPLRPLLLIVGGAKVSSKLTLLKNILDLIDKLIIAGA
MSNTFLKALGYDVQDSSVEDALINDALELLQSAKEKKVKVYLPIDAVTTDDILNPKHIKISPVQDIEPKHKIADIG
PASLKLFSEVIESAPTILWNGPLGVHEKQEFARGTTFLAHKIADTYAFSLIGGGDTIDAINRAGEKDNMSFISTGG
GASLELLEGKILPCFEVLDKRH

Seq ID 291
VVLLTMTKRLFKGLLAVSLAVSLHGGEVKEKKPVKPVKEDPQELAAKRVEAFSRFSNVVSEIEKKYVDKISISEIM
TKAIEGLLSNLDAHSAYLNEKKFKEFQAQTEGEFGGLGITVGMRDGVLTVIAPLEGTPAYKAGVKSGDNILKINNE
STLSMSIDDAINLMRGKPKTPIQITVVRKNEPKPLVFNIIRDIIKLPSVYVKKIKETPYLYVRVSGFDKNVTKSVL
EGLKANPKAKGIVLDLRGNPGGLLNQAVGLSNLFIKEGVLVSQKGKNKEENLEYKANGRAPYTNLPIAVLVNGGSA
SASEIVAGALQDHKRAVIIGEKTFGKGSVQMLLPVNKDEAIKITTARYYLPSGRTIQAKGITPDIVIYPGKVPENE
NKFSLKEADLKHHLEQELKKIDDKTPNSKEADKDKKNEEEKEITPKMINDDIQLKTAIDSLKTWSIVDEKMDEKAP
KKK

Seq ID 292
MNETLYCSFCKKPESRDPKKRRIIFASNLNKDVCVCEYCIDVMHGELHKYDNSLLALKRDRLRRMESSAYEEEFLL
SYIPAPKELKAVLDNYVIGQEQAKKVFSVAVYNHYKRLSFKEKLKKQDNQDSNVELEHLEEVELSKSNILLIGPTG
SGKTLMAQTLAKHLDIPIAISDATSLTEAGYVGEDVENILTRLLQASDWNVQKAQKGIVFIDEIDKISRLSENRSI
TRDVSGEGVQQALLKIVEGSLVNIPPKGGRKHPEGNFIQIDTSDILFICAGAFDGLAEIIKKRTTQNVLGFTQEKM
SKKEQEAILHLVQTHDLVTYGLIPELIGRLPVLSTLDSISLEAMVDILQKPKNALIKQYQQLFKMDEVDLIFEEEA
IKEIAQLALERKTGARGLRAIIEDFCLDIMFDLPKLKGSEVRITKDCVLKQAEPLIIAKTHSKILP

Seq ID 293
MRDFNNAQITRLKVRQNAVFEKLDLEFKDGLSAISGASGVGKSVLIASLLGAFGLKESNASNIEVELIAPFLDTEE
YGIFREDEHEPLVISVIKKEKTRYFLNQTSLSKNTLKALLKGLIKRLSNDRFSQNELNDILMLSLLDGYIQNENKA
FSPLLGALEEKFTRLEKLEKERRLLEDKKRFQKDLEERLNFEKMKLERLDLKEDEYERLLEQKKLLSSKEKLNDKI
ALALEVLENTHKITHALESVGHSAEFLKSALLEASALLEKEQAKLEECERLDIEKVLERLGMLSGIIKDYGSIMHA
KERLGHVKNELHNLKEIDSHCETYHKEIERLKTECLKLCEEISGFRKEYLAGFNALLSAKAKDLLLKSPSLVLEDA
PMSEKGAQKLVLNLQNSQLETLSSGEYSRLRLAFMLLEMEFLKDFKGVLVLDEMDSNLSGEESLAVSKALETLSSH
SQIFAISHQVHIPALAKNHILVFKENHKSLAKTLNNEERVLEIARMIGGSENIESAISFAKEKLKAQE

Seq ID 294
MPDELRAEKSFPSKPYDSLKNKSEFDRVYQKGFKKHNPFFSLFVLDLSQEPPKEKAGFKDPLFCRLKDKKTLYLLG
LSVSKKVGNAVKRNLIKRRLRSLTLKHAALCQGLALVFVPRSDCYHLDFWALEKHFLEMLTSIKNYMNKALKDLKK
GITHTYAKQ

Seq ID 295
MLKLASKTICLSLIGSFTAVEAFQKHQKDGFFIEAGFETGLLQGTQTKEQTIATTQEKPKPKPKPKPITPQSTYGK
YYISQSTVLKNATELFAEDNITNLTFYSLTPVYVTAYNQESAEEAGYGDSSLIMIQNFLPYNLNNIELSYTDNQGN
VVSLGVIETIPKQSQIILPASLFNDPQLNADGFQQLQTATTRFSDASTQNLFDKLSKVTTNLQMTYINYNQFSSGN
GSGSKPPCPPYENQENCTAKVPPPTSQDAKNLTNLMLNMMAVFDSKSWEDAVKNAPFQFSDNNLSAPCYSNYSTCV
NPYNDGLVDPKLIAKNKGDEYNIENGQTGSVILTPQDVIYSYRVTNNLYVNLLPPRGGDLGLGSQYGGPNGPGDDG
TNFGALGILSPFLDPEILFGKELNKVAIMQLRDIIHEYGHTLGYTHNGNMTYQRVRMCEENNGPEERCKGGKIEQV
DGQEVQVFDNGHEVRDTDGSFYDVCSRFGGQNQPAFPSSYPNSIYTDCSQVPAGLIGVTSAVWQQLIDQNALPVDY
TNLSSQTNYLNASLNTQDFATTMLSAISQSLSSTRSSATTYRTSKTSRPFGAPLLGVNLKMGYQKYFNDYLGLSSY
GIIKYNYAQANNEKIQQLSYGVGMDVLFDFITNYTNEKNPKNNLTKKVFTSSLGVFGGLRGLYNSYYLLNQYKGSG
NLNVTGGLNYRYKHSKYSVGISVPLVQLKSRVVSSDGATTNSITLNEGGSHFKVFFNYGWIF

Seq ID 296
MKKIILACLMAFVGANLSAEPKWYSKAYNKTNTQKGYLYGSGSATSKEASKQKALADLVASISVVVNSQIHIQKSR
VDNKLKSSDSQTINLKTDDLELNNVEIVNQEVQKGIYYTRVRINQNLFLQGLRDKYNALYGQFSTLMPKVCKGVFL
QQSKSMGDLLAKAMPIERILKAYSVPVGSLENYEKIYYQNAFKPKVQITFDNNGDAEIKSALISAYARVLTPSDEE
KLYQIKNEVFTDSANGITRIRVVVSASDCQGTPVLNRSLEVDEKNKNFAITRLQSLLYKELKDYANKEGQGNTGL

Seq ID 297
MKENKAFTHLHLHTEYSLLDGANKIKILAKRVKELGMKSVSVTDHGNMFGAIDFYTSMKKEGIKPIIGMEAYIHND
DNLSSKETKQRFHLCLFAKNQEGYENLMFLSSMAYLEGFYYFPRINKKLLKEHSKGIIASSACLQGEVNYHLNTNN
ERNRKYGAKGYDEAKKIACEYQEIFEDDFYLEIMRHGILDQRFIDEQVIKMSLETGLKIIATNDTHYTMPNDAKAQ
EVAMCVAMGKTLNDKGRLKHSVHEFYIKSPEEMAKLFADIPEALENTQEIADKCVLEIDLKDDKKNPPTPPSFKFT
KAYAQNEGLNFEDDASYFAYKAREGLKERLVLVPKEKHDQYKERLEKEIEVITNMKFPGYMLIVWDFIRYAKEMGI
PVGPGRGSAAGSLVAFALKITDIDPLKYDLLFERFLNPERISMPDIDTDFCQRRRKEIIEYMIEKYGKYNVAQVIT
FNKMLAKGVIRDVARVLDMPYKEADDFAKLIPNRLGITLKGYEKNGEFIEGAWELEPKIKELVESNELAKQVWEYS
LNLENLNRNAGVHAAALVVDSQKELWHKTPLFASEKTGGIVTQYSMKYLEPVDLIKFDFLGLKTLTVIDDALKIIK
TQHKISVDFLSLDMDDPKVYKTIQSGDTVGIFQIESGMFQGLNKRLRPSSFEDIIAIIALGRPGPMESGMVDDFVN
RKHGVEPIAYAFKELEPILKPTYGTIVYQEQVMQIVQTIGGFSLGEADLIRRAMGKKDAQIMADNKAKFVEGAKNL
GHDGQKAANLWDLIVKFAGYGFNKSHSAAYAMITFQTAYLKTYYKHEFMAAMLTSESNKIESVARYIDEVRALEIE
VMPPHINSSMQDFSVAEFKNQKGELEKKIVFGLGAIKGVGGEPIKNIIEERAKGDYKSLEDFISRVDFSKLTKKSL
EPLVKSGSLDNLGYTRKTMLANLDLICDAGRAKDKANEMMQGGNSLFGAMEGGTKEQVVLDMIDLGEHDAKTLLEC
EYETLGIHVSGNPLDEFKEEIKGFKNLVKSIDIEELEIGSQAYLLGKIMEVKKKIGKRSGKPYGIADILDRYGKFE
LMLFEKQLNALEELDINKPLVFKCKIEEQEEVVRLRLFEILDLESAREVKIPKARYKDPEKQKEEVREIPPMEMLA
SSSCSLAIVLENDVKKEFLRQIKESALKHQGKRPLYLIIKDKDKQFKIQSDLMVNEKIKDDFKGLEWRDLA

Seq ID 298
MTLLVGLGNPTLRYAHTRHNAGFDILDSLVSELDLSFTFSPKHNAFLCVYKDFIFLKPQTYMNLSGESVLSAKNFY
KTKELLIVHDDLDLPLGVVRFKNGGGNGGHNGLKSIDLLCSNSYYRLRVGISKGIGVIEHVLSKFHKNEEPLKNAA
FEHAKNALKFFIESHDFNAMQNRFTLKKPLKIES

Seq ID 299
MKKSLCLSFFLTFSNPLQALVIELLEEIKTSPHKGTFKAKVLDSKKPRQVLGVYNISPHKKLTLTITHISTAIVYQ
PLDEKLSLETTLNPNRPTIPRNTQIVFSSKELKESHPHQMPSLNAPMQKPQNKPHSSQQPSQNFSYPEPKLGSKNS
KNSLLQPLAIPSKISPTNETQTPTNDTKPPLKHSSEDQESNLFITPPTEKTLPNNTSNADISENNESNENKDNVEK
QAIRDANIKEFACGKWVYDDENLQAYRPSILKRVDEDKQTATDITPCDYSTAENKSGKIITPYTKISVHKTEPLEE
PQTFEAKNNFAILQARSSTEKCKRARARKDGTTRQCYLIEEPLKQAWESEYEITTQLVKAIYERPKQDDQVEPTFY
ETSELAYSSTRKSEITHNELNLNEKFMEFVEVYEGHYLNDIIKESSEYKEWVKNHVRFKEGVCMALEIEEQPRAKS
TPLSIENSRVVCVKKGNYLFNEV

Seq ID 300
MNAFKRIISVGVIALGLFNLLDAKHHKEKKENHKITRELKVGANPVPHAQILQSVVDDLKEKGIKLVIVSFTDYVL
PNLALNDGSLDANYFQHRPYLDRFNLDRKMHLVGLANIHVEPLRFYSQKITDIKNLKKGSVIAVPNDPANQGRALI
LLHKQGLIALKDPSNLYATEFDIVKNPYNIKIKPLEAALLPKVLGDVDGAIITGNYALQAKLTGALFSEDKDSPYA
NLIAAREDNAQDEAIKTLIEALQSEKTRKFILDTYKGAIIPAF

Seq ID 301
MKNLRYKLLLFVFIGFWGLLALNLFILSVKNQEYYEKLAERNMTKKEFLVPTRGNITDRNDEFLATNELVFGVFLP
SGLKQKDLLEKIEIIQKFFPNFSKETLLNNYQKENSLYNHNLIKVVGFIPYATMQPLYAKLIQTQGIFALPLDKRY
YPNNALASHVLGYVGVASLQDLKDDEENQYSQIVGKTGIEKEYNKLLQGKVGYKIMRVNALNQELATLEVVLPSTN
NHLQLSLDKRLQKEADKLFENKRGAILVMDAENGELLVAGSYPEYNLNDFVGGISQDKWQKLQDDIYNPLLNRFAN
ALYPPGSVVKMGVGLSFLENLHITENTTIPTPPFIEVGKHKFRDWKKTGHGNSNLYKAIRESVDVYFYKFGLEISI
EKLSKTLREVGFGEKTGVDLPNEFVGIVPDNLWKLKRFNQDWRVGDTLITAIGQGSFLATPLQVLAYTGLIATGKL
ATPHFAINNKQPLKDPLNSFQKKKLQALRVGMYEVCNHKDGTAYHSTRGSKITLACKTGTAQVVEIAQNIVNRMKE
KDMEYFHRSHAWITAFLPYEKPKYAITILVEHGEGGSKLGGLLVKMSNKLYELGYL

Seq ID 302
MFSGLIHQIAKVKSFHNNILNIESDLNPKLGDSIAINGACLTAIESSKTHFSVELSQKTQNSVALENYKDLVHIEP
ALKADASLDGHFVQGHIDAIGVIEKIIHNANQVDFFISASEETLLLCVEQGSIAVDGVSLTLSKVEEKGFWLTIIP
YTLENTLFKAYKLKRRVNIETDMLVRSVASILKKTKGFEKNFSWNEADALTLGY

Seq ID 303
KKSERFKIELKPFKKRPNRGAHRRALFQAYRSGFAFRRSH

Seq ID 304
WFAKKDFSAWSATKRAF

Seq ID 305
NLQTHLKRLKRSEFVGQKGIRGHGEVFFKRNFNAQPYLIGFTGLDFWQTFRLACECDGFDCHGFNGVL

Seq ID 306
TQAIILKKNQAWGRGWIMRGVASIINSRE

Seq ID 307
AMWILLKTSKTRNSKKIVWNLSKGLMSQSPLSLPLFITLGALSPLKKK

Seq ID 308
KKKKSKNSKNSPWAWKCLSMCGV

Seq ID 309
KKLIKSLALKKDTAIVMKSTPNTAKSGKIRA

Seq ID 310
RGATPPRKKTLFLKKPSVLSRPNS

Seq ID 311
SAQPPSLKRSLGGLKAMA

Seq ID 312
KHDHGFWVRHSREF

Seq ID 313
AKNTALKSLALGIRAMAMCM

Seq ID 314
RFERQNLSLRYGSIGLQQLFIHRKPHYQNKSNGNLCGFDYHHRLIRASQWVLQHSKSAQQTQR

Seq ID 315
SSVSSKKPAKNSLTRFLSSQGIILTGAMNTLKTICISLNPCRLFYMPLL

Seq ID 316
KWNISTPKPPPKNGAIGWGIISLLSKTILIILGI

Seq ID 317
KTRWIPTEKWRNSTMEAARRPFFRPFN

Seq ID 318
KNFRAHDFFERRDCQYFYSVWRRAMGDSSSYHASGWAKLRGGSGSGFYGYRLGRCLDEYDTAFLGFARFSHCGFGR

Seq ID 319
KARLKRFQIIPLISAEKAMLQAMR

Seq ID 320
RAPFRREPWRLGGCCNL

Seq ID 321
FTRHKQTSRSKRSKSLSVKNGVR

Seq ID 322
FFSYIQYERRSSGYHRAWPFFRERFD

Seq ID 323
RDLLAIPQRFARKQAFKKPSL

Seq ID 324
KSPKKATKKRF

Seq ID 325
ALEQRDERFTRGG

Seq ID 326
PISCKAPKFVVSLCNSGMPLDLGPWKGKTATKSLSNSLFLKRSKNSLWVLKTIALALTFLCSSLMAEILITALPKL
PFKILSPPLAAKGSLTGRKISVFRL

Seq ID 327
KSITSRQAIKPILRA

Seq ID 328
FKTLVELFKSQIPGAFRKHSHPRHSNFSVFKKSGKSGV

Seq ID 329
NAIMKPKKPQYLKNSLNSSNFMITPLLKSKP

Seq ID 330
IKALKPSLFERLNSLN

Seq ID 331
AMLFFRFVTVSPTYAQPAPQVLEVTVPDGVPRRLPSLPFSWHTPKESFTNAAGILSKSFTTA

Seq ID 332
GLFQNLTPHSKTPRSLRRANALKQKRVLTPHLLAC

Seq ID 333
FVGPQEVPPIATPKKNPKCKFSRLKIAGLNNTSVPAP

Seq ID 334
IRAFFKGVNLANFIDYGRDSRIFGSDDFISGVSGSGEFACKKTPVFGYFAIDLKIPFANGCLVVLSIQPFKRPSHQ
IAVRKTPVFKRVQFAGIKTRL

Seq ID 335
KFFSNHLRRKVVFIDISLHVNAFLAHSNKSHSMQQSVKAIF

Seq ID 336
SVGVKKSPPNSTSA

Seq ID 337
TLTCKKVASKRALICALISLTLNTSTSSPFYSKRVRSLKSPKNMIKTKNPTPASHNAFCMGVGKVI

Seq ID 338
ASMSLSNPVPLGIAAVTPTIFSSFLANSKRVLEYASVGDKIALLDFLDKPVSKSKGPTPCHFS

Seq ID 339
IFLSNTSLCMGRTNCNTKSNENALASLNSTSKKSMHSKRALLKSFNFSCAFLSMGMELSIPTSSISCWICRLSAIK
KFPVEQPKS

Seq ID 340
RDFQVLKHRLHPFFFIFTQQAMIHKNSDQIILNGSVQQRSDHRRIHAPTHRAQNLSVSDFFFQSCDFSLSEMLHPP
SFFTAAN

Seq ID 341
IIHMRGDHSHHMPSFFQRFKKTKRCHRSAITGVFKTIHD

Seq ID 342
IIIPAVLANDHAHINLRLGVDKKRASFLDIEKGKSGRFAIFHAD

Seq ID 343
KNRPSKNPLAQNAVVSALAPGKTSY

Seq ID 344
KPSSVWIYKPIIRGKNIQTIPS

Seq ID 345
SSVSSKKPAKNSLTRFLSSQGIILTGAMNTLKTICISLNPCRLFYMPLL

Seq ID 346
RARSRSLLGFFLLKASCKTPHKSLNFHLSNSKQGKWRIKSFWK

Seq ID 347
VSEILSTLVSPSKLPEEPKAKLMRWGASAPFLGSNCKRGGFMPASDPSLLKCKRPPSNTLGLAADPPTNSPGSGTI
TLKFHSAPPLL

Seq ID 348
LPNLNKISSSSFTKYTSKTSGLMWHSLKGFHFPFKA

Seq ID 349
SRFRERVAALFTKRAQRKRFRHSFIA

Seq ID 350
NIHWPHAPNRSLLNPKIVAGNPSSLEYRFALNSPQKAPQHR

Seq ID 351
PISCKAPKFVVSLCNSGMPLDLGPWKGKTATKSLSNSLFLKRSKNSLWVLKTIALALTFLCSSLMAEILITALPKL
PFKILSPPLAAKGSLTGRKISVFRL

Seq ID 352
ESLVLKPILGKRRCKGCCPPSKPLLAL

Seq ID 353
GSNERSHKERLSIQTHRIASRDFDICPL

Seq ID 354
LGGNKSFTLYSHHTSQPFFSKRLATCSKTSLSKQGLFVRLSMKKASGTPHFLCRLKHQSGRFSIMVFRRFFPLLGT
NSTFSIASKATSLKVF

Seq ID 355
AFVLKPCKKACSWSFKFSLANSTLESKLLYSFK

Seq ID 356
ESISSLILSKIMIVSLMEYPIKVSKAAITSKFISILKTITELATKITSCTSAMTLAKAKRHS